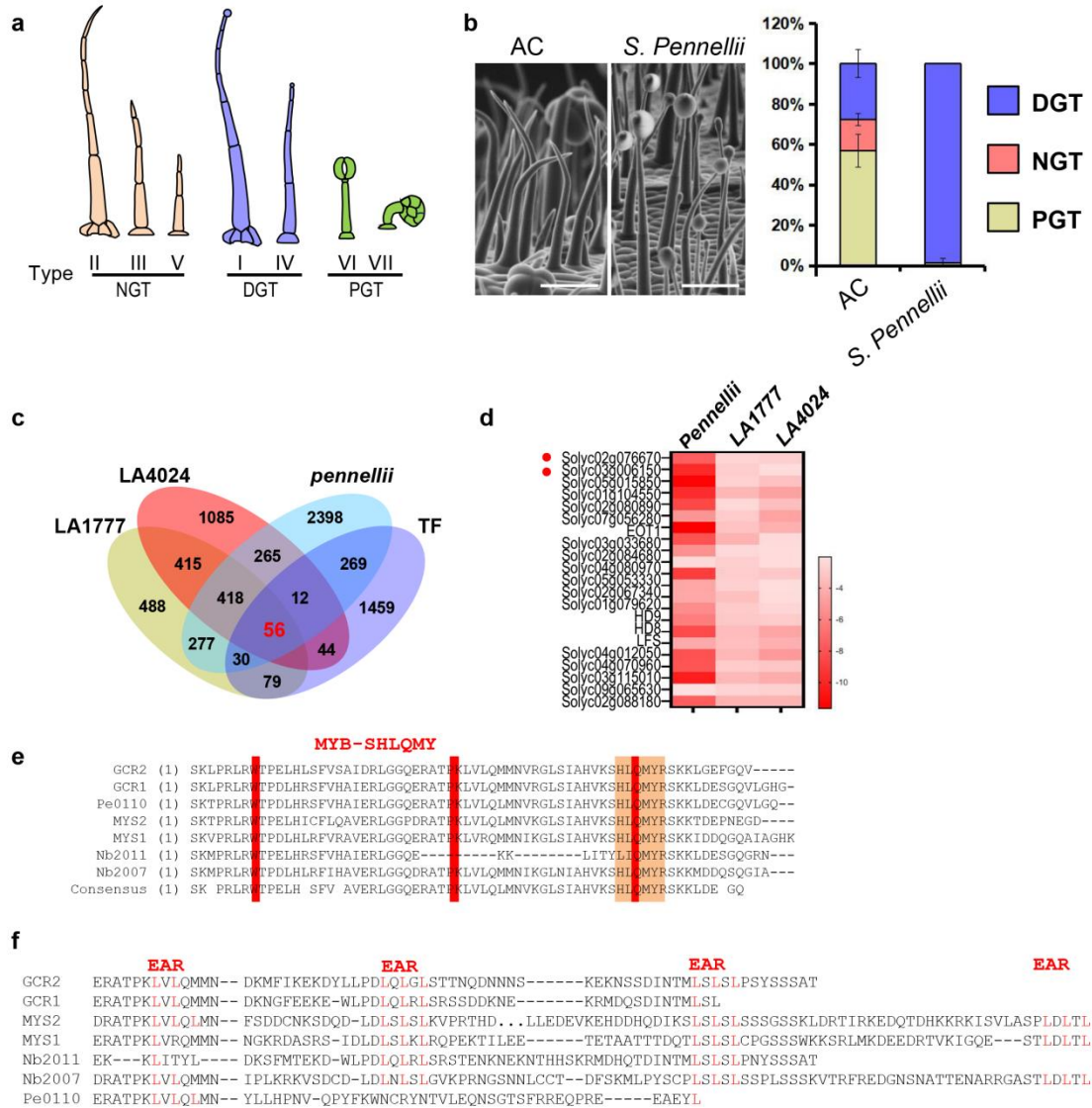


**Spatiotemporal formation of glands in plants is modulated by MYB-like transcription factors**

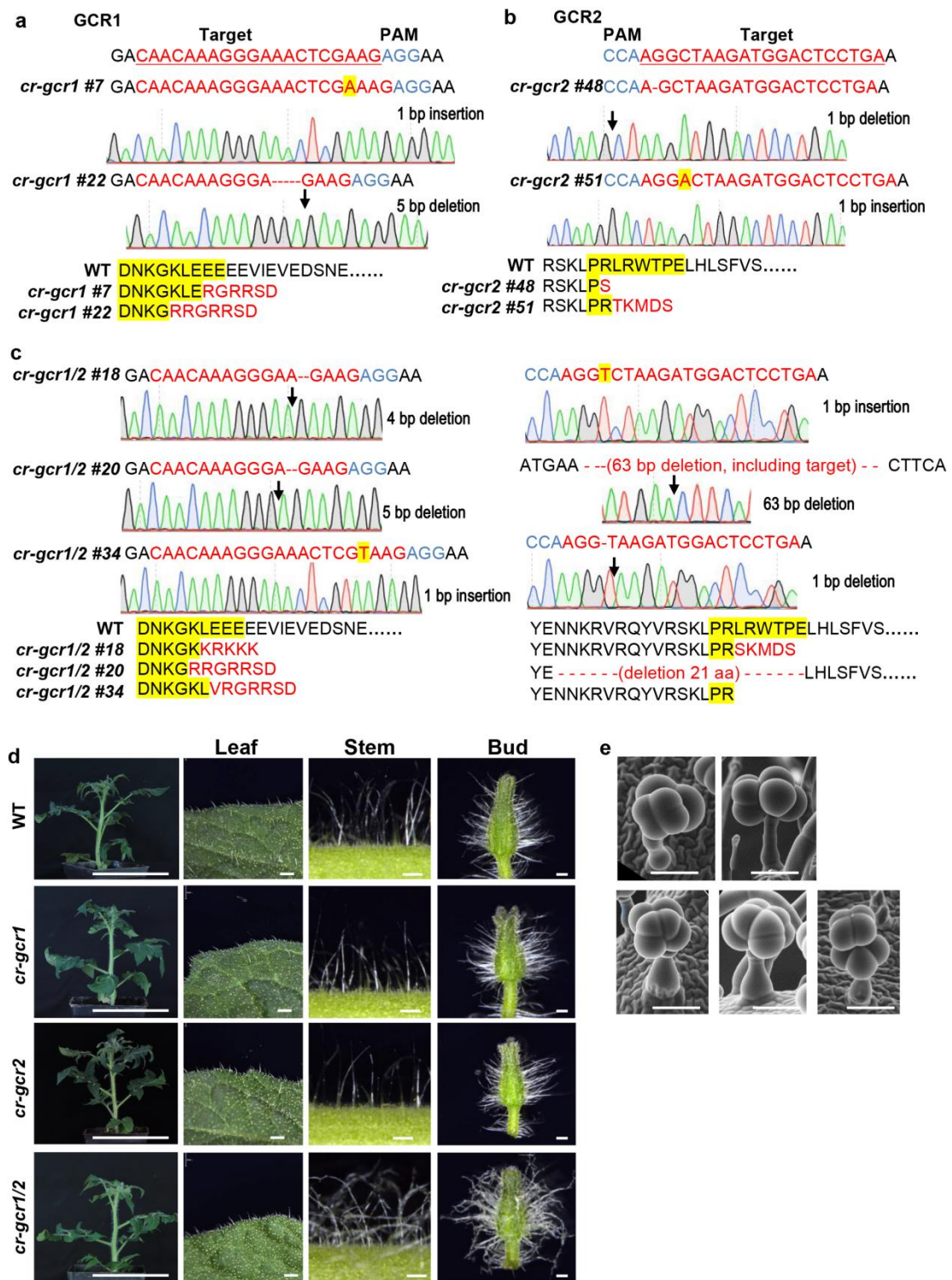
Jiang Chang<sup>1,2</sup>, Shurong Wu<sup>1,2</sup>, Ting You<sup>1,2</sup>, Jianfeng Wang<sup>1</sup>, Bingjing Sun<sup>1</sup>, Bojun Xu<sup>1</sup>, Xiaochun Xu<sup>1</sup>, Yaping Zhang<sup>1</sup>, Shuang Wu<sup>1\*</sup>



**Supplementary Figure 1. Screening for key genes regulating gland development.**

**a** Seven types of trichomes in tomato (type I-VII). Based on the morphology and presence of glandular cell, seven types of trichomes are divided into three categories: NGT (non-glandular trichomes including type II, III and V), DGT (digital glandular trichomes including type I and IV) and PGT (peltate glandular trichomes including type VI and VII). **b** SEM observation and qualification of trichomes on the *S. Pennellii* LA0716. The Y-axis represents the proportion of the three categories of trichomes in the total number of trichomes. Bar: 200  $\mu$ m. *p*-values were calculated by unpaired two-sided *t*-test and exact *p*-values are presented in the Supplementary Table 8. **c** Venn diagram showing the overlap of up-regulated transcription factors in glandular trichomes of *S. Pennellii* LA0716, *S. habrochaites* LA1777 and tomato cultivar *S. lycopersicum* LA4024 ( $\log_2\text{FoldChange}$  (leaf/glandular trichome)  $\leq -1$ ). Transcriptome data of LA4024 and LA1777 was cited from Balcke et al (2016) (25). Transcription factors in tomato were obtained from iTAK ([http://itak.feilab.net/cgi-bin/itak/db\\_browse.cgi](http://itak.feilab.net/cgi-bin/itak/db_browse.cgi)). **d** Heat-map showing transcription

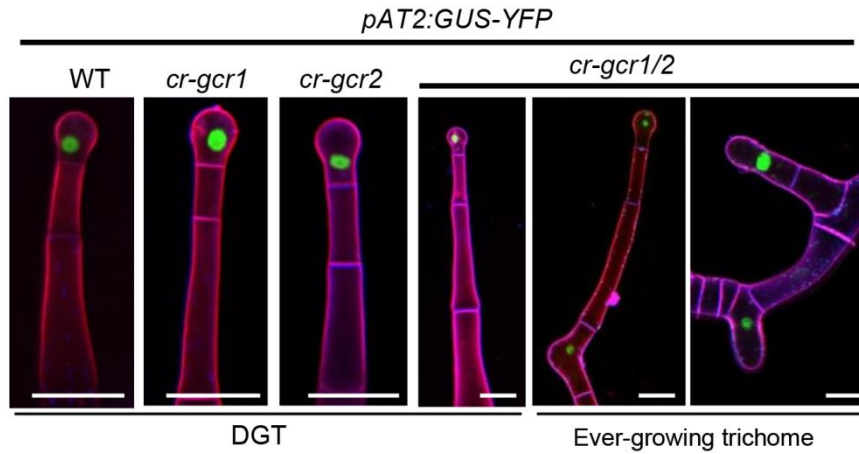
factors highly expressed in the glandular trichomes of *S. Pennellii* LA0716, *S. habrochaites* LA1777 and *S. lycopersicum* LA4024 based on the transcriptome data. Transcription factors with  $\log_2\text{FoldChange (leaf/glandular trichome)} \leq -2$  are shown. Red dots indicate two transcription factors with 81% homology. **e** The MYB-like domain with SHLQMY motif in the N-terminal of GCR1/2. **f** The EAR motif in the C-terminal of GCR1/2 and its homologs.



**Supplementary Figure 2. Knockout of GCR1/2 promotes gland formation in micro-tom tomato.**

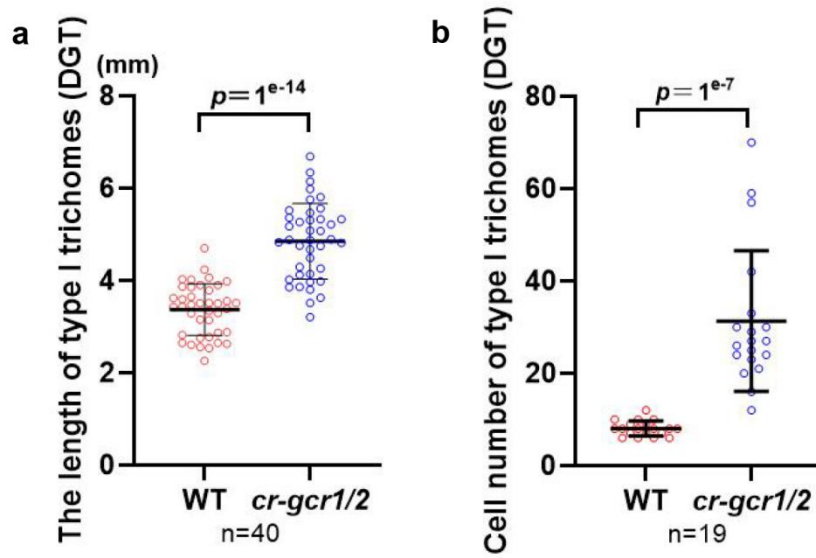
a-c Sequence analysis of *gcr1/2* single (*cr-gcr1*, *cr-gcr2*) and double (*cr-gcr1/2*) mutants generated by CRISPR/Cas9. Both single and double mutants were obtained by stable transformation. Sequences with red underlines are the single guide RNA target sequences of *GCR1* and *GCR2*, which are the same in the single and double mutants. Sequences in blue (AGG, CCA) are the protospacer-adjacent motif (PAM)

sequences. There are 1 base-pair insertion and 5 base-pair deletions of *GCR1* in lines 7 and 22 of *gcr1* single mutant, all resulting in the truncated proteins (highlighted in yellow) **(a)**. There are 1 base-pair deletion and 1 base-pair insertion of *GCR2* in lines 48 and 51 of *gcr2* single mutant, all resulting in the truncated proteins (highlighted in yellow) **(b)**. There are 4 base-pair deletions, 5 base-pair deletions and 1 base-pair insertion of *GCR1* in lines 18, 20 and 34 of *gcr1/2* double mutant, all resulting in the truncated proteins (highlighted in yellow) . There is a 1 base-pair deletion of *GCR2* in lines 18 and 34 of *gcr1/2* double mutant, resulting in the truncated proteins and a 63 base-pair deletion in line 20 which results in a 21 amino acid deletion (highlighted in yellow)**(c)**. **d** The plants, leaves, stems and buds of *gcr1* mutant (*cr-gcr1*), *gcr2* mutant (*cr-gcr2*) and *gcr1/2* double mutant (*cr-gcr1/2*). Bar: 10 cm (plants), 1 mm (Leaves, stems and buds). **e** PGT of *gcr1/2* double mutants (*cr-gcr1/2*) has more than one giant gland with distinct morphology. Bar: 50  $\mu$ m.

