(a)

```
Program TSSPlant
Search for RNA II promoters (TSSs)Input file with query sequence(s): /home/apache/tmp/RRhSfX.TSSPlant
Thresholds, for TATA      promoters:   1.52
                TATA-less promoters:  -0.04
Out of TSSs of different (TATA and TSTS-less) classes located at distance  300bp or less, TSS with higher score is selected
Search only on Sense Strand


Query: >Chr1:29421866..29422452
Length of Query sequence:    587
+ chain  (TATA-) TSS position:    533   TSS score =   1.8436
+ chain  TSS position:    231   TSS score =   1.9844     TATA-box position:    200   TATA-box score =   7.7807
     2 promoter(s) predicted
```

(b)

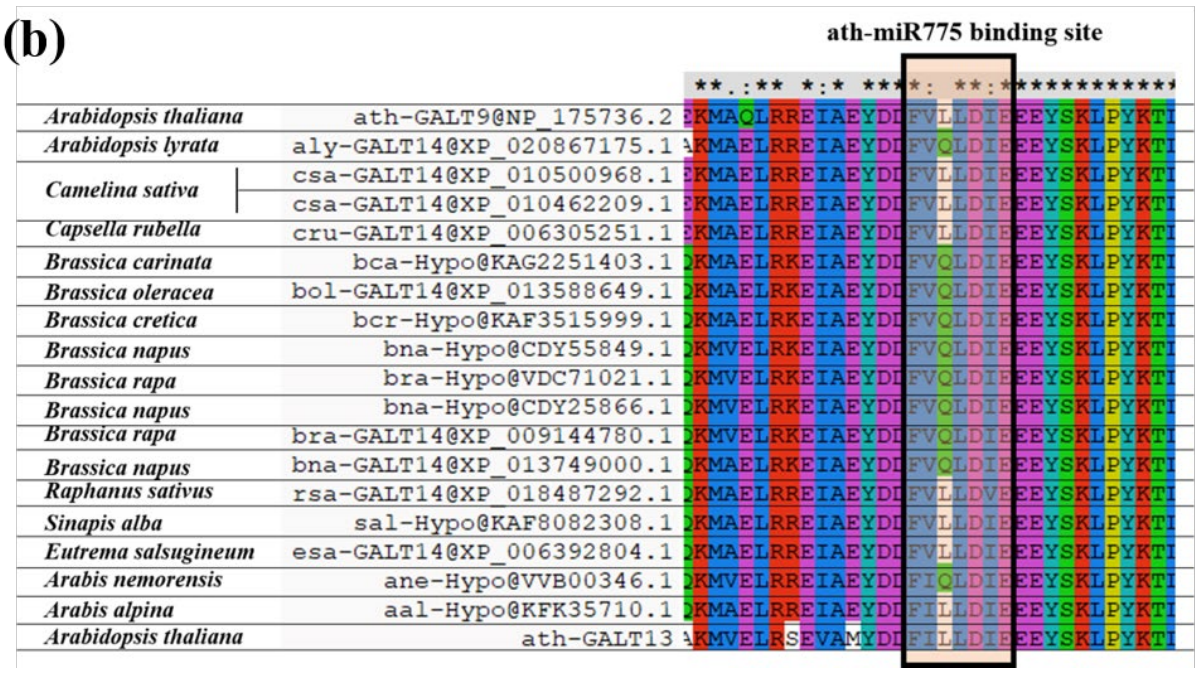


Fig. S1. *In silico* analysis of miR775 and its target GALT9. (a) A screenshot of the result of program TSSPlant showing predicted Transcription Start Site (TSS) and TATA-Box. **(b)** Multiple sequence alignment of *GALT9* homologs showing miR775 binding site conservation.