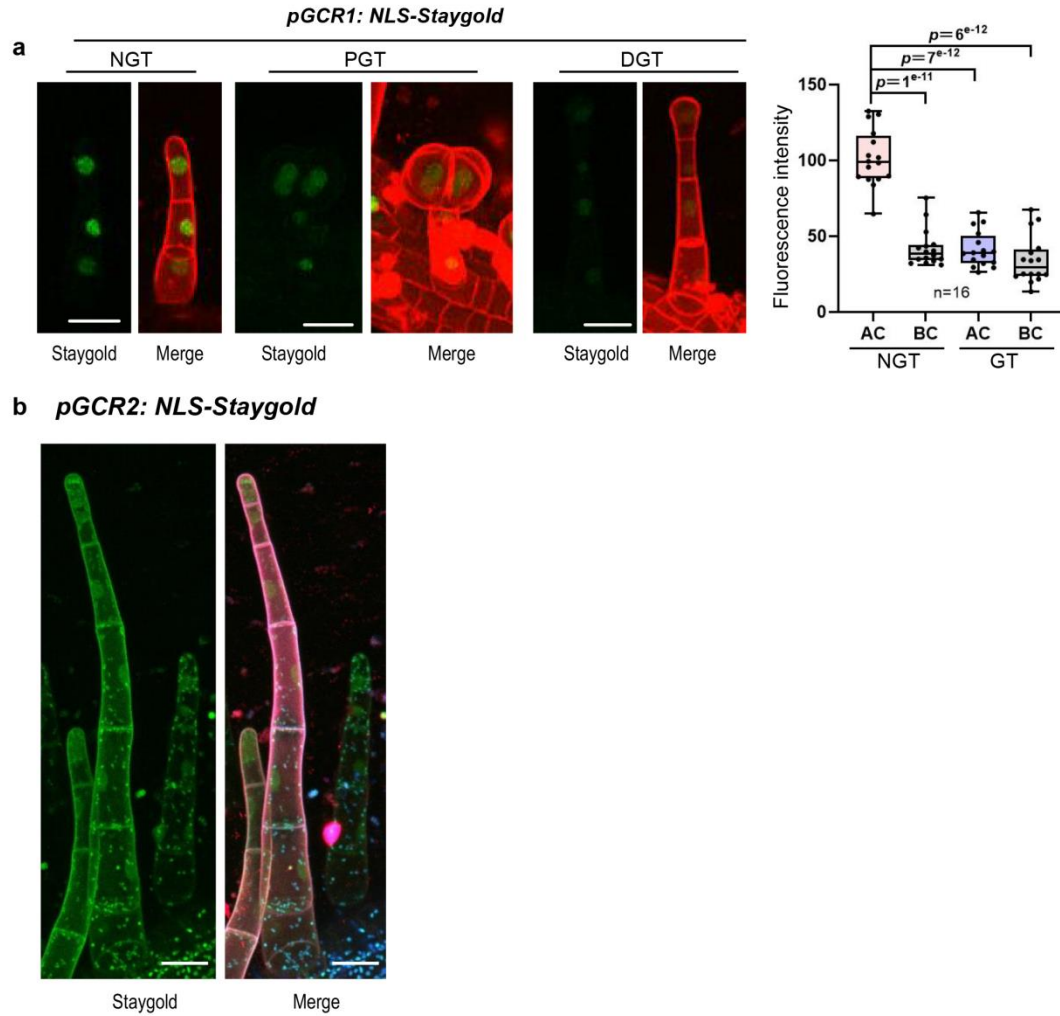


**Supplementary Figure 3. Visualization of glandular marker lines.**

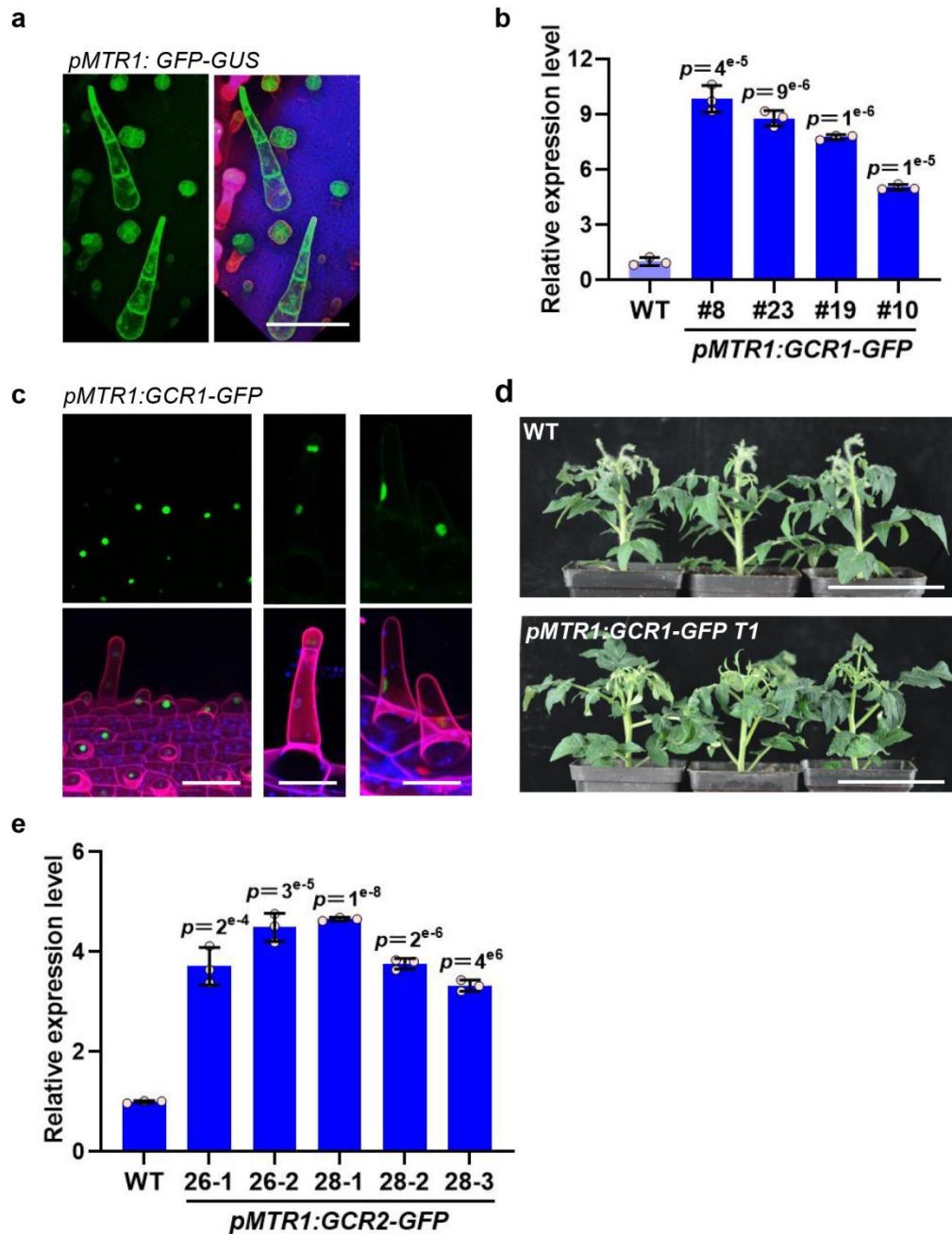
Marker of glandular cells (*pAT2:GUS-YFP*) is introduced into *gcr1* and *gcr2* single mutants and *gcr1/2* double mutant (*cr-gcr1/2*). Propidium Iodide staining is used to show the cell edge. Chloroplast auto-fluorescence is shown in blue. YFP is shown in green. All images processed by maximum intensity projection of z-stacks. Bar: 40  $\mu$ m.



**Supplementary Figure 4. Quantification of trichome length a and cell number b of *cr-gcr1/2*.** n represents the number of trichomes used for the quantification. At least 19 trichomes from two lines were used to quantify. Data are shown as mean  $\pm$  SD. *p*-values were calculated by unpaired two-sided *t*-test.

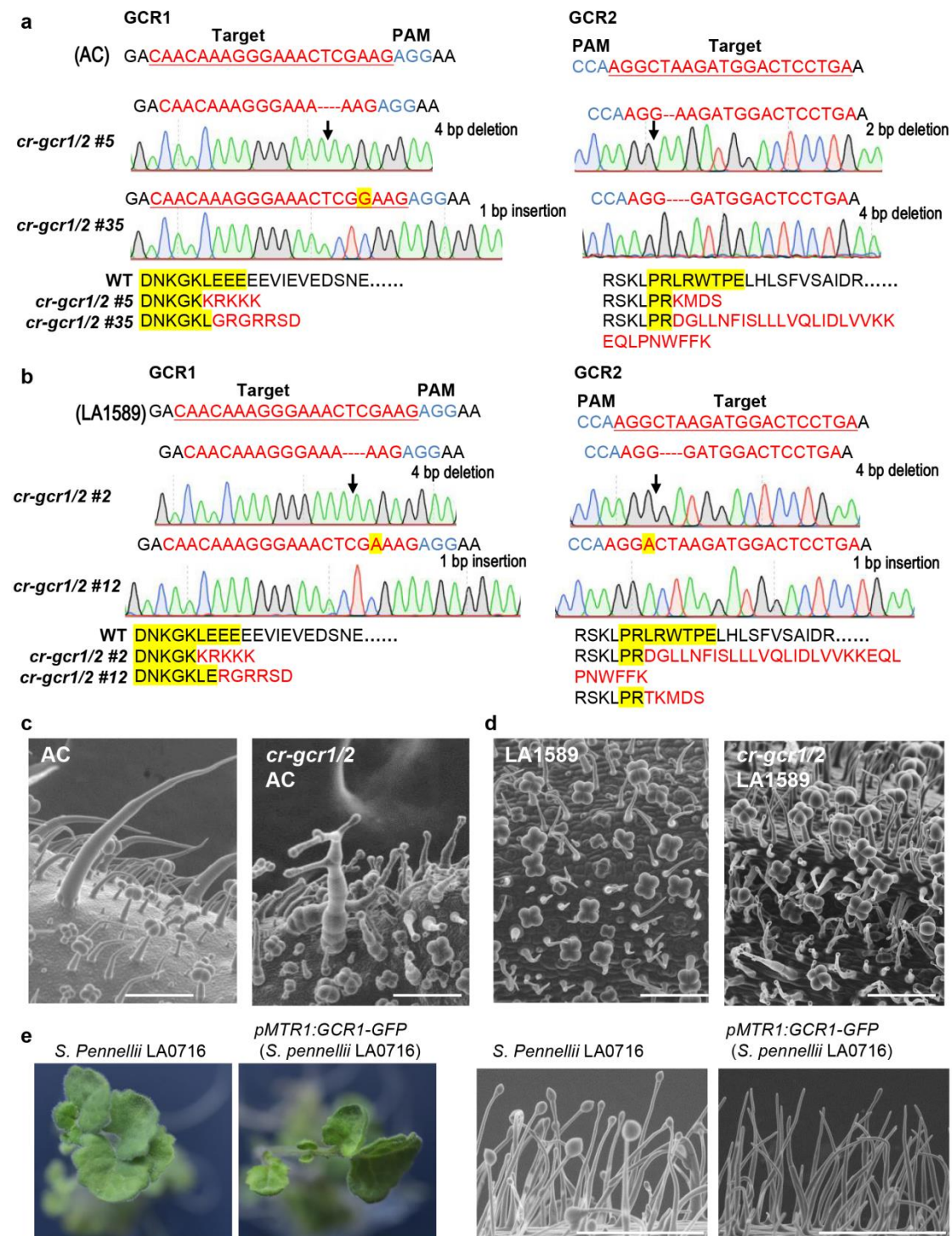


**Supplementary Figure 5. Expression pattern of *GCR1* (a) and *GCR2* (b).** Propidium Iodide staining is used to show the cell edge. Staygold is shown in green. BC: Basal cell; AC: Apical cell. GT: glandular trichomes including DGT and PGT. Bar: 50  $\mu\text{m}$  (a), 20  $\mu\text{m}$  (b). *GCR1* expression is quantified by fluorescence intensity measurement of z-stacked images of *pGCR1:NLS-Staygold*. Box plots show maximum, minimum, first and third quartiles, median (line). n represents the number of trichomes used for the quantification. 16 trichomes from two lines were used to quantify. *p*-values obtained by unpaired *t*-test.



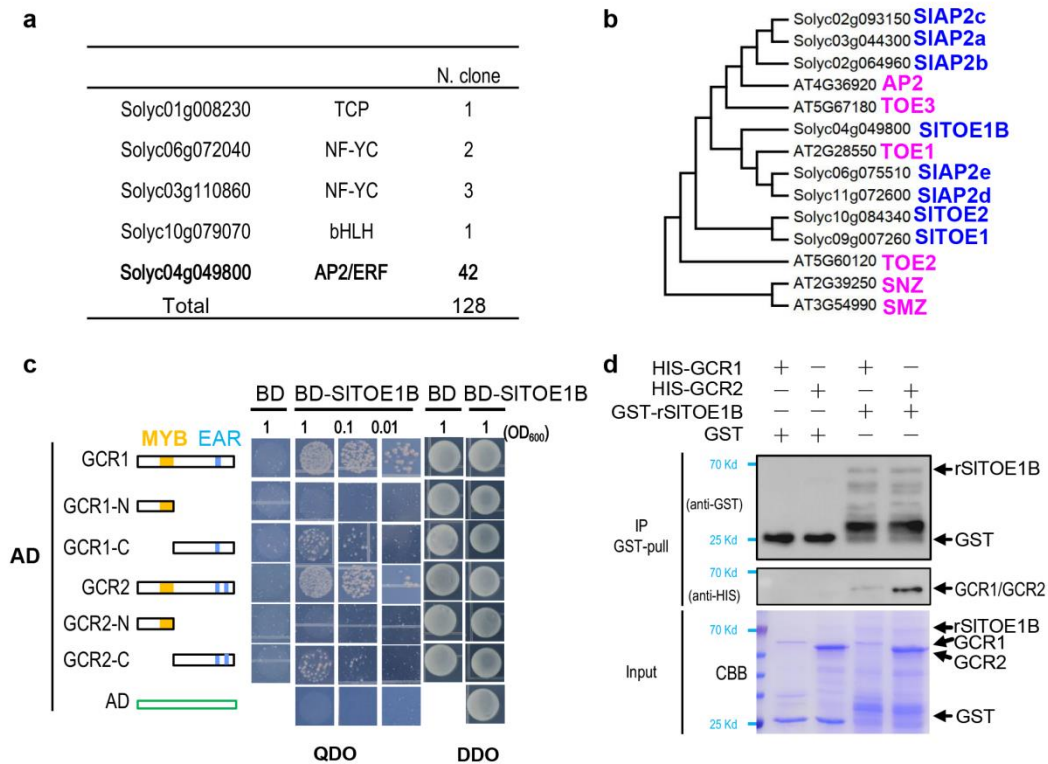
**Supplementary Figure 6. Expression of *GCR1* and *GCR2* inhibits gland formation.**

**a** Expression pattern of *MTR1*. Auto-fluorescence of chloroplast is shown in blue. Fluorescence of PI is shown in red. **b** Relative expression level of *GCR1* in the *pMTR1:GCR1-GFP* transgenic plants. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired *t*-test. **c** *GCR1-GFP* protein in *pMTR1:GCR1-GFP* plants. *GCR1-GFP* protein in nuclei is shown in green. Fluorescence of PI is shown in red. Bar: 20  $\mu$ m. **d** Transgenic plants expressing *GCR1* driven by *MTR1* promoter. Bar: 10 cm. **e** Expression level of *GCR2* in *pMTR1:GCR2-GFP*. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired *t*-test.



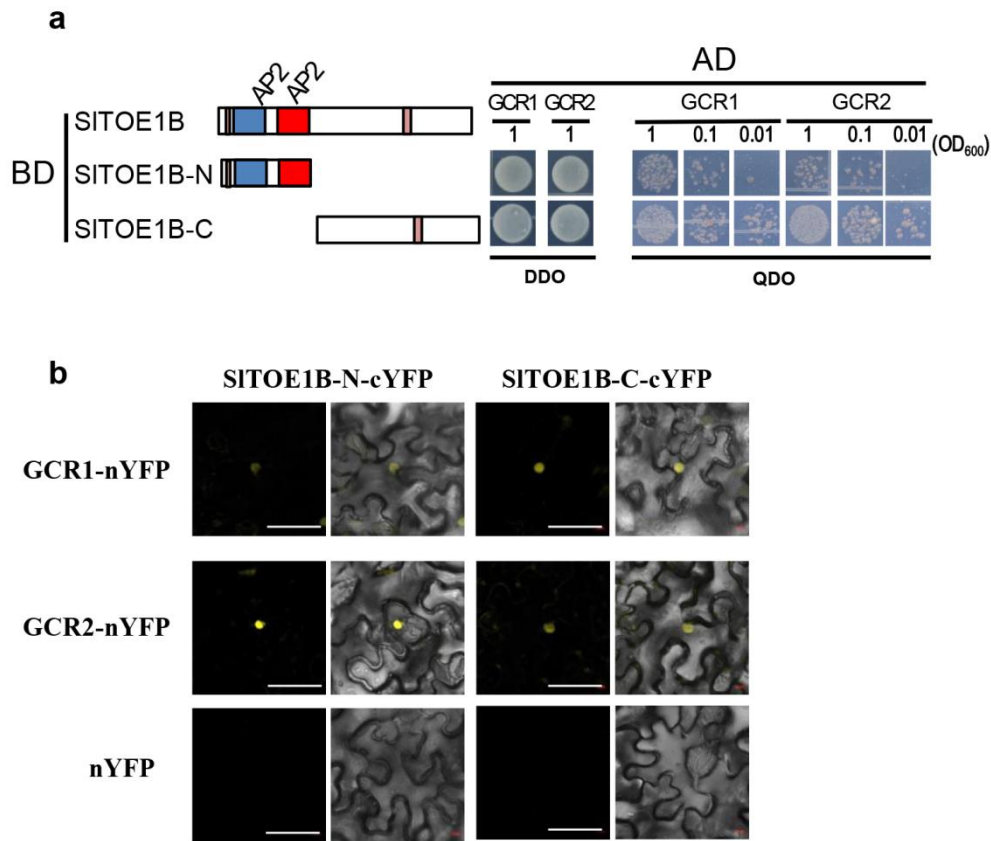
**Supplementary Figure 7. Verification of GCR1/2 function in Alisa Craig (AC), *S. pimpine* LA1589 and *S. pennellii* LA0716.**

**a and b** Sequence analysis of *gcr1/2* double mutants (*cr-gcr1/2*) generated by CRISPR/Cas9 in AC (**a**) and LA1589 (**b**). Sequences with red underlines are the single guide RNA target sequences of GCR1 and GCR2. **c and d** SEM images show that knockout of *GCR1/2* in AC and LA1589 promotes gland formation. Bar: 100  $\mu$ m. **e** Expression of *GCR1* driven by *MTR1* promoter inhibits gland formation in *S. pennellii*. Bar: 300  $\mu$ m (SEM images). At least thirty lines were obtained.



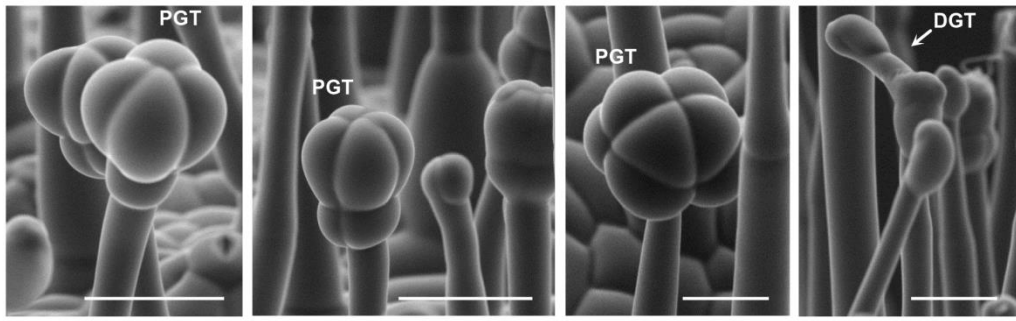
### Supplementary Figure 8. GCR1/2 interact with SITOIE1B.

**a** Yeast-two-hybrid (Y2H) cDNA library screening for GCR1-interacting factors. A total of 128 clones are sequenced, and 42 are the AP2/ERF transcriptional factor Solyc04g049800. **b** Phylogenetic analysis of TOE homology in tomato and *Arabidopsis*. Protein sequences of TOE homology are used. **c** Y2H assays show GCR1/2 interact with SITOIE1B through its C-terminal domain. N-terminal domain of GCR1 (GCR1-N), C-terminal domain of GCR1 (GCR1-C), GCR2-N and GCR2-C are inserted into pGADT7 vector with DNA Gal4-activation domain (AD). SITOIE1B is cloned into pGBKT7 vector with DNA-binding domain (BD). The black boxes represent the coding sequence of GCR1, GCR2 and their fragments used for the interaction verification. The yellow boxes represent the MYB-like domain of GCR1 and GCR2. The blue boxes represent the EAR motif of GCR1 and GCR2. Interaction is tested with gradient cell dilutions (1, 0.1 and 0.01 OD<sub>600</sub>). DDO: SD/-Leu-Trp. QDO: SD/-Ade-His-Leu-Trp. Data represent results of three independent experiments. **d** GST-pull down assay show that GST-SITOIE1B but not GST pulls down HIS-GCR1 and HIS-GCR2. GST beads are used for co-immunoprecipitation and His antibody is used to detect the GCR proteins. Data represent results of three independent experiments.

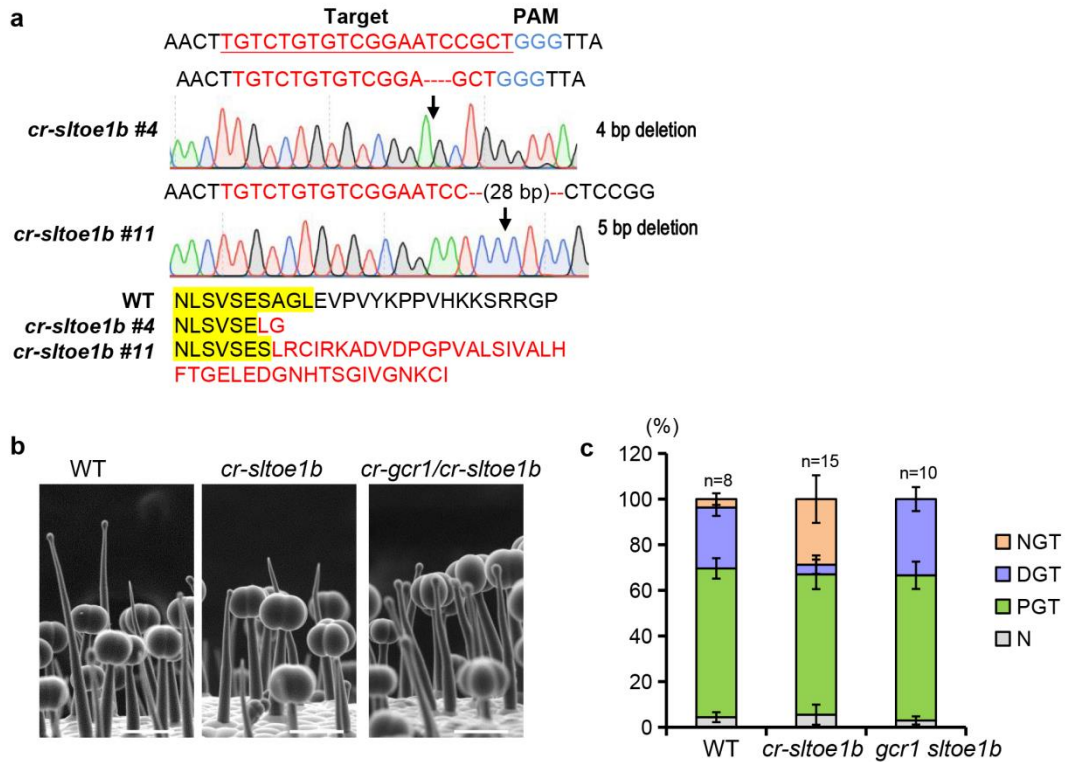


**Supplementary Figure 9. N-terminal and C-terminal domains of SITO E1B interact with GCR1/2.**

**a** Y2H assay. N-terminal and C-terminal domains of SITO E1B are fused with DNA binding domain (BD). GCR1/2 are fused with DNA activation domain (AD). **b** BiFC assays in *N. benthamiana* leaves. N-terminal and C-terminal domains of SITO E1B are fused with cYFP. GCR1/2 are fused with nYFP. Bar: 50  $\mu$ m. Data represent results of three independent experiments in a and b.

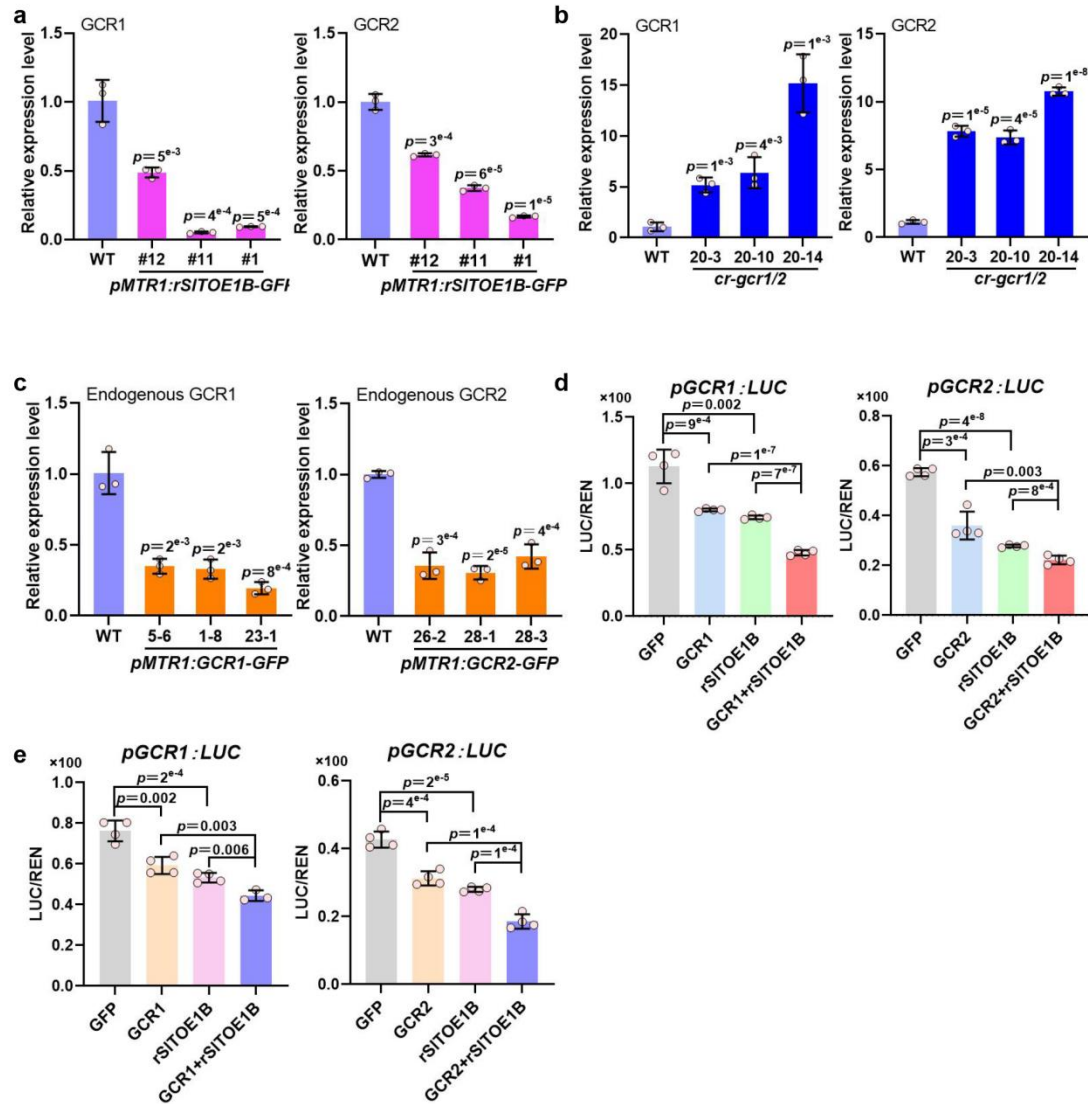


**Supplementary Figure 10. PGT and DGT of *pMTR1:SITOE1B* plants form more than one glanular cells. Bar: 50  $\mu$ m.**



**Supplementary Figure 11. Sequence analysis of *sltoe1b* mutant and phenotype of *sltoe1b gcr1* double mutant.**

**a** Sequence analysis of *sltoe1b* mutant generated by CRISPR/Cas9. **b** Phenotypes of *cr-sltoe1b* and *sltoe1b gcr1* double mutant (*cr-sltoe1b/cr-gcr1*). **c** Quantification of the trichomes on the juvenile stems. The Y-axis represents the proportion of the three categories of trichomes in the total number of trichomes. n represents the number of SEM images used for the quantification. For each line, at least 8 different SEM images from four to five individual plants are used for trichome quantification. Data are shown as mean  $\pm$  SD. *p*-values were obtained by unpaired two-sided *t*-test and exact *p*-values are presented in the Supplementary Table 9.

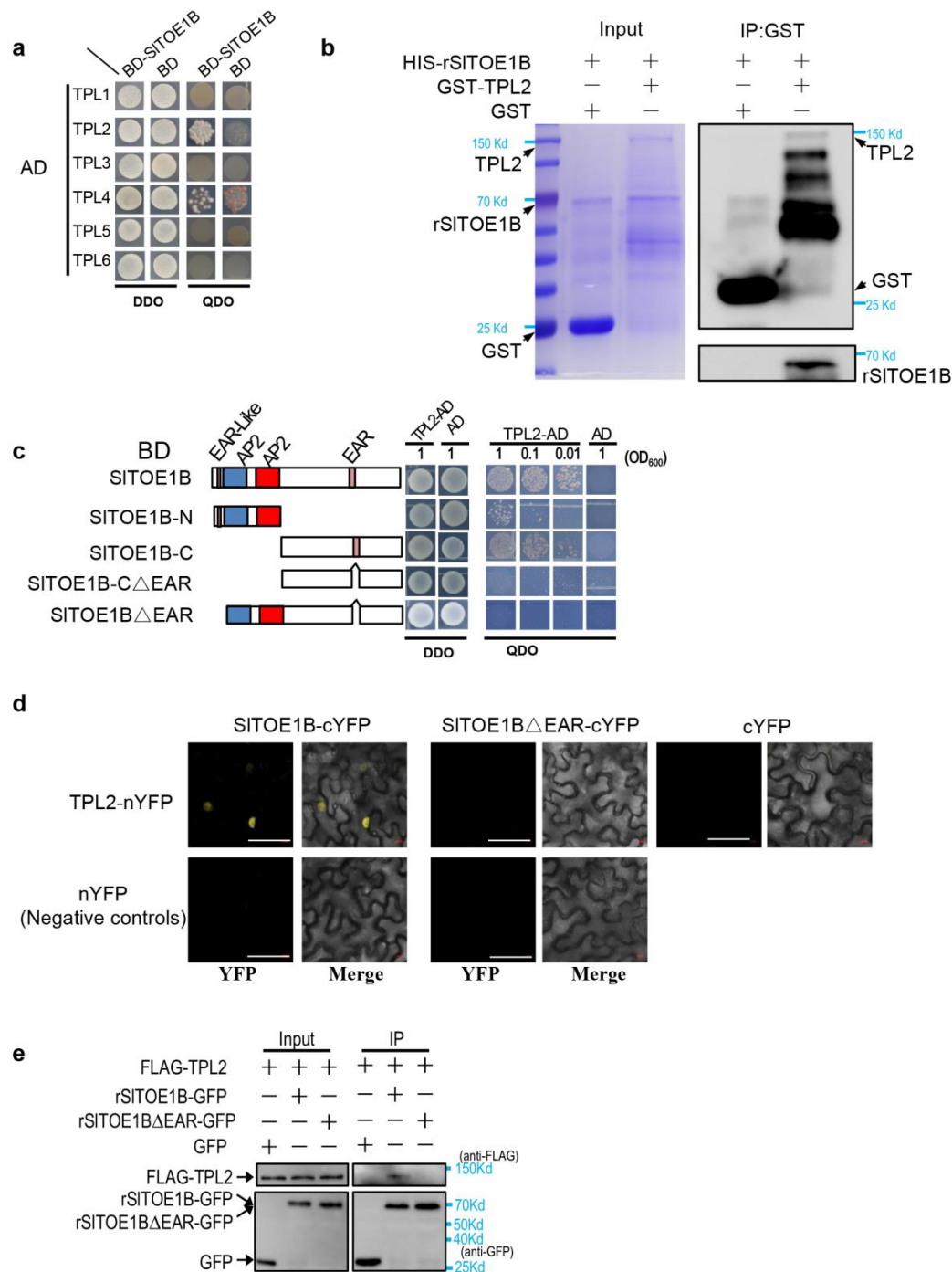


**Supplementary Figure 12. *SITOE1B* and *GCR1/2* regulate the expression of *GCR1/2*.**

**a** Relative expression of *GCR1/2* in the *pMTR1:rSITOE1B* transgenic plants. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired *t*-test. **b** Relative expression of *GCR1/2* in *gcr1/2* double mutants (*cr-gcr1/2*). Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired *t*-test. **c** Relative expression of endogenous *GCR1* and *GCR2* in the *pMTR1:GCR1* and the *pMTR1:GCR2* transgenic plants. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired *t*-test. **d** and **e** LUC assay in WT (**d**) and *cr-gcr1/2* (**e**) protoplasts. *GCR1/2* inhibits the transcriptional activity of *GCR1/2* promoters and such inhibition is significantly enhanced when *SITOE1B* proteins are present. *p*-values were calculated by unpaired two-sided *t*-test. n = 3~4 biological replicates.

| Motif   | Sequence | <i>pGCR1</i>                     | <i>pGCR2</i>                                            | <i>pLFS</i>                          | PJG-GCR1 | PJG-GCR2 | PJG | Promoter fragment                 |
|---------|----------|----------------------------------|---------------------------------------------------------|--------------------------------------|----------|----------|-----|-----------------------------------|
| Motif1  | AAGAATAA | -2837 ~ -2830<br>-808 ~ -801     |                                                         | -2173 ~ -2166(-)<br>-1330 ~ -1323(-) |          |          |     | <i>pGCR1-1</i> ;<br><i>pLFS-2</i> |
| Motif2  | AAGAATTA | -2097 ~ -2090                    | -2507 ~ -2500                                           |                                      |          |          |     |                                   |
| Motif3  | GGGAATCT | -969 ~ -962                      |                                                         |                                      |          |          |     | <i>pGCR1-2</i>                    |
| Motif4  | GGGAATAA |                                  | -200~-193(-)                                            |                                      |          |          |     |                                   |
| Motif5  | ACATTCTT |                                  |                                                         | -2786 ~ -2779(-)                     |          |          |     |                                   |
| Motif6  | AAATTCTA | -2882 ~ -2875 (-)<br>-614 ~ -607 |                                                         | -1290 ~ -1283(-)<br>-246 ~ -239      |          |          |     | <i>pLFS-4</i>                     |
| Motif7  | AAATTCTT | -1174 ~ -1167 (-)                |                                                         | -163 ~ -156                          |          |          |     | <i>pLFS-5</i>                     |
| Motif8  | ACATTCTC |                                  | -1890~-1833                                             | -92 ~ -85                            |          |          |     | <i>pLFS-5</i>                     |
| Motif9  | ATATTCTT | -339 ~ -332 (-)                  | -2894 ~ -2887 (-)<br>-1423 ~ -1416 (-)                  | -30 ~ -23                            |          |          |     | <i>pLFS-5</i> ;<br><i>pGCR2-1</i> |
| Motif10 | TTATTCTC | -1581 ~ -1574 (-)                | -2412 ~ -2405                                           |                                      |          |          |     | <i>pGCR2-2</i>                    |
| Motif11 | AGGAATAT | -1345 ~ -1338                    |                                                         |                                      |          |          |     |                                   |
| Motif12 | GAGAATTT | -2508 ~ -2501 (-)                |                                                         |                                      |          |          |     |                                   |
| Motif13 | TAGAATTA | -2969 ~ -2962                    |                                                         |                                      |          |          |     |                                   |
| Motif14 | TGGAATTA | -1711 ~ -1704(-)                 | -2984 ~ -2977<br>-2774 ~ -2767 (-)<br>-1379 ~ -1372 (-) |                                      |          |          |     |                                   |
| Motif15 | TGGAATAA |                                  | -2659 ~ -2652                                           | -2257 ~ -2250(-)                     |          |          |     |                                   |
| Motif16 | AGGAATAA |                                  |                                                         | -1067 ~ -1060(-)                     |          |          |     |                                   |
| Motif17 | AGGAATGA |                                  |                                                         | -1543 ~ -1536(-)                     |          |          |     |                                   |
| Motif18 | GGGAATAT |                                  |                                                         | -1731 ~ -1724(-)                     |          |          |     |                                   |

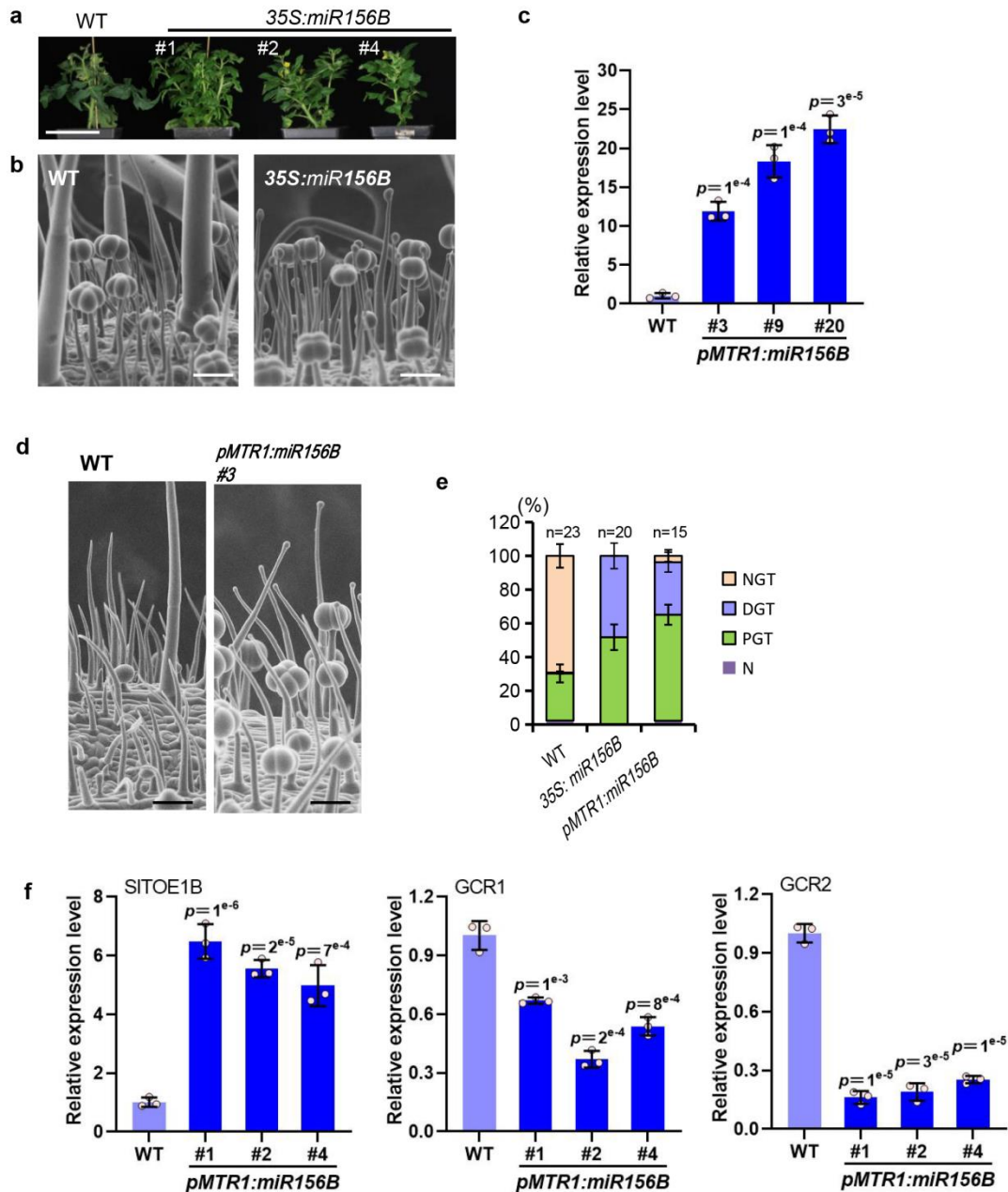
**Supplementary Figure 13. Screening for GCR-binding motifs.** Ten motifs are selected for the interaction verification. Data in columns 3-5 show the position of these motifs in *GCR1*, *GCR2* and *LFS* promoters. The last column shows the promoter fragments that contain the corresponding motifs and are used for Y1H assays (in support of Figure 6a and Figure 7d). Data represent results of three independent experiments.