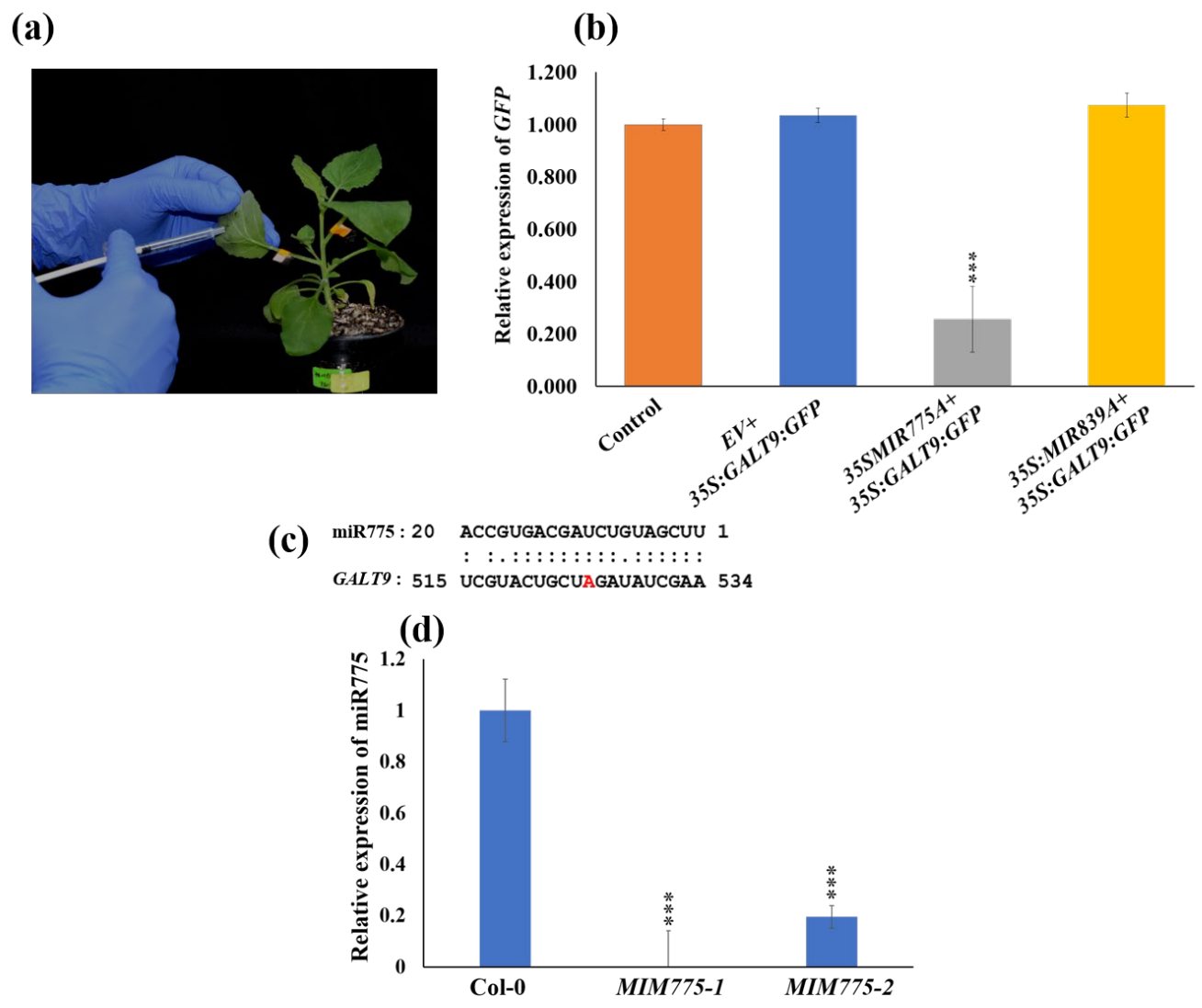


Fig. S2. miR775 *c*leaves its predicted target *GALT9* in a transient assay carried out in tobacco (*N. benthamiana)* leaves. (a) Co-infiltration of *MIR775A* and *GALT9* (*35S:MIR775A+35S:GALT9:GFP*) wiin leaf of tobacco plants (~4 weeks old). **(b)** Relative expression level of *GFP* in control (*35S:GALT9:GFP*), EV *+35S:GALT9:GFP*, *35S:MIR775A+35S:GALT9:GFP*, and *35S:MIR839A+35S:GALT9:GFP*. **(c)** Sequence alignment of the mature miR775 with the target *GALT9*. **(d)** Relative expression of mature miR775 in *MIM775* lines.

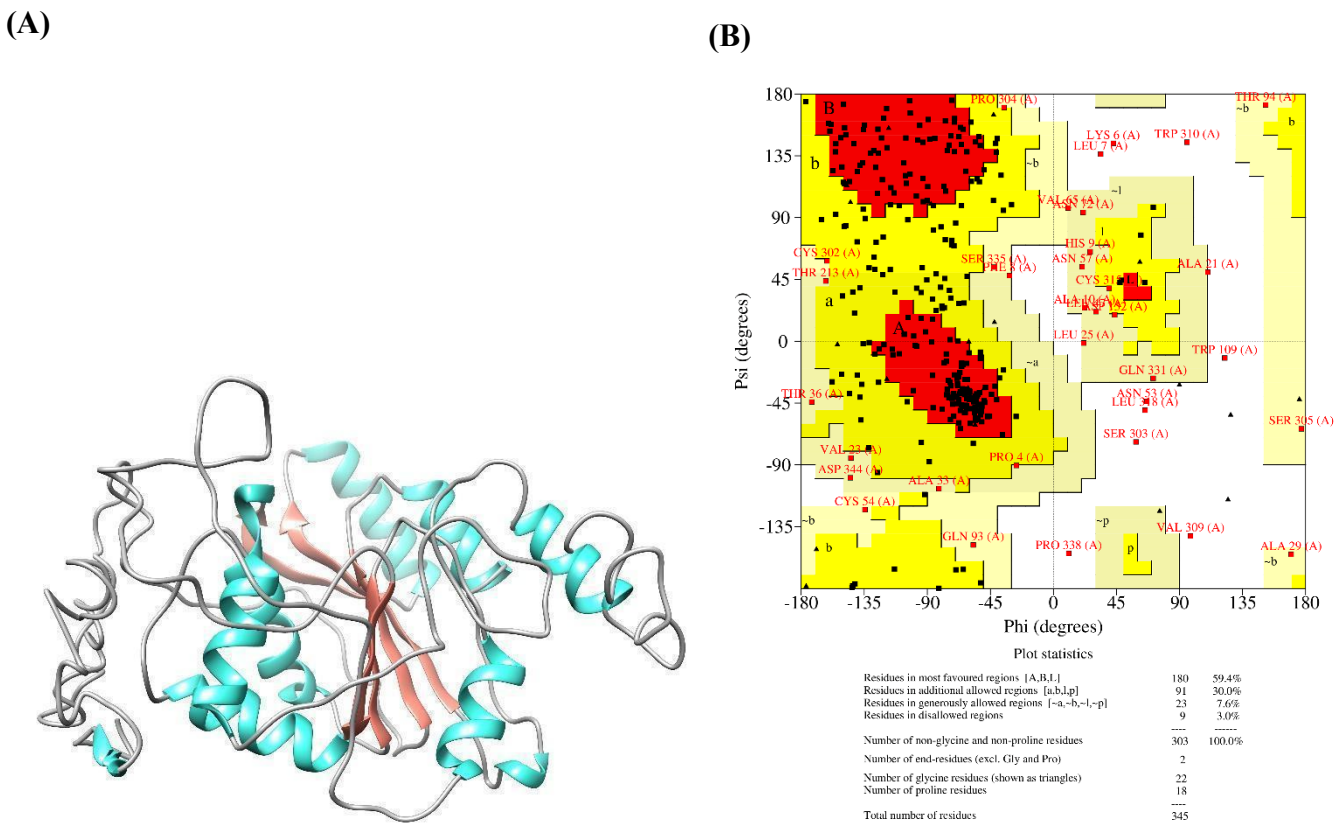