### Supplementary Figure 14. SITOE1B interacts with TPL2.

**a** Y2H assay. SITPLs are in pGADT7 and SITOE1B is in pGBKT7. DDO: SD/-Leu-Trp. QDO: SD/-Ade-His-Leu-Trp. **b** GST-pull down assay. GST-TPL2 but not GST pulls down His-SITOE1B. GST beads are used for co-immunoprecipitation and His antibody is used to detect SITOE1B protein. **c** Y2H shows that both EAR-like motif and EAR motif are required for the interaction between SITOE1B and TPL2. **d** BiFC assays show that deletion of EAR and EAR-like motifs of SITOE1B abolishes the interaction between SITOE1B and TPL2. Bar: 50  $\mu$ m. **e** Co-IP assay shows that

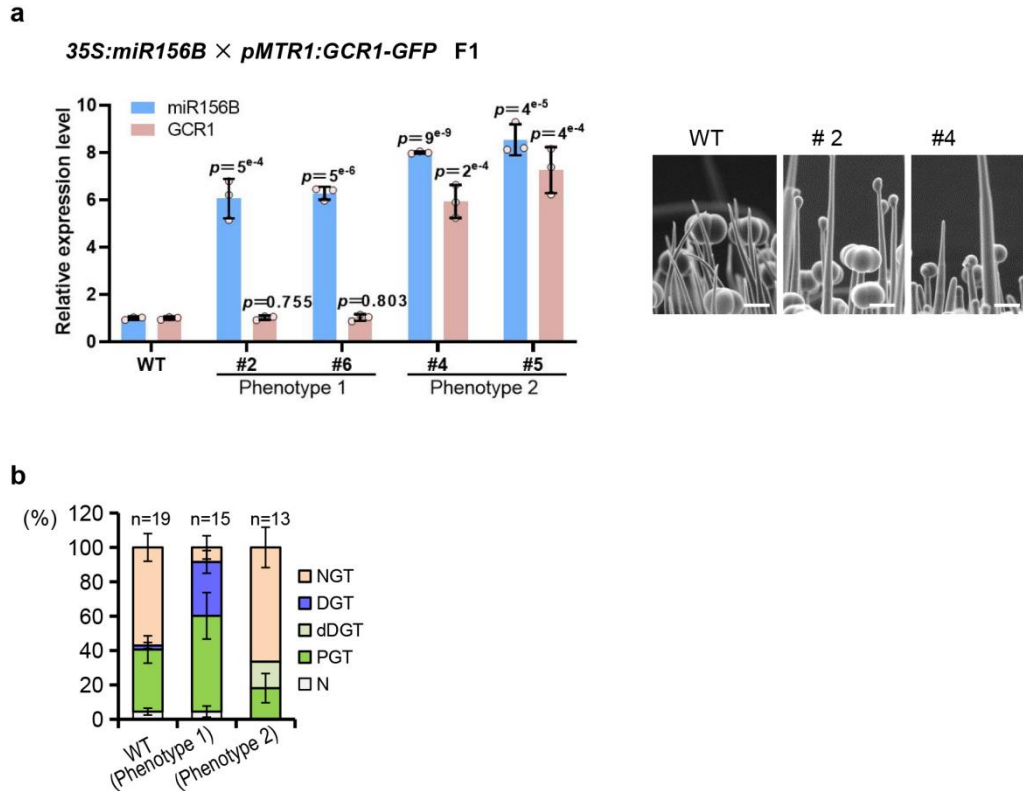
SLTOE1B interacts with TPL2. GFP (left lane; negative control) or GFP fused with the target protein (the other lanes) are used as bait to bind to the GFP beads. Immuno-precipitated proteins are detected by anti-FLAG antibody. Data represent results of three independent experiments including Y2H assays; GST-pull down assay; BiFC assays and Co-IP assay.



**Supplementary Figure 15. GCR1/2 are required for miR156-induced glandular trichome formation.**

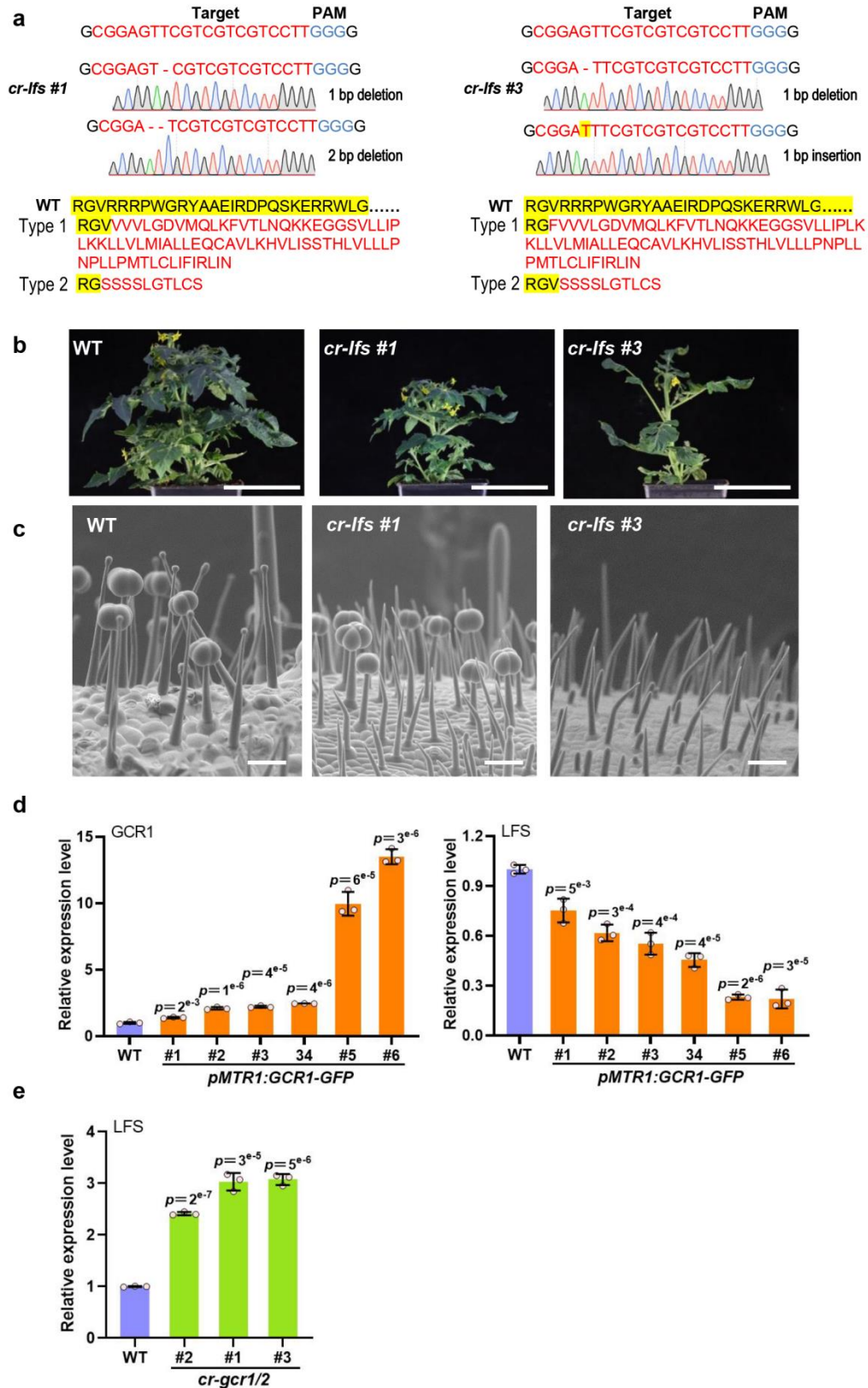
**a** Transgenic plants with *miR156B* overexpression. Bar: 10 cm. **b** SEM images show that *miR156B* overexpression induces DGT formation. Bar: 100  $\mu$ m. **c** and **d** Expression of *miR156B* driven by *MTR1* promoter induces DGT formation. Relative expression level of *miR156B* in *pMTR1:miR156B* transgenic lines (**c**). Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired two-sided *t*-test. SEM images show DGT in *pMTR1:miR156B* transgenic line #3 (**d**). Bar: 100  $\mu$ m. **e** Quantification of trichomes in *35S:miR156B* and *pMTR1:miR156B*. The Y-axis represents the proportion of three categories of trichomes in the total number of trichomes. n represents the number of SEM images used for the quantification. At

least 15 different SEM images from three to four individual plants are used for trichome quantification. Data are shown as mean  $\pm$  SD. *p*-values were calculated by unpaired two-sided *t*-test and presented in the Supplementary Table 10. **f** Relative expression level of *GCR1*, *GCR2* and *SITOE1B* in *pMTR1: miR156B* lines. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired two-sided *t*-test.



**Supplementary Figure 16. GCR1 is epistatic to miR156B in the gland formation pathway.**

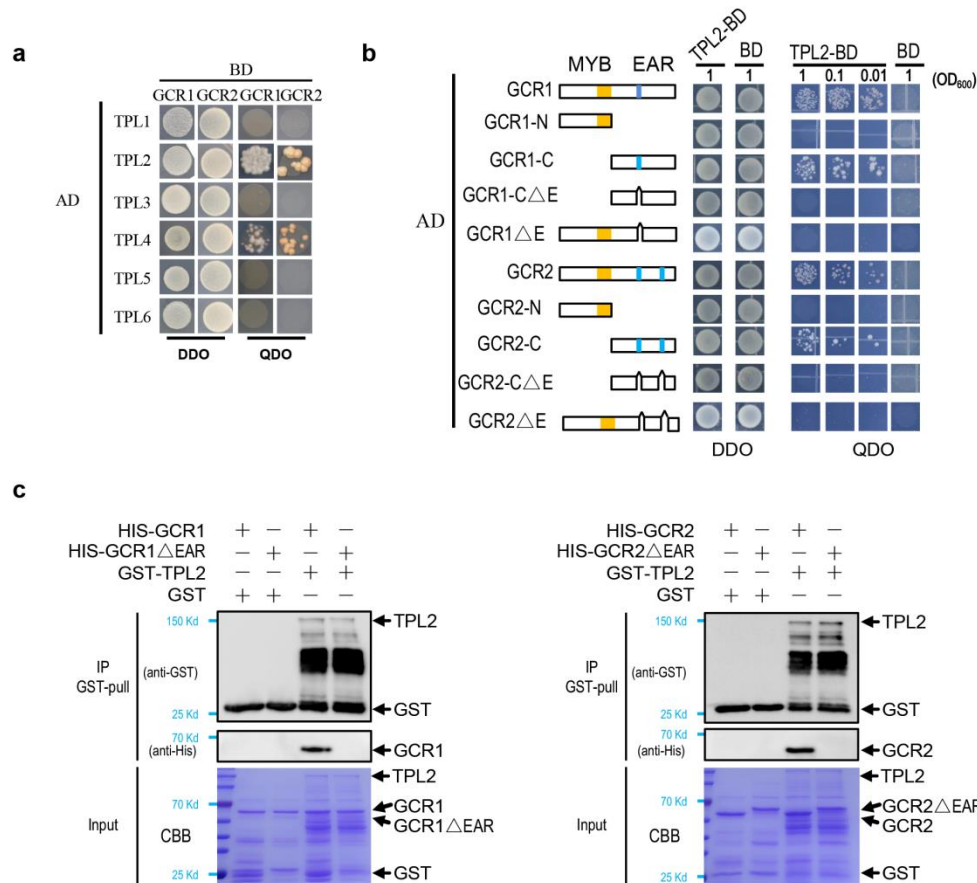
**a** Gland development is inhibited in F1 plants of the cross between *pMTR1:GCR1-GFP* and *35S:miR156B*. Data are shown as mean  $\pm$  SD (n=3 technical replicates). Exact *p*-values were calculated by unpaired two-sided *t*-test. Trichome phenotype of Line 2 (#2) and Line 6 (#6) is the same as *35S:miR156B* plants (Phenotype 1) and trichome phenotype of Line 4 (#4) and Line 5 (#5) is the same as *pMTR1: GCR1-GFP* plants (Phenotype 2). SEM images show trichomes of line 2 (#2) and line 4 (#4). Bar: 50  $\mu$ m. **b** Quantification of trichomes on the adult stems of F1 plants shown in (a). n represents the number of SEM images used for the quantification. For each line, at least 13 different SEM images from three to five individual plants were used for trichome quantification. Data are shown as mean  $\pm$  SD. *p*-values were calculated by unpaired two-sided *t*-test and presented in the Supplementary Table 11.



**Supplementary Figure 17. Genotype and phenotype of *lfs* mutant.**

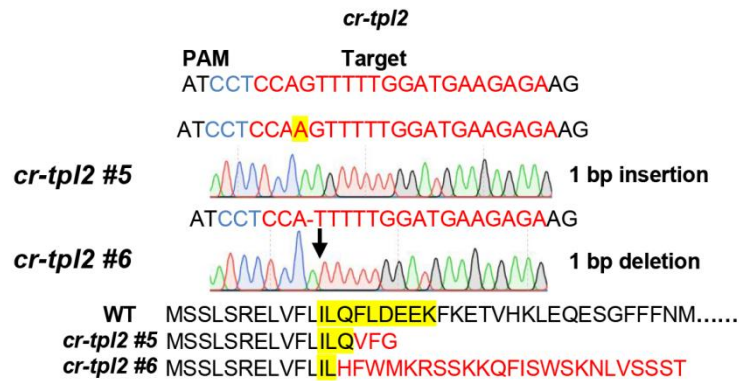
**a** Knockout of *LFS* by CRISPR/Cas9 (*cr-lfs*). The red lines indicate the single guide

RNA target sequences. The sequences in blue indicate the protospacer-adjacent motif (PAM) sequences. Two knockout lines of LFS are shown: *cr-lfs* #1 and *cr-lfs* #3. *cr-lfs* #1 is a heterozygous mutant with a single DNA strand edited. Two types of mutations are generated in *cr-lfs* #1: type 1 with 1 base-pair deletion and type 2 with 2 base-pairs deletion, both of which result in the truncated proteins. All DNA strands of *cr-lfs* #3 are edited and two types of mutations are identified: type 1 with 1 base-pair deletion and type 2 with 1 base-pair deletion insertion, both of which result in the truncated proteins. **b** *lfs* mutant plants. Bar: 10 cm. **c** SEM images of juvenile stems show that knockout of *LFS* inhibits gland formation. Bar: 100  $\mu$ m. **d** Relative expression level of *GCR1* and *LFS* in *pMTR1:GCR1-GFP* lines. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired two-sided *t*-test. **e** Relative expression level of *LFS* in *cr-gcr1/2* lines. Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired two *t*-test.



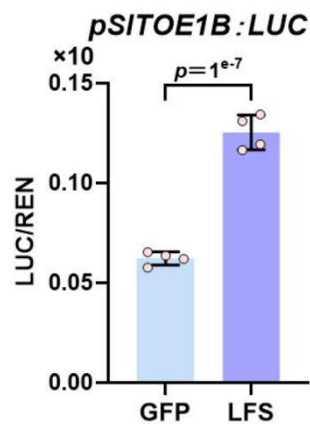
### Supplementary Figure 18. GCR1/2 interact with TPL.

**a** Y2H assays show that GCR1/2 interact with TPL2 and TPL4. **b** Y2H assays show GCR1 and GCR2 interact with TPL2 by EAR motif. GCR1/2-N represents the N-terminal of GCR1/2; GCR1/2-C represents the C-terminal of GCR1/2; GCR1/2-CΔE represents the C-terminal of GCR1/2 with EAR motif deletion. GCR1/2ΔE represents the full length of GCR1/2 with EAR motif deletion. DDO: SD/-Leu-Trp. QDO: SD/-Ade-His-Leu-Trp. Three dilutions for each interaction are presented. **c** GST-pull down assay. HIS-GCR1/2 with EAR motif deletion is marked as HIS-GCR1ΔEAR and HIS-GCR2ΔEAR. GFP (left two lanes; negative control) or GFP fused with the target protein (the other lanes) are used as bait to bind to the GFP beads. Immuno-precipitated proteins are detected by anti-HIS antibody. Data represent results of three independent experiments including Y2H assays and GST-pull down assays.