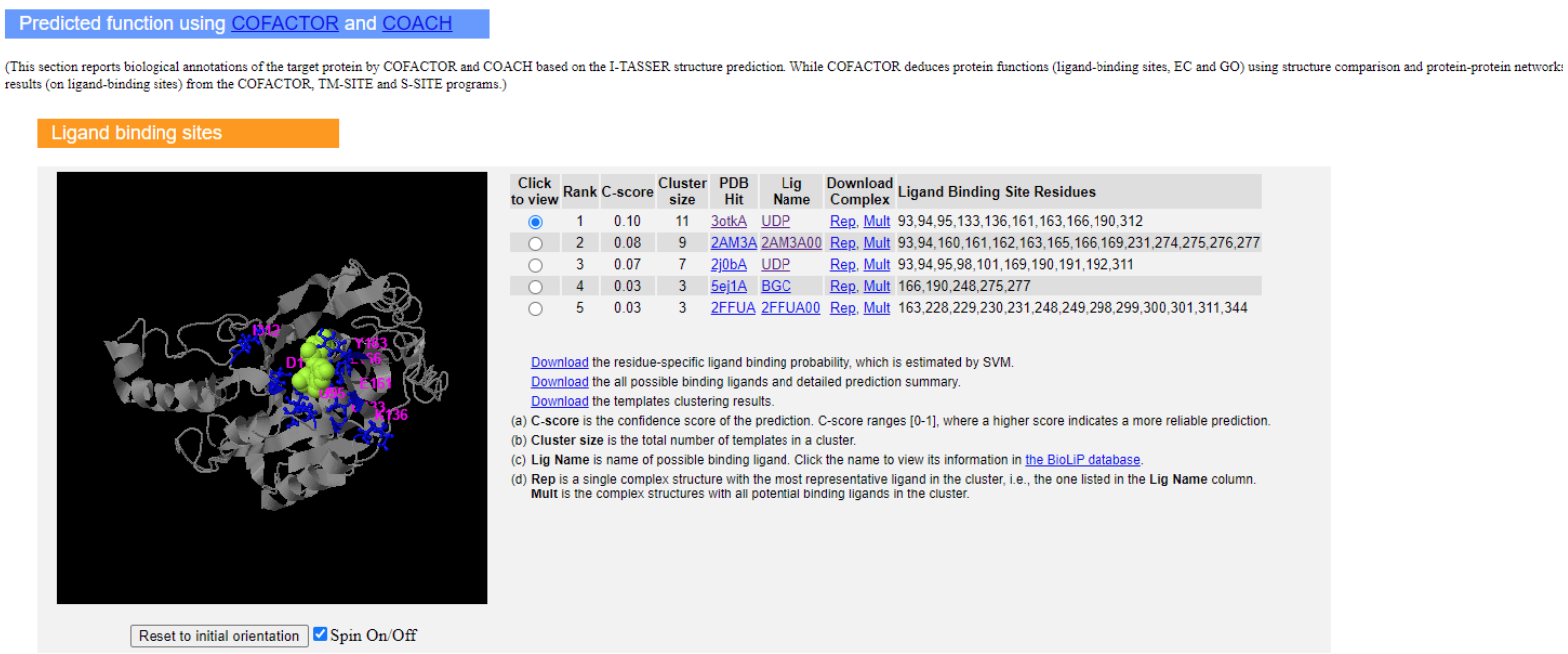


Fig. S3. **Modeled 3D structure of GALT9 and its quality check. (A)** Best predicted model of GALT9 through I-TASSER and visualized through UCSF Chimera v1.14. The α-helix is represented in cyan, β-sheets in brown and the coiled coil in grey. **(B)** Stereochemical quality was checked through Ramachandran plot available online at PROCHECK server (https://saves.mbi.ucla.edu/), showing 97% of amino acids were in allowed region.

(A)



Predicted function using COFACTOR and COACH

(This section reports biological annotations of the target protein by COFACTOR and COACH based on the I-TASSER structure prediction. While COFACTOR deduces protein functions (ligand-binding sites, EC and GO) using structure comparison and protein-protein network results (on ligand-binding sites) from the COFACTOR, TM-SITE and S-SITE programs.)

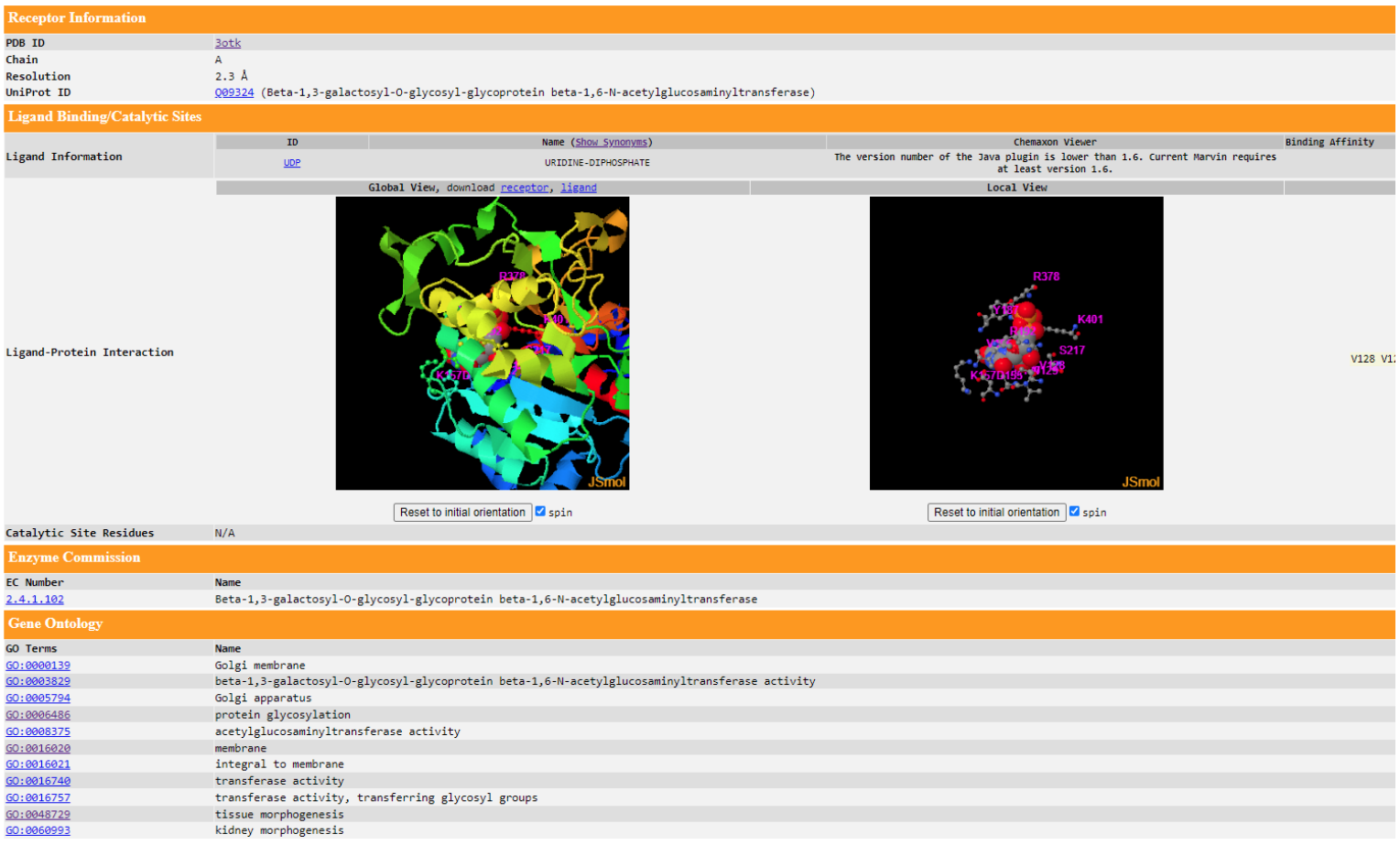
Ligand binding sites

Click to view	Rank	C-score	Cluster size	PDB Hit	Lig Name	Download Complex	Ligand Binding Site Residues
◉	1	0.10	11	3otkA	UDP	Rep, Mult	93,94,95,133,136,161,163,166,190,312
○	2	0.08	9	2AM3A	2AM3A00	Rep, Mult	93,94,160,161,162,163,165,166,169,231,274,275,276,277
○	3	0.07	7	2j0bA	UDP	Rep, Mult	93,94,95,98,101,169,190,191,192,311
○	4	0.03	3	5ej1A	BGC	Rep, Mult	166,190,248,275,277
○	5	0.03	3	2FFUA	2FFUA00	Rep, Mult	163,228,229,230,231,248,249,298,299,300,301,311,344

Download the residue-specific ligand binding probability, which is estimated by SVM.
Download the all possible binding ligands and detailed prediction summary.
Download the templates clustering results.

(a) **C-score** is the confidence score of the prediction. C-score ranges [0-1], where a higher score indicates a more reliable prediction.
(b) **Cluster size** is the total number of templates in a cluster.
(c) **Lig Name** is name of possible binding ligand. Click the name to view its information in the BioLiP database.
(d) **Rep** is a single complex structure with the most representative ligand in the cluster, i.e., the one listed in the **Lig Name** column. **Mult** is the complex structures with all potential binding ligands in the cluster.