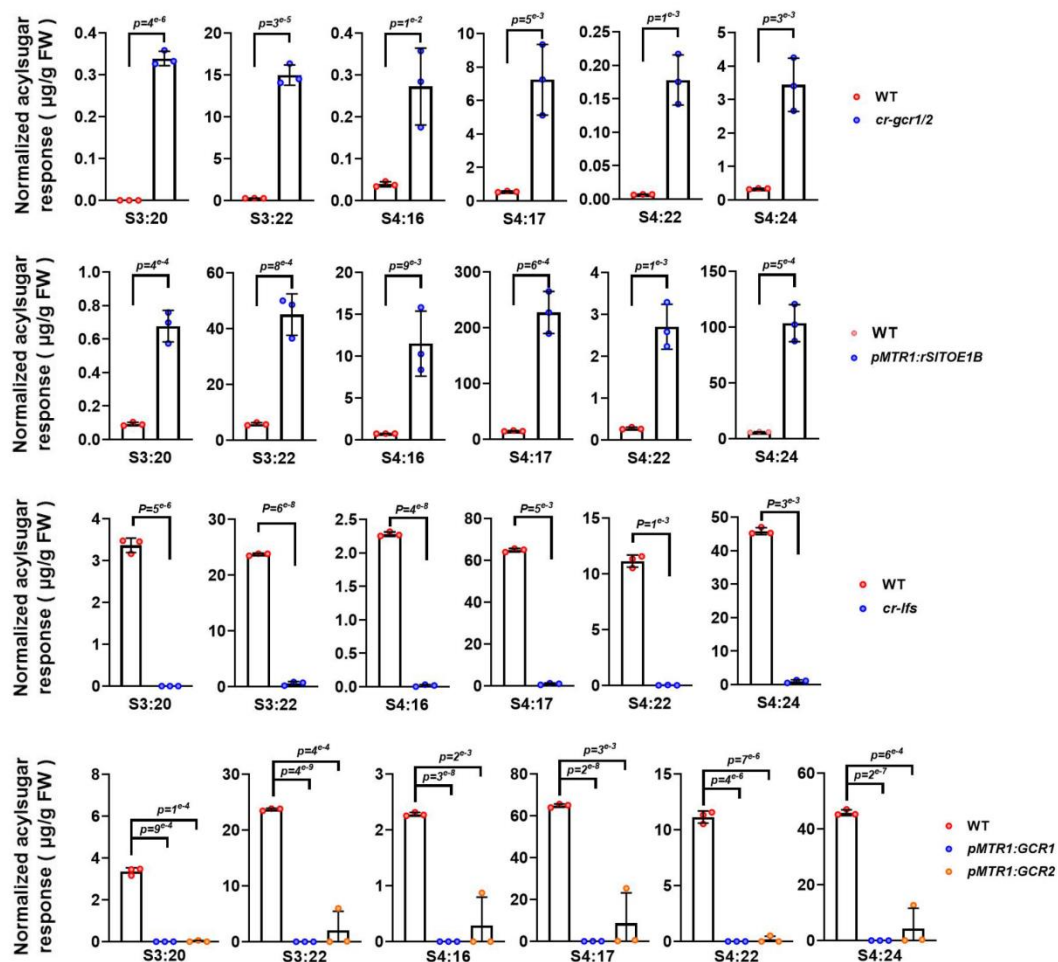
**Supplementary Figure 19. Sequence analysis of *tpl2* mutant generated by CRISPR/Cas9.**

The red lines indicate the single guide RNA target sequences. The sequences in blue indicate the protospacer-adjacent motif (PAM) sequences. Two knockout lines of TPL2 are shown: *cr-tpl2* #5 and #6. There are 1 base-pair insertion in *cr-tpl2* #5 and 1 base-pair deletion in *cr-tpl2* #6 which result in the truncated proteins.



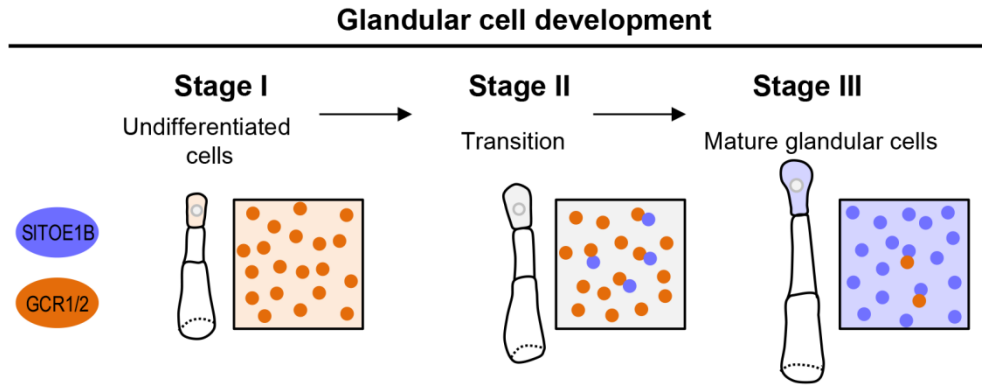
**Supplementary Figure 20. LUC assay shows LFS activates the transcriptional activity of *SITOE1B* promoters in tobacco protoplasts.**

n = 4 biological replicates. *p*-values were calculated by unpaired two-sided *t*-test.



**Supplementary Figure 21. Measurement of acylsugars by LC-MS according to the previously published method.**

Data are shown as mean  $\pm$  SD (n=3 biological replicates). *p*-values obtained by unpaired two-sided *t*-test.



**Supplementary Figure 22. A putative model depicting the coordination of GCR1/2 and SITO1B during glandular cell formation.**

Supplementary Table 1. Annotation of positive clones in Y2H screening using GCR1 as a bait.

| Gene ID        | Number of positive clone | Percentage of total positive clones | Protein name     | Homolog of Arabidopsis | Annotation                                                  |
|----------------|--------------------------|-------------------------------------|------------------|------------------------|-------------------------------------------------------------|
| Solyc04g049800 | 42                       | 32.81%                              | TOE1             | AT2G28550              | AP2 family transcription factor                             |
| Solyc03g110860 | 3                        | 2.34%                               | NF-YC1           | AT3G48590              | Nuclear transcription factor Y subunit C-1                  |
| Solyc06g072040 | 2                        | 1.56%                               | <i>CIP2a</i>     | AT3G48590              | Nuclear transcription factor Y subunit C-1                  |
| Solyc04g077490 | 1                        | 0.78%                               | ANT              | AT4G37750              | A putative transcriptional regulator similar to AP2         |
| Solyc10g079070 | 1                        | 0.78%                               | <i>SlbHLH065</i> | AT3G57800              | Regulate hypocotyl elongation                               |
| Solyc01g008230 | 1                        | 0.78%                               | <i>SITCP15</i>   | AT5G23280              | Involved in leaf development and axillary shoots formation. |
| Solyc02g085950 | 18                       | 14.06%                              | RBCS3B           | AT5G38410              | Rubisco small subunit (RBCS) multigene family               |
| Solyc03g034220 | 10                       | 7.81%                               | Slss5            | AT5G38410              | Rubisco small subunit (RBCS) multigene family               |
| Solyc12g005630 | 8                        | 6.25%                               | PETC, PGR1       | AT4G03280              | Cytochrome b6-f complex iron-sulfur subunit                 |
| Solyc10g086580 | 5                        | 3.91%                               |                  | AT2G39730              | Ribulose-1,5-bisphosphate carboxylase/oxygenase activase 1  |
| Solyc01g105050 | 4                        | 3.13%                               |                  | AT1G15820              | Chlorophyll a-b binding protein                             |
| Solyc01g096150 | 2                        | 1.56%                               |                  | AT1G01225              | NC domain-containing protein                                |
| Solyc01g097010 | 2                        | 1.56%                               |                  | AT3G04610              | Nucleic acid binding protein                                |
| Solyc04g015020 | 2                        | 1.56%                               | ATHMP35          | AT4G16380              | Proline-rich protein                                        |
| Solyc06g083620 | 2                        | 1.56%                               |                  | AT4G29040              | 26S protease regulatory subunit 4                           |
| Solyc08g008470 | 2                        | 1.56%                               |                  |                        |                                                             |
| Other clones   | 23                       | 17.97%                              |                  |                        |                                                             |

Supplementary Table 2. P-value of quantification of trichomes in figure 1e.

|                  | NGT      |          |                                                                                                                                                                                                         |
|------------------|----------|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                  | Average  | SD       | P-Value                                                                                                                                                                                                 |
| WT               | 76.74854 | 3.20844  |                                                                                                                                                                                                         |
| <i>cr-gcr1</i>   | 56.08000 | 13.51929 | 0.00144, ** ( <i>cr-gcr1</i> vs WT)                                                                                                                                                                     |
| <i>cr-gcr2</i>   | 75.19709 | 3.39759  | 0.1939, ( <i>cr-gcr2</i> vs WT)                                                                                                                                                                         |
| <i>cr-gcr1/2</i> | 4.27852  | 1.65451  | 2.73262 <sup>e-32</sup> , *** ( <i>cr-gcr1/2</i> vs WT)<br>1.70071 <sup>e-13</sup> , *** ( <i>cr-gcr1/2</i> vs <i>cr-gcr1</i> )<br>4.27538 <sup>e-31</sup> , *** ( <i>cr-gcr1/2</i> vs <i>cr-gcr2</i> ) |
|                  | DGT      |          |                                                                                                                                                                                                         |
|                  | Average  | SD       | P-Value                                                                                                                                                                                                 |
| WT               | 0.00000  | 0.00000  |                                                                                                                                                                                                         |
| <i>cr-gcr1</i>   | 26.63346 | 9.62693  | 4.29132 <sup>e-12</sup> , *** ( <i>cr-gcr1</i> vs WT)                                                                                                                                                   |
| <i>cr-gcr2</i>   | 0.00000  | 0.00000  |                                                                                                                                                                                                         |
| <i>cr-gcr1/2</i> | 79.80067 | 2.36857  | 4.38918 <sup>e-42</sup> , *** ( <i>cr-gcr1/2</i> vs WT)<br>6.74871 <sup>e-17</sup> , *** ( <i>cr-gcr1/2</i> vs <i>cr-gcr1</i> )<br>2.39097 <sup>e-37</sup> , *** ( <i>cr-gcr1/2</i> vs <i>cr-gcr2</i> ) |
|                  | PGT      |          |                                                                                                                                                                                                         |
|                  | Average  | SD       | P-Value                                                                                                                                                                                                 |
| WT               | 23.25146 | 3.20844  |                                                                                                                                                                                                         |
| <i>cr-gcr1</i>   | 17.28653 | 5.59106  | 0.00092, *** ( <i>cr-gcr1</i> vs WT)                                                                                                                                                                    |
| <i>cr-gcr2</i>   | 24.80291 | 3.39759  | 0.22999, ( <i>cr-gcr2</i> vs WT)                                                                                                                                                                        |
| <i>cr-gcr1/2</i> | 15.92081 | 2.14219  | 4.12274 <sup>e-08</sup> , *** ( <i>cr-gcr1/2</i> vs WT)<br>0.40568, ( <i>cr-gcr1/2</i> vs <i>cr-gcr1</i> )<br>1.14870 <sup>e-08</sup> , *** ( <i>cr-gcr1/2</i> vs <i>cr-gcr2</i> )                      |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 3. P-value of quantification of trichomes in figure 2d.

|                    | NGT      |          |                                                            |
|--------------------|----------|----------|------------------------------------------------------------|
|                    | Average  | SD       | P-Value                                                    |
| WT                 | 1.93699  | 2.66827  |                                                            |
| <i>pMTR1:GCR1</i>  | 51.09046 | 9.08866  | 7.04127 <sup>e-23</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)   |
| <i>pMTR1:GCR2</i>  | 52.54066 | 8.02333  | 2.92651 <sup>e-24</sup> , *** ( <i>pMTR1:GCR2</i> vs WT)   |
| <i>pMTR1:NbGCR</i> | 45.91640 | 5.43791  | 2.45399 <sup>e-24</sup> , *** ( <i>pMTR1:NbGCR1</i> vs WT) |
| <i>pMTR1:PeGCR</i> | 46.47423 | 5.79386  | 4.09252 <sup>e-17</sup> , *** ( <i>pMTR1:PeGCR1</i> vs WT) |
|                    | DGT      |          |                                                            |
|                    | Average  | SD       | P-Value                                                    |
| WT                 | 45.56827 | 11.16015 |                                                            |
| <i>pMTR1:GCR1</i>  | 0.00000  | 0.00000  | 1.00647 <sup>e-16</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)   |
| <i>pMTR1:GCR2</i>  | 0.00000  | 0.00000  | 5.52419 <sup>e-16</sup> , *** ( <i>pMTR1:GCR2</i> vs WT)   |
| <i>pMTR1:NbGCR</i> | 0.00000  | 0.00000  | 1.10232 <sup>e-13</sup> , *** ( <i>pMTR1:NbGCR1</i> vs WT) |
| <i>pMTR1:PeGCR</i> | 0.00000  | 0.00000  | 1.00647 <sup>e-16</sup> , *** ( <i>pMTR1:PeGCR1</i> vs WT) |
|                    | dPGT     |          |                                                            |
|                    | Average  | SD       | P-Value                                                    |
| WT                 | 0.00000  | 0.00000  |                                                            |
| <i>pMTR1:GCR1</i>  | 25.67144 | 4.62728  | 3.76427 <sup>e-24</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)   |
| <i>pMTR1:GCR2</i>  | 25.77243 | 5.19004  | 3.33244 <sup>e-22</sup> , *** ( <i>pMTR1:GCR2</i> vs WT)   |
| <i>pMTR1:NbGCR</i> | 33.98648 | 5.90426  | 1.99334 <sup>e-16</sup> , *** ( <i>pMTR1:NbGCR1</i> vs WT) |
| <i>pMTR1:PeGCR</i> | 32.78665 | 4.67172  | 1.97684 <sup>e-26</sup> , *** ( <i>pMTR1:PeGCR1</i> vs WT) |
|                    | PGT      |          |                                                            |
|                    | Average  | SD       | P-Value                                                    |
| WT                 | 49.54519 | 8.96585  |                                                            |
| <i>pMTR1:GCR1</i>  | 21.14755 | 5.48796  | 2.44081 <sup>e-12</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)   |
| <i>pMTR1:GCR2</i>  | 19.07359 | 5.53306  | 1.29389 <sup>e-12</sup> , *** ( <i>pMTR1:GCR2</i> vs WT)   |
| <i>pMTR1:NbGCR</i> | 17.74634 | 3.47535  | 4.49866 <sup>e-13</sup> , *** ( <i>pMTR1:NbGCR1</i> vs WT) |
| <i>pMTR1:PeGCR</i> | 18.94579 | 6.08689  | 6.21863 <sup>e-12</sup> , *** ( <i>pMTR1:PeGCR1</i> vs WT) |
|                    | N        |          |                                                            |
|                    | Average  | SD       | P-Value                                                    |
| WT                 | 2.91798  | 2.69085  |                                                            |
| <i>pMTR1:GCR1</i>  | 2.09055  | 2.25785  | 0.34628, ( <i>pMTR1:GCR1</i> vs WT)                        |
| <i>pMTR1:GCR2</i>  | 2.61331  | 2.05595  | 0.72757, ( <i>pMTR1:GCR2</i> vs WT)                        |
| <i>pMTR1:NbGCR</i> | 2.35078  | 1.52178  | 0.45200, ( <i>pMTR1:NbGCR1</i> vs WT)                      |
| <i>pMTR1:PeGCR</i> | 0.01793  | 0.02184  | 0.00079, *** ( <i>pMTR1:PeGCR1</i> vs WT)                  |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 4. P-value of quantification of trichomes in figure 4e.

|                       | NGT      |         |                                                              |
|-----------------------|----------|---------|--------------------------------------------------------------|
|                       | Average  | SD      | P-Value                                                      |
| WT                    | 64.80523 | 5.55099 |                                                              |
| <i>pMTR1:rSITOE1B</i> | 0.00000  | 0.00000 | 1.14848 <sup>e-52</sup> , *** ( <i>pMTR1:rSITOE1B</i> vs WT) |
|                       | DGT      |         |                                                              |
|                       | Average  | SD      | P-Value                                                      |
| WT                    | 1.57385  | 2.50852 |                                                              |
| <i>pMTR1:rSITOE1B</i> | 58.13140 | 6.51422 | 7.04748 <sup>e-41</sup> , *** ( <i>pMTR1:rSITOE1B</i> vs WT) |
|                       | PGT      |         |                                                              |
|                       | Average  | SD      | P-Value                                                      |
| WT                    | 25.68163 | 2.82098 |                                                              |
| <i>pMTR1:rSITOE1B</i> | 35.45805 | 7.44657 | 1.93096 <sup>e-07</sup> , *** ( <i>pMTR1:rSITOE1B</i> vs WT) |
|                       | N        |         |                                                              |
|                       | Average  | SD      | P-Value                                                      |
| WT                    | 7.93928  | 4.91125 |                                                              |
| <i>pMTR1:rSITOE1B</i> | 7.26955  | 4.17810 | 0.31868, ( <i>pMTR1:rSITOE1B</i> vs WT)                      |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 5. P-value of quantification of trichomes in figure 4g.

|                   | NGT      |          |                                         |
|-------------------|----------|----------|-----------------------------------------|
|                   | Average  | SD       | P-Value                                 |
| WT                | 8.02515  | 7.74626  |                                         |
| <i>cr-sltoe1b</i> | 18.25261 | 10.68665 | 0.00170, *** ( <i>cr-sltoe1b</i> vs WT) |
|                   | DGT      |          |                                         |
|                   | Average  | SD       | P-Value                                 |
| WT                | 19.58280 | 8.22352  |                                         |
| <i>cr-sltoe1b</i> | 8.22430  | 3.08835  | 0.00021, *** ( <i>cr-sltoe1b</i> vs WT) |
|                   | PGT      |          |                                         |
|                   | Average  | SD       | P-Value                                 |
| WT                | 69.73267 | 7.84332  |                                         |
| <i>cr-sltoe1b</i> | 72.24430 | 13.55013 | 0.38353, ( <i>cr-sltoe1b</i> vs WT)     |
|                   | N        |          |                                         |
|                   | Average  | SD       | P-Value                                 |
| WT                | 2.65939  | 3.48240  |                                         |
| <i>cr-sltoe1b</i> | 1.27878  | 1.46680  | 0.22268, ( <i>cr-sltoe1b</i> vs WT)     |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 6. P-value of quantification of trichomes in figure 5b.

|                       | NGT      |          |                                                                                                                                          |
|-----------------------|----------|----------|------------------------------------------------------------------------------------------------------------------------------------------|
|                       | Average  | SD       | P-Value                                                                                                                                  |
| WT                    | 53.50468 | 10.06659 |                                                                                                                                          |
| <i>pMTR1:rSITOE1B</i> | 0.00000  | 0.00000  | 1.30491 <sup>e-32</sup> , *** ( <i>pMTR1:rSITOE1B</i> vs WT)                                                                             |
| <i>pMTR1:GCR1</i>     | 74.99150 | 9.65256  | 1.18776 <sup>e-07</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>1.15134 <sup>e-39</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>pMTR1:rSITOE1B</i> ) |
|                       | DGT      |          |                                                                                                                                          |
|                       | Average  | SD       | P-Value                                                                                                                                  |
| WT                    | 0.63989  | 1.13032  |                                                                                                                                          |
| <i>pMTR1:rSITOE1B</i> | 57.35540 | 7.23384  | 4.03145 <sup>e-35</sup> , *** ( <i>pMTR1:rSITOE1B</i> vs WT)                                                                             |
| <i>pMTR1:GCR1</i>     | 0.00000  | 0.00000  | 0.02185, ( <i>pMTR1:GCR1</i> vs WT)<br>1.89038 <sup>e-34</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>pMTR1:rSITOE1B</i> )                      |
|                       | dPGT     |          |                                                                                                                                          |
|                       | Average  | SD       | P-Value                                                                                                                                  |
| WT                    | 0.00000  | 0.00000  |                                                                                                                                          |
| <i>pMTR1:rSITOE1B</i> | 0.00000  | 0.00000  |                                                                                                                                          |
| <i>pMTR1:GCR1</i>     | 14.53673 | 4.53742  | 6.92987 <sup>e-16</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>1.06967 <sup>e-22</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>pMTR1:rSITOE1B</i> ) |
|                       | PGT      |          |                                                                                                                                          |
|                       | Average  | SD       | P-Value                                                                                                                                  |
| WT                    | 35.61300 | 6.32415  |                                                                                                                                          |
| <i>pMTR1:rSITOE1B</i> | 33.39627 | 5.50705  | 0.19788, ( <i>pMTR1:rSITOE1B</i> vs WT)                                                                                                  |
| <i>pMTR1:GCR1</i>     | 10.47177 | 7.48332  | 5.70469 <sup>e-13</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>2.74430 <sup>e-16</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>pMTR1:rSITOE1B</i> ) |
|                       | N        |          |                                                                                                                                          |
|                       | Average  | SD       | P-Value                                                                                                                                  |
| WT                    | 10.15373 | 6.86552  |                                                                                                                                          |
| <i>pMTR1:rSITOE1B</i> | 9.24833  | 4.93418  | 0.64042, ( <i>pMTR1:rSITOE1B</i> vs WT)                                                                                                  |
| <i>pMTR1:GCR1</i>     | 0.00000  | 0.00000  | 3.41059 <sup>e-07</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>3.39005 <sup>e-10</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>pMTR1:rSITOE1B</i> ) |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 7. P-value of quantification of trichomes in figure 8b.

|                                  | NGT       |         |                                                                                                                                                                  |
|----------------------------------|-----------|---------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                  | Average   | SD      | P-Value                                                                                                                                                          |
| WT                               | 87.47876  | 3.65358 |                                                                                                                                                                  |
| <i>cr-lfs</i>                    | 100.00000 | 0.00000 | 1.91693 <sup>e-13</sup> , *** ( <i>cr-lfs</i> vs WT)                                                                                                             |
| <i>cr-gcr1/2</i>                 | 0.00000   | 0.00000 | 6.93438 <sup>e-40</sup> , *** ( <i>cr-gcr1/2</i> vs WT)                                                                                                          |
| <i>cr-gcr1/2</i> × <i>cr-lfs</i> | 100.00000 | 0.00000 | 1.59019 <sup>e-16</sup> , ***( <i>cr-gcr1/2</i> × <i>cr-lfs</i> vs WT)                                                                                           |
|                                  | DGT       |         |                                                                                                                                                                  |
|                                  | Average   | SD      | P-Value                                                                                                                                                          |
| WT                               | 0.00000   | 0.00000 |                                                                                                                                                                  |
| <i>cr-lfs</i>                    | 0.00000   | 0.00000 |                                                                                                                                                                  |
| <i>cr-gcr1/2</i>                 | 92.84777  | 5.43531 | 2.18511 <sup>e-38</sup> , *** ( <i>cr-gcr1/2</i> vs WT)                                                                                                          |
| <i>cr-gcr1/2</i> × <i>cr-lfs</i> | 0.00000   | 0.00000 | 4.38918 <sup>e-42</sup> , ***( <i>cr-gcr1/2</i> × <i>cr-lfs</i> vs WT)<br>2.18512 <sup>e-38</sup> , *** ( <i>cr-gcr1/2</i> × <i>cr-lfs</i> vs <i>cr-gcr1/2</i> ) |
|                                  | PGT       |         |                                                                                                                                                                  |
|                                  | Average   | SD      | P-Value                                                                                                                                                          |
| WT                               | 12.52124  | 3.65358 |                                                                                                                                                                  |
| <i>cr-lfs</i>                    | 0.00000   | 0.00000 | 1.91693 <sup>e-13</sup> , *** ( <i>cr-lfs</i> vs WT)                                                                                                             |
| <i>cr-gcr1/2</i>                 | 7.15223   | 5.43531 | 0.00214, ** ( <i>cr-gcr1/2</i> vs WT)                                                                                                                            |
| <i>cr-gcr1/2</i> × <i>cr-lfs</i> | 0.00000   | 0.00000 | 1.59019 <sup>e-16</sup> , ***( <i>cr-gcr1/2</i> × <i>cr-lfs</i> vs WT)<br>2.00219 <sup>e-06</sup> , *** ( <i>cr-gcr1/2</i> × <i>cr-lfs</i> vs <i>cr-gcr1/2</i> ) |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 8. P-value of quantification of trichomes in figure S1b.

|                     | NGT      |         |                                                     |
|---------------------|----------|---------|-----------------------------------------------------|
|                     | Average  | SD      | P-Value                                             |
| AC                  | 15.41000 | 2.98915 |                                                     |
| <i>S. Pennellii</i> | 0.00000  | 0.00000 | $6.11548^{e-28}$ *** ( <i>S. Pennellii</i> vs AC)   |
|                     | DGT      |         |                                                     |
|                     | Average  | SD      | P-Value                                             |
| AC                  | 27.61137 | 6.98275 |                                                     |
| <i>S. Pennellii</i> | 98.40385 | 1.90934 | $1.78130^{e-37}$ , *** ( <i>S. Pennellii</i> vs AC) |
|                     | PGT      |         |                                                     |
|                     | Average  | SD      | P-Value                                             |
| AC                  | 56.97863 | 8.06392 |                                                     |
| <i>S. Pennellii</i> | 1.59615  | 1.90934 | $2.14884^{e-31}$ , *** ( <i>S. Pennellii</i> vs AC) |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 9. P-value of quantification of trichomes in figure S11c.

|                           | NGT      |          |                                                                                                                        |
|---------------------------|----------|----------|------------------------------------------------------------------------------------------------------------------------|
|                           | Average  | SD       | P-Value                                                                                                                |
| WT                        | 3.69006  | 2.54926  |                                                                                                                        |
| <i>cr-sltoe1b</i>         | 28.74175 | 10.42325 | 1.46897e-06, *** ( <i>cr-sltoe1b</i> vs WT)                                                                            |
| <i>cr-sltoe1b/cr-gcr1</i> | 0.00000  | 0.00000  | 0.00029, *** ( <i>cr-sltoe1b/cr-gcr1</i> vs WT)<br>1.07797e-08, *** ( <i>cr-sltoe1b/cr-gcr1</i> vs <i>cr-sltoe1b</i> ) |
|                           | DGT      |          |                                                                                                                        |
|                           | Average  | SD       | P-Value                                                                                                                |
| WT                        | 26.69287 | 3.67950  |                                                                                                                        |
| <i>cr-sltoe1b</i>         | 4.23503  | 4.04797  | 1.51363e-11, *** ( <i>cr-sltoe1b</i> vs WT)                                                                            |
| <i>cr-sltoe1b/cr-gcr1</i> | 33.40297 | 5.24900  | 0.00754, ** ( <i>cr-sltoe1b/cr-gcr1</i> vs WT)<br>8.97323e-14, *** ( <i>cr-sltoe1b/cr-gcr1</i> vs <i>cr-sltoe1b</i> )  |
|                           | PGT      |          |                                                                                                                        |
|                           | Average  | SD       | P-Value                                                                                                                |
| WT                        | 65.22112 | 4.47421  |                                                                                                                        |
| <i>cr-sltoe1b</i>         | 61.52907 | 6.47896  | 0.24348, ( <i>cr-sltoe1b</i> vs WT)                                                                                    |
| <i>cr-sltoe1b/cr-gcr1</i> | 63.63138 | 5.98381  | 0.54178, ( <i>cr-sltoe1b/cr-gcr1</i> vs WT)<br>0.59267, ( <i>cr-sltoe1b/cr-gcr1</i> vs <i>cr-sltoe1b</i> )             |
|                           | N        |          |                                                                                                                        |
|                           | Average  | SD       | P-Value                                                                                                                |
| WT                        | 4.39595  | 2.17300  |                                                                                                                        |
| <i>cr-sltoe1b</i>         | 5.49416  | 4.40600  | 0.51744, ( <i>cr-sltoe1b</i> vs WT)                                                                                    |
| <i>cr-sltoe1b/cr-gcr1</i> | 2.96565  | 1.78862  | 0.14464, ( <i>cr-sltoe1b/cr-gcr1</i> vs WT)<br>0.10011, ( <i>cr-sltoe1b/cr-gcr1</i> vs <i>cr-sltoe1b</i> )             |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 10. P-value of quantification of trichomes in figure S15e.

|                      | NGT      |         |                                                               |
|----------------------|----------|---------|---------------------------------------------------------------|
|                      | Average  | SD      | P-Value                                                       |
| WT                   | 69.20174 | 6.99667 |                                                               |
| <i>35S:miR156B</i>   | 0        | 0       | $3.36490 \times 10^{-36}$ , *** ( <i>35S:miR156B</i> vs WT)   |
| <i>pMTR1:miR156B</i> | 3.75435  | 3.52980 | $1.03779 \times 10^{-28}$ , *** ( <i>pMTR1:miR156B</i> vs WT) |
|                      | DGT      |         |                                                               |
|                      | Average  | SD      | P-Value                                                       |
| WT                   | 0.50627  | 0.84314 |                                                               |
| <i>35S:miR156B</i>   | 48.24196 | 7.58475 | $1.55470 \times 10^{-29}$ , *** ( <i>35S:miR156B</i> vs WT)   |
| <i>pMTR1:miR156B</i> | 31.14024 | 5.85880 | $2.90898 \times 10^{-24}$ , *** ( <i>pMTR1:miR156B</i> vs WT) |
|                      | PGT      |         |                                                               |
|                      | Average  | SD      | P-Value                                                       |
| WT                   | 27.96025 | 5.34091 |                                                               |
| <i>35S:miR156B</i>   | 51.71338 | 7.59273 | $5.58875 \times 10^{-15}$ , *** ( <i>35S:miR156B</i> vs WT)   |
| <i>pMTR1:miR156B</i> | 62.90222 | 5.94822 | $3.07086 \times 10^{-20}$ , *** ( <i>pMTR1:miR156B</i> vs WT) |
|                      | N        |         |                                                               |
|                      | Average  | SD      | P-Value                                                       |
| WT                   | 2.33172  | 2.80952 |                                                               |
| <i>35S:miR156B</i>   | 0.04464  | 0.19964 | 0.00079, ** ( <i>35S:miR156B</i> vs WT)                       |
| <i>pMTR1:miR156B</i> | 2.20316  | 2.47396 | 0.88605, ( <i>pMTR1:miR156B</i> vs WT)                        |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 11. P-value of quantification of trichomes in figure S16b.

|                    | NGT      |          |                                                                                                                                       |
|--------------------|----------|----------|---------------------------------------------------------------------------------------------------------------------------------------|
|                    | Average  | SD       | P-Value                                                                                                                               |
| WT                 | 57.05781 | 8.06261  |                                                                                                                                       |
| <i>35S:miR156B</i> | 8.43720  | 6.78074  | 8.72100 <sup>e-19</sup> , *** ( <i>35S:miR156B</i> vs WT)                                                                             |
| <i>pMTR1:GCR1</i>  | 66.43301 | 11.73391 | 0.01359, * ( <i>pMTR1:GCR1</i> vs WT)<br>7.37283 <sup>e-15</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>35S:miR156B</i> )                    |
|                    | DGT      |          |                                                                                                                                       |
|                    | Average  | SD       | P-Value                                                                                                                               |
| WT                 | 2.32611  | 1.74707  |                                                                                                                                       |
| <i>35S:miR156B</i> | 31.35628 | 6.60291  | 1.32535 <sup>e-18</sup> , *** ( <i>35S:miR156B</i> vs WT)                                                                             |
| <i>pMTR1:GCR1</i>  | 0        | 0        | 0.00004, *** ( <i>pMTR1:GCR1</i> vs WT)<br>1.19211 <sup>e-15</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>35S:miR156B</i> )                  |
|                    | dPGT     |          |                                                                                                                                       |
|                    | Average  | SD       | P-Value                                                                                                                               |
| WT                 | 0        | 0        |                                                                                                                                       |
| <i>35S:miR156B</i> | 0        | 0        | ( <i>35S:miR156B</i> vs WT)                                                                                                           |
| <i>pMTR1:GCR1</i>  | 15.43239 | 5.51496  | 8.30439 <sup>E-13</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>8.52421 <sup>E-11</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>35S:miR156B</i> ) |
|                    | PGT      |          |                                                                                                                                       |
|                    | Average  | SD       | P-Value                                                                                                                               |
| WT                 | 36.15156 | 7.95586  |                                                                                                                                       |
| <i>35S:miR156B</i> | 55.73454 | 13.53319 | 9.04981 <sup>e-06</sup> , *** ( <i>35S:miR156B</i> vs WT)                                                                             |
| <i>pMTR1:GCR1</i>  | 18.13459 | 8.50002  | 1.34237 <sup>e-06</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>4.99305 <sup>e-09</sup> , *** ( <i>pMTR1:GCR1</i> vs <i>35S:miR156B</i> ) |
|                    | N        |          |                                                                                                                                       |
|                    | Average  | SD       | P-Value                                                                                                                               |
| WT                 | 4.46450  | 1.98304  |                                                                                                                                       |
| <i>35S:miR156B</i> | 4.47196  | 3.24916  | 0.99346, ( <i>35S:miR156B</i> vs WT)                                                                                                  |
| <i>pMTR1:GCR1</i>  | 0        | 0        | 5.16256 <sup>e-09</sup> , *** ( <i>pMTR1:GCR1</i> vs WT)<br>0.00004, *** ( <i>pMTR1:GCR1</i> vs <i>35S:miR156B</i> )                  |

*p*-values were obtained by unpaired two-sided *t*-test.

Supplementary Table 12. Primers used in this study.