(B)



Receptor Information

PDB ID	3otk
Chain	A
Resolution	2.3 Å
UniProt ID	Q09324 (Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase)

Ligand Binding/Catalytic Sites

	ID	Name (Show Synonyms)	Chemaxon Viewer	Binding Affinity
Ligand Information	UDP	URIDINE-DIPHOSPHATE	The version number of the Java plugin is lower than 1.6. Current Marvin requires at least version 1.6.	

Ligand-Protein Interaction

Catalytic Site Residues: N/A

Enzyme Commission

EC Number	Name
2.4.1.102	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase

Gene Ontology

GO Terms	Name
GO:0000139	Golgi membrane
GO:0003829	beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase activity
GO:0005794	Golgi apparatus
GO:0006486	protein glycosylation
GO:0008375	acetylglucosaminyltransferase activity
GO:0016020	membrane
GO:0016021	integral to membrane
GO:0016740	transferase activity
GO:0016757	transferase activity, transferring glycosyl groups
GO:0048729	tissue morphogenesis
GO:0060993	kidney morphogenesis

Fig. S4. Functional annotation of GALT9 through in silico analysis. (A) Screenshot of I-TASSER result showing predicted biological annotation of GALT9. **(B)** Screenshot of BioLiP (biologically relevant ligand-protein binding interactions) database 50wing the Function Annotation of 3otk, which is a significant PDB hit of predicted GALT9 3D structure.

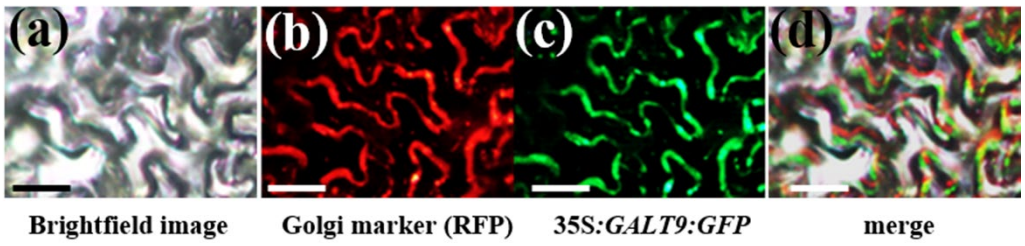


Fig. S5. GALT9 localizes in the Golgi apparatus of a cell. The fluorescent protein-tagged GALT9 fusion proteins were co-expressed with GmMan*I*-pBIN2 (mCherry Golgi apparatus marker) 6into the abaxial side of a young in tobacco (*N. benthamiana)* leaf epidermis. The signals were visualized 6 under a fluorescence microscope. **(a)** Bright field image of leaf epidermal cells. **(b)** Fluorescence image of *GmManI-pBIN2* (Golgi apparatus marker). **(c)** Fluorescence image of *35S:GALT9:GFP*. **(d)** Image was merged with fluorescence image of GmMan*I*-pBIN2 and *35S:GALT9:GFP.* Scale bar = 50 µm.

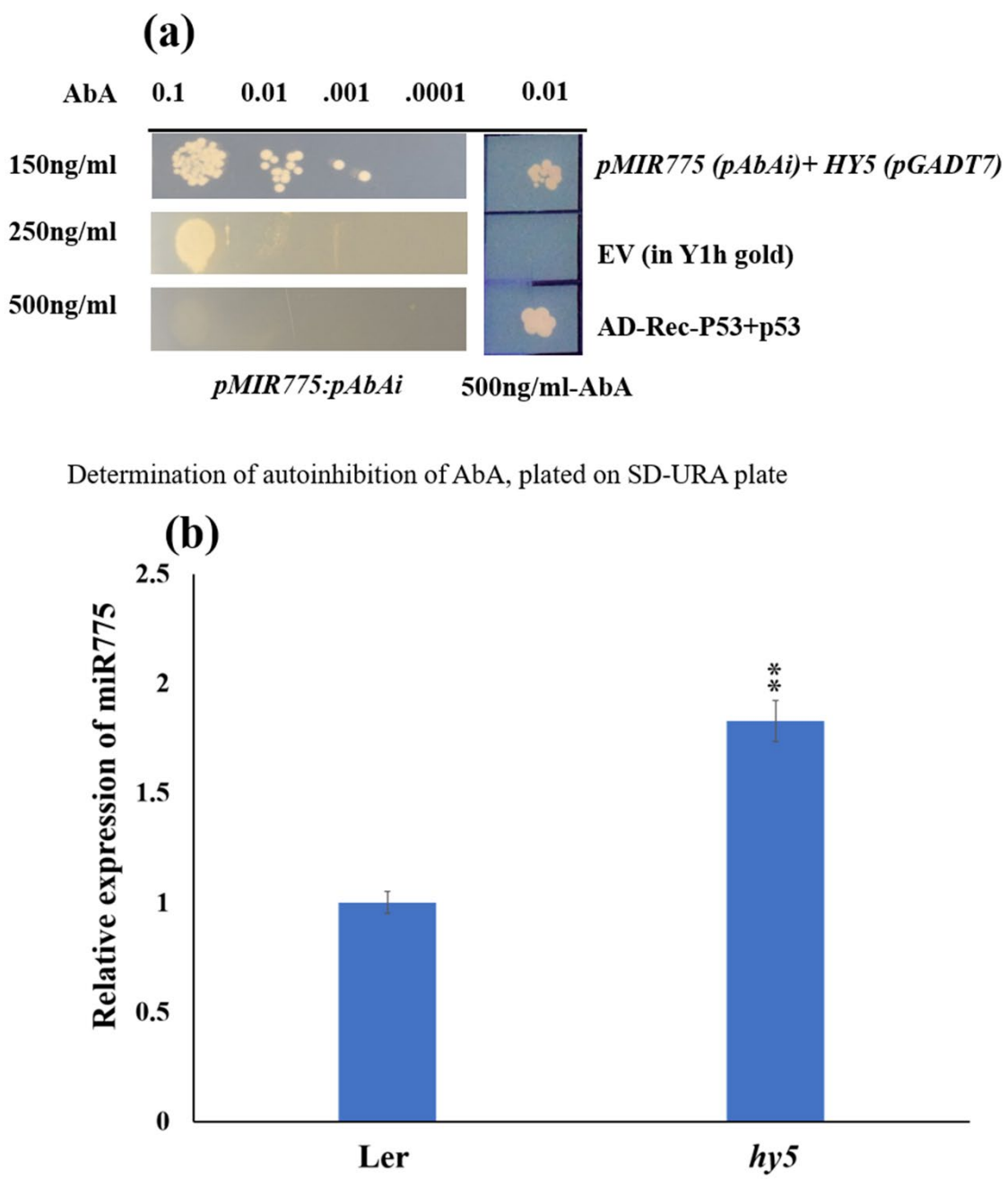


Fig. S6. HY5 binds to the promoter of *MIR775A* and regulates its expression. (a) Determination of autoactivation, represents Yeast one hybrid (Y1H) assay showing the interaction of HY5 with *pMIR775A*. *HY5* CDS + *pGADT7* transformed into *pMIR775A* + pAbAi was used to check the interaction. pGADT7-Rec-p53/ p53-AbAi was used as a positive control. pGADT7 transformed into a Y1H gold cell used a negative control. **(b)** Expression of miR775 in hy5 mutant background.