| Analysis                    | Primer name        | Sequence(5' to 3')                                            | Usage                        |
|-----------------------------|--------------------|---------------------------------------------------------------|------------------------------|
| <b>Vector Construct ion</b> | CR-GCR1-F          | GAATCTAACAGTGTAGTTTGCAACAAAGGGAAACTCGAAGGTTTATAGAGCTAGAAATAG  | <i>gcr1</i> mutant           |
|                             | CR-GCR1-R          | GCTATTTCTAGCTCTAAAACACGTAGCCTTGGCAATTTTGCAAACTACACTGTTAGATT   |                              |
|                             | CR-GCR2-F          | GAATCTAACAGTGTAGTTTGTTCAGGAGTCCATCTTAGCCTGTTTATAGAGCTAGAAATAG | <i>gcr2</i> mutant           |
|                             | CR-GCR2-R          | GCTATTTCTAGCTCTAAAACAGGCTAAGATGGACTCCTGACAACTACACTGTTAGATT    |                              |
|                             | CR-SITPL2-F        | GAATCTAACAGTGTAGTTTGTCTCTTCATCCAAAACTGGGTTTATAGAGCTAGAAATAG   | <i>slpl2</i> mutant          |
|                             | CR-SITPL2-R        | GCTATTTCTAGCTCTAAAACCCAGTTTTTGGATGAAGAGACAACTACACTGTTAGATT    |                              |
|                             | CR-SITOE1B-F       | GAATCTAACAGTGTAGTTTGTGTCTGTGTGCGAATCCGCTGTTTATAGAGCTAGAAATAG  | <i>SltOE1b</i> mutant        |
|                             | CR-SITOE1B-R       | GCTATTTCTAGCTCTAAAACGAGGTTTGTAAACAGGCACTCAAACCTACACTGTTAGATT  |                              |
|                             | 35S-miR156b-F      | CATTGAGAGGACACGCTCGAGGACAAAACATCATGTCTCTCCATT                 | <i>35S:miR156B</i>           |
|                             | 35S-miR156b-R      | TCTCATTAAAGCAGGACTCTAGACAAACTCAAACGCAAGACTTTTC                |                              |
|                             | 35S-GCR1-F         | CATTGAGAGGACACGCTCGAGATGGAATGCATCTTCTCATCCA                   | <i>35S:GCR1</i>              |
|                             | 35S-GCR1-R         | TCGCCCTTGCTCACCATGAATCAAGAGAAAGCAITGTGTTTATATCT               |                              |
|                             | pMTR1-F            | TGCATCCAACGCGTTGGGAGCTCCAGGTCGTGCAAGGTTTC                     | <i>pMTR1:GCR1</i>            |
|                             | pMTR1-GCR1-R       | GAAGATGCATTTTCCATCTCGAGCTAAAATCAAACAAAATAAAAAATA              |                              |
|                             | pMTR1-GCR2-F       | TTTGATTTAGGAGCTCCTCGAGATGACAAGTGATTCCATTGATCTGA               | <i>pMTR1:GCR2</i>            |
|                             | pMTR1-GCR2-R       | AGCTTGGTACCGGTACCTCGAGGGTGCACCTTGATGAATAAGAAGGC               |                              |
|                             | pMTR1-miR156b-F    | TTTGATTTAGGAGCTCCTCGAGGACAAAACATCATGTCTCTCCATT                | <i>pMTR1:miR156B</i>         |
|                             | pMTR1-miR156b-R    | AGCTTGGTACCGGTACCTCGAGCAAACTCAAACGCAAGACTTTTC                 |                              |
|                             | pMTR1- NbGCR-F     | TTTGATTTAGGAGCTCCTCGAGATGATCATATAGGCTTGTCTCT                  | <i>pMTR1:NbGCR</i>           |
|                             | pMTR1- NbGCR-R     | AGCTTGGTACCGGTACCTCGAGGGTGCACCTTGATGAATAATTGGC                |                              |
|                             | pMTR1- PeGCR-F     | TTTGATTTAGGAGCTCCTCGAGATGGAATACATTACGGGAAAAGCCT               | <i>pMTR1:PeGCR</i>           |
|                             | pMTR1- PeGCR-R     | AGCTTGGTACCGGTACCTCGAGCAAGTACTCAGCCTCCTCTCTAGGC               |                              |
|                             | pMTR1- rSITOE1B-F1 | TTTGATTTAGGAGCTCCTCGAGATGTTGGATCTGAATAATGATAG                 | <i>pMTR1:rSITOE1B</i>        |
|                             | pMTR1- rSITOE1B-R1 | AAAAGCCGACGAGGCGCCGGAAGAAGAAAATACTGGCACTGGA                   |                              |
|                             | pMTR1- rSITOE1B-F2 | TCCGCGGCTCGTCCGGCTTTTCTACTGTACCCTCTGCATAC                     | <i>pGCR1:NLS-Staygold</i>    |
|                             | pMTR1- rSITOE1B-R2 | AGCTTGGTACCGGTACCTCGAGGTTGGTGGGAGACGTAGTTG                    |                              |
|                             | pGCR1-nStayGold-F  | TGCATCCAACGCGTTGGGAGCTCGGATTAITTAGTGGCAAGTTTG                 | <i>pGCR2:NLS-Staygold</i>    |
|                             | pGCR1-nStayGold-R  | AGCTTGGTACCGGTACCTCGAGGACTAATATACGTCTTGTCT                    |                              |
|                             | pGCR2-nStaygold-F  | TGCATCCAACGCGTTGGGAGCTCTCCGAAAAAGAAAACCTCAAAG                 | <i>pSITOE1B:NLS-Vneus</i>    |
|                             | pGCR2-nStaygold-R  | AGCTTGGTACCGGTACCTCGAGGATTAITTAITGATGCAAGAACAATCTCTG          |                              |
|                             | pSITOE1B-nVenus-F  | TGCATCCAACGCGTTGGGAGCTCTTTTCTAGTATTGGTTGGCAGTGG               | <i>GCR1-AD and GCR1ΔE-AD</i> |
|                             | pSITOE1B-nVenus-R  | AGCTTGGTACCGGTACCTCGAGGCTCCGTTTTTTGCAAAITATTAC                |                              |
| <b>Y2H</b>                  | GCR1-AD-F          | GTACCAGATTACGCTCATATGATGGAATGCATCTTCTTCATCCA                  | <i>GCR2-AD and GCR2ΔE-AD</i> |
|                             | GCR1-AD-R          | CAGCTCGAGCTCGATGGATCCAAGAGAAAGCAITGTGTTTATATCT                |                              |
|                             | GCR2-AD-F          | GTACCAGATTACGCTCATATGATGACAAGTGATTCCATTGATCTGA                | <i>SITOE1B-AD</i>            |
|                             | GCR2-AD-R          | CAGCTCGAGCTCGATGGATCCGTTGCACTTGATGAATAAGAAGGC                 |                              |
|                             | SITOE1B-AD-F       | GTACCAGATTACGCTCATATGATGTTGGATCTGAATAATGATAGTG                | <i>SITPL1-AD</i>             |
|                             | SITOE1B-AD-R       | CAGCTCGAGCTCGATGGATCCTTAGTGTGGGAGACGTAGTTGGTTG                |                              |
|                             | SITPL1-AD-F        | GTACCAGATTACGCTCATATGATGTCATCTCTCAGTAGAGA                     | <i>SITPL2-AD</i>             |
|                             | SITPL1-AD-R        | CAGCTCGAGCTCGATGGATCCTCATCTTGGTGCTTGATCGG                     |                              |
|                             | SITPL2-AD-F        | GTACCAGATTACGCTCATATGATGTCCTTCTTAGTAGGGA                      | <i>SITPL3-AD</i>             |
|                             | SITPL2-AD-R        | CAGCTCGAGCTCGATGGATCCTACCTTGAAGGTGTTTCTG                      |                              |
|                             | SITPL3-AD-F        | GTACCAGATTACGCTCATATGATGTCCTTCTTACGAGAGA                      | <i>SITPL4-AD</i>             |
|                             | SITPL3-AD-R        | CAGCTCGAGCTCGATGGATCCTCATCTTTGAACTTGGTCAG                     |                              |
|                             | SITPL4-AD-F        | GTACCAGATTACGCTCATATGATGACTTCTTAAGCAGAGA                      |                              |
|                             | SITPL4-AD-R        | CAGCTCGAGCTCGATGGATCCTACCTTGATGCTTGATCAA                      |                              |

|             |                         |                                                                |                                |
|-------------|-------------------------|----------------------------------------------------------------|--------------------------------|
|             | SITPL5-AD-F             | GTACCAGATTACGCTCATATGATGAGGCATTTTGATGAAAT                      | SITPL5-AD                      |
|             | SITPL5-AD-R             | CAGCTCGAGCTCGATGGATCCCTACCTTTGAGGTTGATCTG                      |                                |
|             | SITPL6-AD-F             | GTACCAGATTACGCTCATATGATGTCTCTTAGTAAAGGACCT                     | SITPL6-AD                      |
|             | SITPL6-AD-R             | CAGCTCGAGCTCGATGGATCCCTATATTTGGTTGCTCATTGG                     |                                |
|             | GCR1-N-AD-F             | GTACCAGATTACGCTCATATGATGGAAAATGCATCTTCTTC                      | GCR1-N-AD                      |
|             | GCR1-N-AD-R             | CAGCTCGAGCTCGATGGATCCTCATTGTCCAGATTCATCAA                      |                                |
|             | GCR1-C-AD-F             | GTACCAGATTACGCTCATATGATGGTGTAGGGCATGGTAAT                      | GCR1-C-AD                      |
|             | GCR1-C-AD-R             | CAGCTCGAGCTCGATGGATCCCTAAAGAGAAAGCATTG                         |                                |
|             | GCR1-C $\Delta$ E-AD-R  | GAAAAAGAATGGTTACCTGATAGCAGAAGCTCAGATGACAAG                     | GCR1-C $\Delta$ E-AD           |
|             | GCR1-C $\Delta$ E-AD-F  | CTTGTCATCTGAGCTTCTGCTATCAGGTAACCATTTCTTTTC                     |                                |
|             | GCR2-N-AD-F             | GTACCAGATTACGCTCATATGATGACAAGTGATTCCATTG                       | GCR2-N-AD                      |
|             | GCR2-N-AD-R             | CAGCTCGAGCTCGATGGATCCTTATACTTGTCCAAATTCTC                      |                                |
|             | GCR2-C-AD-F             | GTACCAGATTACGCTCATATGATGCTAGGCCATGCTTATAGAAC                   | GCR2-C-AD                      |
|             | GCR2-C-AD-R             | CAGCTCGAGCTCGATGGATCCTTAGGTTGCACTTGATGAATAAG                   |                                |
|             | GCR2-C $\Delta$ E-AD-R1 | CTATTATTATTGCTTGATTAGTTGTAGGCAGCAAATAATCTTTTC                  |                                |
|             | GCR2-C $\Delta$ E-AD-F2 | GAAAAAGATTATTTGCTGCCTACAATAATCAAGACAATAAATAG                   | GCR2-C $\Delta$ E-AD           |
|             | GCR2-C $\Delta$ E-AD-R2 | CAGCTCGAGCTCGATGGATCCTTAGGTTGCACTTGATGAATAAGAAGTGT<br>TTATACTG |                                |
|             | GCR1-BD-F               | TCAGAGGAGGACCTGCATATGATGGAAAATGCATCTTCTTCATCCA                 | GCR1-BD                        |
|             | GCR1-BD-R               | CTAGTTATGCGGCCGCTGCAGAAAGAGAAAGCATTGTGTTTATATCT                |                                |
|             | GCR2-BD-F               | TCAGAGGAGGACCTGCATATGATGACAAGTGATTCCATTGATCTGA                 | GCR2-BD                        |
|             | GCR2-BD-R               | CTAGTTATGCGGCCGCTGCAGGGTTGCACTTGATGAATAAGAAGGC                 |                                |
|             | SITOE1B-BD-F            | TCAGAGGAGGACCTGCATATGATGTTGGATCTGAATAATGATAGTG                 | SITOE1B-BD                     |
|             | SITOE1B-BD-R            | CTAGTTATGCGGCCGCTGCAGCTAGTTGGTGGGGAGACGTAA                     |                                |
|             | SITOE1B-C-DE-BD-F       | TCAGAGGAGGACCTGCATATGATGGAGAATTGGATTCTCTGCC                    | SITOE1B-C- $\Delta$<br>EAR -BD |
|             | SITPL2-BD-F             | TCAGAGGAGGACCTGCATATGATGTCTTCCCTGAGTAGGG                       | SITPL2-BD                      |
|             | SITPL2-BD-R             | CTAGTTATGCGGCCGCTGCAGTCACCTTGAAGGTGTTTCTG                      |                                |
|             | SITOE1B-DE-BD-F         | TCAGAGGAGGACCTGCATATGATGGATAGTGTTTTTTTCAAGG                    | SITOE1B- $\Delta$              |
|             | SITOE1B-DE-BD-R         | CTAGTTATGCGGCCGCTGCAGGTTGGTGGGGAGACGTAGTTGGTT                  | EAR-BD                         |
| <b>BIFC</b> | GCR1-2YN-F              | CATTTACGAACGATAGTTAATTAACATGGAAAATGCATCTTCTTC                  | GCR1-nYFP and                  |
|             | GCR1-2YN-R              | CCACCTCCTCCACTAGTGGCGCGCCCAAGAGAAAGCATTGTG                     | GCR1 $\Delta$ EAR -<br>nYFP    |
|             | GCR1-N-2YN-F            | CATTTACGAACGATAGTTAATTAACATGGAAAATGCATCTTCTTC                  | GCR1-N-nYFP                    |
|             | GCR1-N-2YN-R            | CCACCTCCTCCACTAGTGGCGCGCCCTGTGCCAGATTCATCAA                    |                                |
|             | GCR1-C-2YN-F            | CATTTACGAACGATAGTTAATTAACATGGTGTAGGGCATGGTAAT                  | GCR1-C-nYFP                    |
|             | GCR1-C-2YN-R            | CCACCTCCTCCACTAGTGGCGCGCCCAAGAGAAAGCATTGTG                     |                                |
|             | GCR2-2YN-F              | CATTTACGAACGATAGTTAATTAACATGACAAGTGATTCCATTG                   | GCR2-nYFP and                  |
|             | GCR2-2YN-R              | CCACCTCCTCCACTAGTGGCGCGCCCGGTTGCACTTGATGAATAAG                 | GCR2 $\Delta$ EAR -<br>nYFP    |
|             | GCR2-N-2YN-F            | CATTTACGAACGATAGTTAATTAACATGACAAGTGATTCCATTG                   | GCR2-N-nYFP                    |
|             | GCR2-N-2YN-R            | CCACCTCCTCCACTAGTGGCGCGCCCTACTTGTCCAAATCTC                     |                                |
|             | GCR2-C-2YN-F            | CATTTACGAACGATAGTTAATTAACATGCTAGGCCATGCTTATAGAAC               | GCR2-C-nYFP                    |
|             | GCR2-C-2YN-R            | CCACCTCCTCCACTAGTGGCGCGCCCGGTTGCACTTGATGAATAAG                 |                                |
|             | SITPL2-2YC-F            | CATTTACGAACGATAGTTAATTAACATGTCTTCCCTTGAGTAGGGA                 | SITPL2-cYFP                    |
|             | SITPL2-2YC-R            | CCACCTCCTCCACTAGTGGCGCGCCCCCTTGAAGGTGTTTCTG                    |                                |
|             | SITPL2-2YN-F            | CATTTACGAACGATAGTTAATTAACATGTCTTCCCTTGAGTAGGGA                 | SITPL2-nYFP                    |
|             | SITPL2-2YN-R            | CCACCTCCTCCACTAGTGGCGCGCCCCCTTGAAGGTGTTTCTG                    |                                |
|             | SITOE1B-N-2YC-F         | CATTTACGAACGATAGTTAATTAACATGTTGGATCTGAATAATGATAGTG             | SITOE1B-N-<br>cYFP             |
|             | SITOE1B-N-2YC-R         | CCACCTCCTCCACTAGTGGCGCGCCCACTACCACCATCTC                       |                                |
|             | SITOE1B-C-2YC-F         | CATTTACGAACGATAGTTAATTAACATGGAGAATCTTGATCTGAACC                | SITOE1B-C-<br>cYFP             |
|             | SITOE1B-C-2YC-R         | CCACCTCCTCCACTAGTGGCGCGCCCGTTGGTGGGGAGACGTAG                   |                                |
|             | SITOE1B-DE-2YC-F        | CATTTACGAACGATAGTTAATTAACATGGATAGTGTTTTTTTCAAGG                | SITOE1B- $\Delta$ EAR          |
|             | SITOE1B-DE-2YC-R        | CCACCTCCTCCACTAGTGGCGCGCCCGTTGGTGGGGAGACGTAGTTGGT<br>T         | -cYFP                          |
|             | 2YNC-F                  | GAAITCTCAACACAACATATAC                                         | nYFP                           |
|             | 2YN-R                   | CGTCGCCGTCCAGCTCGACCAG                                         |                                |

|                      | 2YC-R                 | GTGTTCTGCTGGTAGTGG                                          | eYFP                                    |
|----------------------|-----------------------|-------------------------------------------------------------|-----------------------------------------|
| <b>PULL<br/>DOWN</b> | NpGEX4T-GST-GCR1-F    | CCGCGTGGATCCCCGGAATTCATGGAAAATGCATCTTCTTC                   | GST-GCR1                                |
|                      | NpGEX4T-GST-GCR1-R    | GTCACGATGCGGCCGCTCGAGCTAAAGAGAAAGCATTGTGT                   |                                         |
|                      | NpGEX4T-GST-SITOE1B-F | CCGCGTGGATCCCCGGAATTCATGTTGGATCTGAATAATGATAGTG              | GST-rSITOE1B                            |
|                      | NpGEX4T-GST-SITOE1B-R | CCGCGTGGATCCCCGGAATTCATGTTGGATCTGAATAATGATAGTG              |                                         |
|                      | pET28a-HIS-SITOE1B-F  | AGAGAACAGATTGGTGGATCCATGTTGGATCTGAATAATGA                   | pET28a-HIS-rSITOE1B                     |
|                      | pET28a-HIS-rSITOE1B-R | GTGGTGGTGGTGGTCTCGAGCTAGTTGGTGGGAGACGTA                     |                                         |
|                      | NpGEX4T-GST-TPL2-F    | CCGCGTGGATCCCCGGAATTCATGCTTCTTGGATAGGGA                     | GST-TPL2                                |
|                      | NpGEX4T-GST-TPL2-R    | GTCACGATGCGGCCGCTCGAGCTACCTTGAAGGTGTTTCTGATG                |                                         |
|                      | pET28a-HIS-GCR1-F     | AGAGAACAGATTGGTGGATCCATGGAAAATGCATCTTCTTC                   | pET28a-HIS-GCR1 and<br>pET28a-HIS-mGCR1 |
|                      | pET28a-HIS-GCR1-R     | GTGGTGGTGGTGGTCTCGAGCTAAAGAGAAAGCATTGTGT                    |                                         |
|                      | pET28a-HIS-GCR2-F     | AGAGAACAGATTGGTGGATCCATGACAAGTGATTCCATTGATCTGA              | pET28a-HIS-GCR2 and<br>pET28a-HIS-mGCR2 |
|                      | pET28a-HIS-GCR2-R     | GTGGTGGTGGTGGTCTCGAGTTAGGTTGCACTTGATGAATAAG                 |                                         |
| <b>Y1H</b>           | GCR1-pJG-F            | CAGATTATGCCTCTCCCGAATTCATGGAAAATGCATCTTCTTC                 | GCR1-pJG                                |
|                      | GCR1-pJG-R            | GAAGAAGTCCAAAGCTTCTCGAGCTAAAGAGAAAGCATTGTG                  |                                         |
|                      | GCR2-pJG-F            | CAGATTATGCCTCTCCCGAATTCATGACAAGTGATTCCATTG                  | GCR2-pJG                                |
|                      | GCR2-pJG-R            | GAAGAAGTCCAAAGCTTCTCGAGTTAGGTTGCACTTGATGAA                  |                                         |
|                      | GCR1-mMYB-pJG-F       | CAGATTATGCCTCTCCCGAATTCATGGAAAATGCATCTTCTTC                 | GCR1mMYB-pJG                            |
|                      | GCR1-mMYB-pJG-R       | GAAGAAGTCCAAAGCTTCTCGAGAAGAGAAAGCATTGTGTTTATCT              |                                         |
|                      | GCR2-mMYB-pJG-F       | CAGATTATGCCTCTCCCGAATTCATGACAAGTGATTCCATTG                  | GCR2mMYB-pJG                            |
|                      | GCR2-mMYB-pJG-R       | GAAGAAGTCCAAAGCTTCTCGAGTTAGGTTGCACTTGATGAATAAG              |                                         |
|                      | pGCR1-1-placzi-F:     | GATGAATTGAAAAGCTTGAATTCCTGGAAGATCCTGCCCAGATG                | pGCR1-1-placzi                          |
|                      | pGCR1-1-placzi-R:     | ACATACAGAGCACATGCCTCGAGGGACAATGTCAAAATCAAACTG               |                                         |
|                      | pGCR1-2-placzi-F:     | GATGAATTGAAAAGCTTGAATTCCTTCTTATACATATGTTG                   | pGCR1-2-placzi                          |
|                      | pGCR1-2-placzi-R:     | ACATACAGAGCACATGCCTCGAGTTAGAAGAAGGATCAGACCAG                |                                         |
|                      | pGCR2-1-placzi-F:     | GATGAATTGAAAAGCTTGAATTCGTACAATCCATAAAGAAAAG                 | pGCR2-1-placzi                          |
|                      | pGCR2-1-placzi-R:     | ACATACAGAGCACATGCCTCGAGCAITTTTTTAAAAAATTGTGTTT              |                                         |
|                      | pGCR2-2-placzi-F:     | GATGAATTGAAAAGCTTGAATTCGAAATGAAGAAGAAACTTC                  | pGCR2-2-placzi                          |
|                      | pGCR2-2-placzi-R:     | ACATACAGAGCACATGCCTCGAGGAGACTTTATAATATTATATTATC             |                                         |
|                      | pLFS-2-placzi-F:      | GATGAATTGAAAAGCTTGAATTCGGATAAAATTACAAGTTAAC                 | pLFS-2-placzi                           |
|                      | pLFS-2-placzi-R:      | ACATACAGAGCACATGCCTCGAGCTGTATTACTCTGAGGACGC                 |                                         |
|                      | pLFS-4-placzi-F:      | GATGAATTGAAAAGCTTGAATTCATCACGACGCTAGATTGAC                  | pLFS-4-placzi                           |
|                      | pLFS-4-placzi-R:      | ACATACAGAGCACATGCCTCGAGCGATGTCGTTGCATATATTG                 |                                         |
|                      | pLFS-5-placzi-F:      | GATGAATTGAAAAGCTTGAATTCCTTCTATTTAATGCCCGTG                  | pLFS-5-placzi                           |
|                      | pLFS-5-placzi-R:      | ACATACAGAGCACATGCCTCGAGCGTTTTTGTAAATATGAA                   |                                         |
|                      | Motif1-placzi-F       | GATGAATTGAAAAGCTTGAATTCATAAGAATAATAAGAATAATAAGAA<br>TAA     | Motif1-placzi                           |
|                      | Motif1-placzi-R       | ACATACAGAGCACATGCCTCGAGTTATTCTTTATTATTCTTTATTCTTTA          |                                         |
|                      | Motif2-placzi-F       | GATGAATTGAAAAGCTTGAATTCATAAGAATAATAAGAATAATAAGAAT<br>TA     | Motif2-placzi                           |
|                      | Motif2-placzi-R       | ACATACAGAGCACATGCCTCGAGTAATTCTTATTAATTCTTATTAATTCTTA<br>T   |                                         |
|                      | Motif3-placzi-F       | GATGAATTGAAAAGCTTGAATTCAGGGAATCTAAGGGAATCTAAGGGA<br>ATCT    | Motif3-placzi                           |
|                      | Motif3-placzi-R       | ACATACAGAGCACATGCCTCGAGAGATTCCCTTAGAATCCCTTAGATTCC<br>CTT   |                                         |
|                      | Motif4-placzi-F       | GATGAATTGAAAAGCTTGAATTCATAATGGGAATAAATGGGAATAAATGG<br>GAA   | Motif4-placzi                           |
|                      | Motif4-placzi-R       | ACATACAGAGCACATGCCTCGAGTTCCCAITTTATCCCAITTTATCCCAITTT<br>A  |                                         |
|                      | Motif5-placzi-F       | GATGAATTGAAAAGCTTGAATTCACATTCTTTCCACATTCTTTCCACATT<br>CTTTC | Motif5-placzi                           |
|                      | Motif5-placzi-R       | ACATACAGAGCACATGCCTCGAGGAAAGAATGTGGAAAGAATGTGGAA            |                                         |