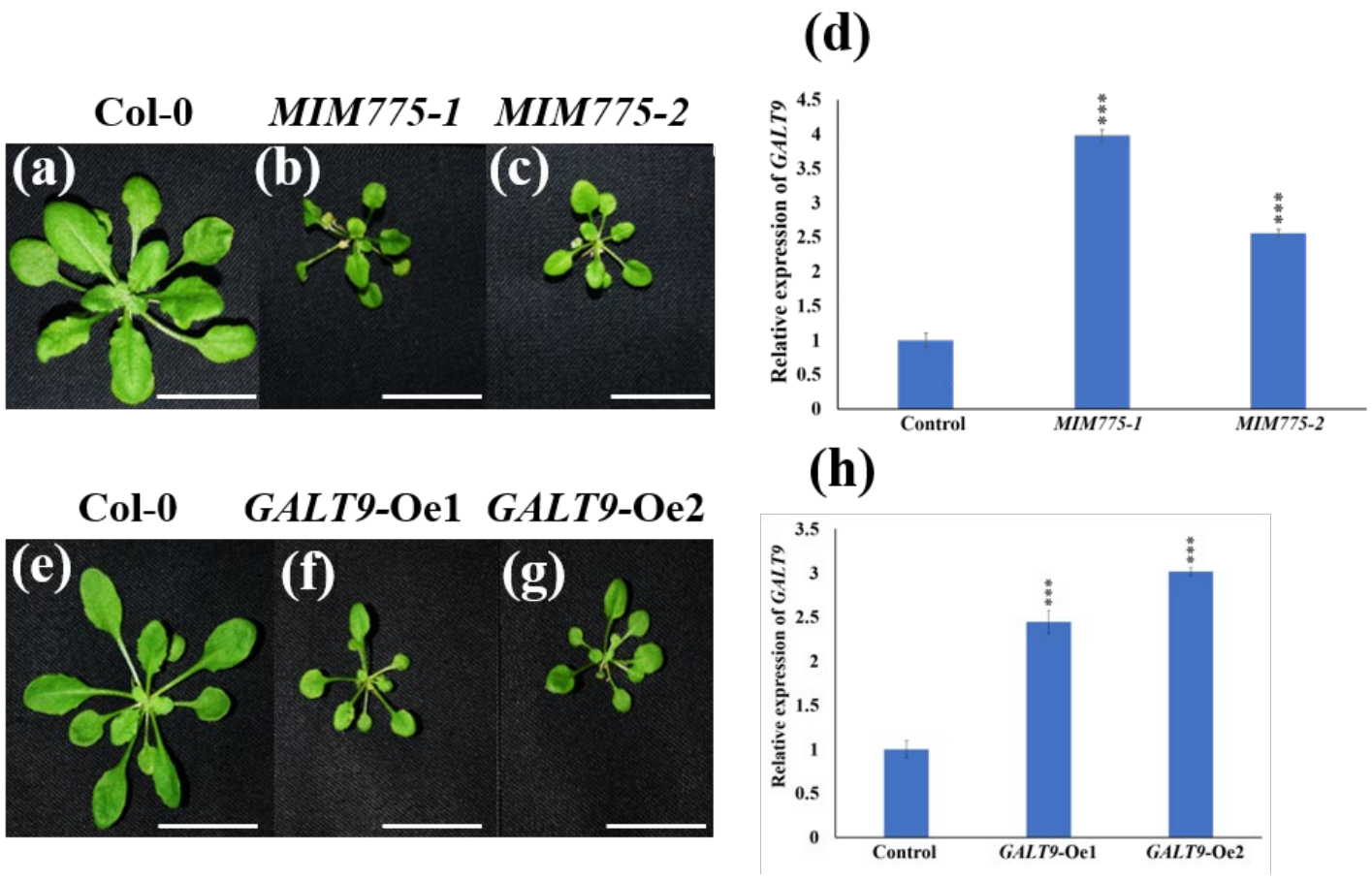


Fig. S7. Phenotypic comparison of *MIM775* and *GALT9* regulating leaf sizes in *A. thaliana*. **(a-c)** Phenotypic comparison of *MIM775* in two independent lines of *MIM775* (*MIM775-1*, *MIM775-2*). **(d)** Relative expression of *GALT9* in two independent lines *MIM775-1* and *MIM775-2*. **(e-g)** Phenotypic comparison of *GALT9* in two independent lines of *GALT9* overexpression (*GALT9*-Oe1 and *GALT9*-Oe2). **(h)** Relative expression of *GALT9* in two independent lines of *GALT9*-Oe1 and *GALT9*-Oe2. Scale bar= 2.5 cm.

Table S1. List of probable targets of miR775 validated through cleaveland software using degradome PARE data of 11-days seedling (SRR3143654).

Click here to download Table S1

Table S2. List of probable targets of miR775 validated through cleaveland software using degradome PARE data of Sample leaf of stage 5 (SRR3143654).

Click here to download Table S2

Table S3. List of primers used in the study.

Click here to download Table S3

Table S4. List of coexpressed gene with GALT9.

Click here to download Table S4