|                                         |                  |                                                            |                |
|-----------------------------------------|------------------|------------------------------------------------------------|----------------|
|                                         |                  | AGAAATGTG                                                  |                |
|                                         | Motif6-placzi-F  | GATGAATTGAAAAGCTTGAATTCCAAATTCCTATACAAATTCCTATACAAATTCTATA |                |
|                                         | Motif6-placzi-R  | ACATACAGAGCACATGCCTCGAGTATAGAATTTGTATAGAATTTGTATAGAATTTG   | Motif6-placzi  |
|                                         | Motif7-placzi-F  | GATGAATTGAAAAGCTTGAATTCCTAAATTCCTCTTAAATTCCTCTTAAATTCCTCT  |                |
|                                         | Motif7-placzi-R  | ACATACAGAGCACATGCCTCGAGAGAAGAATTTAAGAAGAATTTAAGAA          | Motif7-placzi  |
|                                         | Motif8-placzi-F  | GATGAATTGAAAAGCTTGAATTCACATTCCTCTACATTCCTCTCTACATTCTCTC    |                |
|                                         | Motif8-placzi-R  | ACATACAGAGCACATGCCTCGAGGAGAGAATGTAGAGAGAATGTAGAGAGAATGTA   | Motif8-placzi  |
|                                         | Motif9-placzi-F  | GATGAATTGAAAAGCTTGAATTCATATCTTTTAATATCTTTTAATATCTTTT       |                |
|                                         | Motif9-placzi-R  | ACATACAGAGCACATGCCTCGAGAAAAGAATATTAAGAATATTAAGAA           | Motif9-placzi  |
|                                         | Motif10-placzi-F | GAATTGAAAAGCTTAAAAATATCTCTTAAAAATATCTCTTAAAAATATCTCTT      |                |
|                                         | Motif10-placzi-R | TACAGAGCACATGCAAGAGAATAATTTTAAGAGAATAATTTTAAGAGAATAATTTT   | Motif10-placzi |
|                                         | Motif11-placzi-F | GATGAATTGAAAAGCTTGAATTCAGGAATATAGGAATATAGGAATAT            |                |
|                                         | Motif11-placzi-R | ACATACAGAGCACATGCCTCGAGATATTCCTATATTCCTATATTCCT            | Motif11-placzi |
|                                         | Motif12-placzi-F | GATGAATTGAAAAGCTTGAATTCGAGAGAATTTGAGAATTTGAGAATTT          |                |
|                                         | Motif12-placzi-R | ACATACAGAGCACATGCCTCGAGAAATTCCTCAAATTCCTCAAATTCCTC         | Motif12-placzi |
|                                         | Motif13-placzi-F | GATGAATTGAAAAGCTTGAATTCAGAAATATAGAATATAGAATTA              |                |
|                                         | Motif13-placzi-R | ACATACAGAGCACATGCCTCGAGTAATTCATAATTCATAATTCATA             | Motif13-placzi |
|                                         | Motif14-placzi-F | GATGAATTGAAAAGCTTGAATTCGGAATTAAGGAATTAAGGAATTA             |                |
|                                         | Motif14-placzi-R | ACATACAGAGCACATGCCTCGAGTAATCCATAATTCATAATTCATA             | Motif14-placzi |
|                                         | Motif15-placzi-F | GATGAATTGAAAAGCTTGAATTCGGAATAATGGAATAATGGAATAA             |                |
|                                         | Motif15-placzi-R | ACATACAGAGCACATGCCTCGAGTATTCATTAATTCATTAATTCATA            | Motif15-placzi |
|                                         | Motif16-placzi-F | GATGAATTGAAAAGCTTGAATTCAGGAATAAAGGAATAAAGGAATAA            |                |
|                                         | Motif16-placzi-R | ACATACAGAGCACATGCCTCGAGTATTCCTTTATTCCTTTATTCCT             | Motif16-placzi |
|                                         | Motif17-placzi-F | GATGAATTGAAAAGCTTGAATTCAGGAATGAAGGAATGAAGGAATGA            |                |
|                                         | Motif17-placzi-R | ACATACAGAGCACATGCCTCGAGTCATTCCTTCATTCCTTCATTCCT            | Motif17-placzi |
|                                         | Motif18-placzi-F | GATGAATTGAAAAGCTTGAATTCGGAATATGGAATATGGAATAT               |                |
|                                         | Motif18-placzi-R | ACATACAGAGCACATGCCTCGAGATATTCCTATATTCCTATATTCCT            | Motif18-placzi |
| <b>Luciferase assay and Co-IP assay</b> | 0800-GCR1-F      | CACTATAGGGCGAATTGGGTACCGGATTATTTAGTGGCAAGTTTG              |                |
|                                         | 0800-GCR1-R      | ATCGATACCGTCGACCTCGAGAATATATCCACTGAATATTTTCC               | 0800-pGCR1     |
|                                         | 0800-GCR2-F      | CACTATAGGGCGAATTGGGTACCTCCGAAAAAGAAAACCCAAAAG              |                |
|                                         | 0800-GCR2-R      | ATCGATACCGTCGACCTCGAGGATTATTAATGATGCAAGAACAATCCTG          | 0800-pGCR2     |
|                                         | pHBT-GCR1-F      | CTCCCTTGCTCCGTGGATCCATGGAATATGCAATCTTCTTATCCA              |                |
|                                         | pHBT-GCR1-R      | CTCGCCCTTGCTCACAGGCCTAAGAGAAAGCAATGTGTTTATATCT             | pHBT-pGCR1     |
|                                         | pHBT-GCR2-F      | CTCCCTTGCTCCGTGGATCCATGACAAGTGATTCATGTATCTGA               |                |
|                                         | pHBT-GCR2-R      | CTCGCCCTTGCTCACAGGCCTGGTTGCACCTTGATGAATAAGAAGGC            | pHBT-pGCR2     |
|                                         | pHBT-SITPL2-F    | CTCCCTTGCTCCGTGGATCCATGCTTCTCTTGAGTAGGGA                   |                |
|                                         | pHBT-SITPL2-R    | CTCGCCCTTGCTCACAGGCCTCTTGAAGGTGTTTCTGATG                   | pHBT-SITPL2    |
|                                         | pHBT-mSITOE1B-F1 | CTCCCTTGCTCCGTGGATCCATGGATAGTGTTTTTTCAAGG                  |                |
|                                         | pHBT-mSITOE1B-R1 | CTCCAAGGCAGAGAAATCCAAATCTCACCCTACCACCATC                   | pHBT-rSITOE1B  |
|                                         | pHBT-mSITOE1B-F2 | GATGGTGGTAGTGGTGAGAATGGATTTCTCTGCCTTTGGAG                  | △EAR           |
|                                         | pHBT-mSITOE1B-R2 | CTCGCCCTTGCTCACAGGCCTGTGGTGGGAGACGTAGTTGGTT                |                |
|                                         | pHBT-mGCR1-F1    | CTCCCTTGCTCCGTGGATCCATGGAATATGCAATCTTCTTC                  |                |
|                                         | pHBT-mGCR1-R1    | TTGTATCTGAGCTTCTGCTATCAGGTAAACCATTC                        | pHBT-GCR1 △    |
|                                         | pHBT-mGCR1-F2    | GAATGGTTACCTGATAGCAGAAGCTCAGATGACAA                        | EAR            |
|                                         | pHBT-mGCR1-R2    | CTCGCCCTTGCTCACAGGCCTAAGAGAAAGCAATGTGTTA                   |                |
|                                         | pHBT-mGCR2-F1    | CTCCCTTGCTCCGTGGATCCATGACAAGTGATTCATG                      | pHBT-GCR2 △    |

|                            |                     |                                                                |                |
|----------------------------|---------------------|----------------------------------------------------------------|----------------|
|                            | pHBT-mGCR2-R1       | GTCTTGATTAGTTGTGCTATCAGGCAGCAAATAATC                           | EAR            |
|                            | pHBT-mGCR2-F2       | GATTATTGCTGCCTGATAGCACAACTAATCAAGAC                            |                |
|                            | pHBT-mGCR2-R2       | TCGCCCTTGCTCAGAGCCTGGTTGCACTTGATGAATAAGAAGGCATAGT<br>GTTTATATC |                |
|                            | pHBT-GCR1mMYB-R1    | GAACGATGAAGGTCTGGAGTCGAACGTAGCCTTGCCAATT                       |                |
|                            | pHBT-GCR1mMYB-F2    | AATTGCCAAGGCTACGTTTCGACTCCAGACCTTCATCGTTC                      |                |
|                            | pHBT-GCR1-mMYB-R2   | CATCATTGTAGAACCAACTTGAGTGTGGCTCTTTCTTGAC                       | pHBT-          |
|                            | pHBT-GCR1-mMYB-F3   | GTCAAGAAAGAGCCACATCCAAGTTGGTTCTACAAATGATG                      | GCR1mMYB       |
|                            | pHBT-GCR1-mMYB-R3   | CTTGCTTCGATACATCTGGGAATGACTTTTACATGAG                          |                |
|                            | pHBT-GCR1-mMYB-F4   | CTCATGTAAAAAGTCATTCAGATGTATCGAAGCAAG                           |                |
|                            | pHBT-GCR2-mMYB-R1   | GAGAGATGAAGTTCAGGAGTCGATCTTAGCCTTGGCAATT                       |                |
|                            | pHBT-GCR2-mMYB-F2   | AATTGCCAAGGCTAAGATCGACTCCTGAACCTCATCTCTC                       |                |
|                            | pHBT-GCR2-mMYB-R2   | CATCATTGAAGAACCAATTGGAAGTTGCTCTTTCTTGAC                        | pHBT-          |
|                            | pHBT-GCR2-mMYB-F3   | GTCAAGAAAGAGCAACTTCCAAATGGTTCTTCAAATGATG                       | GCR2mMYB       |
|                            | pHBT-GCR2-mMYB-R3   | GTTTCTTGCTTCGATACATCTGGGAGTGACTTTTACATGGG                      |                |
|                            | pHBT-GCR2-mMYB-F4   | CCCATGTAAAAAGTCACTCCAGATGTATCGAAGCAAGAAAC                      |                |
|                            | pHBT-GCR1-NF        | CTCCCTTGCTCCGTGGATCCATGGAAAATGCATCTTCTTC                       | PHBT-GCR1-N    |
|                            | pHBT-GCR1-NR        | CTCGCCCTTGCTCAGGCTTGTGTCAGATTCATCAAGTTTC                       |                |
|                            | pHBT-GCR1-C-F       | CTCCCTTGCTCCGTGGATCCATGGTTAGGGCATGGTAAT                        | PHBT-GCR1-C    |
|                            | pHBT-GCR1-C-R       | CTCGCCCTTGCTCAGGCTAAGAGAAAGCATGTGTG                            |                |
|                            | pHBT-GCR2-NF        | CTCCCTTGCTCCGTGGATCCATGACAAGTGATCCATTG                         |                |
|                            | pHBT-GCR2-NR        | CTCGCCCTTGCTCAGGCTTACTTGTCCAAATCTCCAAG                         | PHBT-GCR2-N    |
|                            | pHBT-GCR2-C-F       | CTCCCTTGCTCCGTGGATCCATGCTAGGCCATGCTTATAGAAC                    |                |
|                            | pHBT-GCR2-C-R       | CTCGCCCTTGCTCAGGCTGGTTGCACTTGATGAATAAG                         | PHBT-GCR2-C    |
|                            | PXSN-Flag-SITOE1B-F | ATGATGATAAGCCAATACTTATGTTGGATCTGAATAATG                        |                |
|                            | PXSN-Flag-SITOE1B-R | GCTAGTGGATCCCCAATACTTAGTTGGTGGGAGACGTAG                        | FLAG-SITOE1B   |
|                            | PXSN-Flag-TPL2-F    | ATGATGATAAGCCAATACTTATGTTCTTCTTGAGTAGGGAAGTG                   |                |
|                            | PXSN-Flag-TPL2-R    | GCTAGTGGATCCCCAATACTTCAGTTAGATCCTTGGCTAAGATTC                  | FLAG-SITPL2    |
| <b>Quantitative RT-PCR</b> | GCR1-qPCR-F1        | TGGGTTTGAGGAAAAAGAATGG                                         | GCR1-GFP qRCR  |
|                            | GCR1-qPCR-R1        | GGACACGCTGAACCTGTGGC                                           |                |
|                            | GCR1-qPCR-F2        | GTCAATGGAGGAAAATAATTCAGTGG                                     | Endogenous     |
|                            | GCR1-qPCR-R2        | GCCTTGGCAATTTTGATCGA                                           | GCR1 qRCR      |
|                            | GCR2-qPCR-F         | ATGGAATTGCACATATAACAGCC                                        |                |
|                            | GCR2-qPCR-R         | ATATCTGATGAGTTTCTCTCTTCTG                                      | GCR2 qRCR      |
|                            | GCR2-qPCR-F2        | CACTATGCTCTCTCTTCTTTTGCTCTCT                                   |                |
|                            | GCR2-qPCR-R2        | ACCAACCCGGTGAACAGCT                                            | GCR2-GFP qRCR  |
|                            | GCR2-qPCR-F3        | TTGGGATTGAGCACAACTAATCAAG                                      | Endogenous     |
|                            | GCR2-qPCR-R3        | TCCATCCATTTGTGACACATCA                                         | GCR2 qRCR      |
|                            | PeGCR-qPCR-F        | AGTGGGGAGGAATGTAGTGAGAAAA                                      | PeGCR qPCR     |
|                            | PeGCR-qPCR-R        | GTGAAGGTCAGGAGTCCAACGAA                                        |                |
|                            | NbGCR-qPCR-F        | CTCCTGAACCTCCATCGCTCCTT                                        |                |
|                            | NbGCR-qPCR-R        | GCTTCTCCCTTGCAATTGCTTTAT                                       | NbGCR qPCR     |
|                            | SITOE1B-qPCR-F      | CTCCTCCTTCCAGCCTTCACTTT                                        |                |
|                            | SITOE1B-qPCR-R      | ACCCAGCGGATTCGGACAC                                            | SITOE1B qPCR   |
|                            | LFS-qPCR-F          | GCCCAAGCCCATTAATCTGTGA                                         |                |
|                            | LFS-qPCR-R          | GTCTCCCATATGTTGTCTCCTG                                         | LFS qPCR       |
|                            | miR156B-RT          | GTGTAATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGTGCTC             |                |
|                            | miR156B-F           | GCGGCGGTGACAGAAGAGAGT                                          |                |
|                            | miRNA-R             | GTGCAGGGTCCGAGGTATTC                                           | miR156B qRCR   |
|                            | U6-F                | TCTAACAGTGTAGTTTGTCCCTTCG                                      |                |
|                            | U6-R                | TTGTGCGTGTATCCTTGC                                             |                |
|                            | ChipQ-pGCR1-1-F     | CGTGAAGATCCTGGCCGCATG                                          | pGCR1-1 ChipQ- |
|                            | ChipQ-pGCR1-1-R     | GGACAATGTTCAAATCAAACTG                                         | qRCR           |
|                            | ChipQ-pGCR1-2-F     | CTTTCCTCTTATACATATGTTG                                         | pGCR1-2        |
|                            | ChipQ-pGCR1-2-R     | TTAGAAGAAGGATCAGACCAG                                          | ChipQ-qRCR     |

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|                |                         |            |
|----------------|-------------------------|------------|
| ChipQ-pLFS-2-F | TCTTCGATCAAATGCGTCCTC   | pLFS-2     |
| ChipQ-pLFS-2-R | CGGTGTATTCAAAGAAGCGTTGT | ChipQ-qRCR |
| ChipQ-pLFS-5-F | GTGCAACGCGTAAATTCTTC    | pLFS-5     |
| ChipQ-pLFS-5-R | CGAAGTAGTTTGTGCAGGAGAG  | ChipQ-qRCR |

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