Table S1. *LpGDSL* open reading frame sequence

name	sequence
The open reading frame sequence of *LpGDSL*	ATGGTCAGCACTGGATTTATTGTTCATCATGTGGTG GTGGCTGCGGCTGCATTAGTCCTCATCTTGTCTGCA CTTCCCAGCGGAAGTGCACAGCCACTCGTTCCGGC CATCATCACATTTGGCGACTCAGCAGTCGATGTGGG AAACAATGACTACCTCCCTACCCTCTTCAAAGCTGA TTTCCCTCCTTATGGGCGGGATTACAAAAACCATCA AGCCACCGGGAGGTTCTGTAACGGGAAATTGGCTA CTGATATCACTGCTGAAACTCTGGGATTCACGAGCG TCCCCCCGCCATACCTCAGCCCACAGGCCTCGGGAA AGAACCTTCTCATAGGAGCTAATTTTGCTTCAGCTGC CTCTGGGTATTATGATGAAACTGCCATTTTGTATAAAG CCATCCCATTATCTCAACAGTTGGAGTACTACAAAGA GTACCAGTCCAAGTTGAAGTCTGTTGCTGGGAGTGG GAAGGCGACCTCCATCCTATCAGGGGCGCTGTACATC ATTGGCGCTGGGAGCAGCGACTTCATACAAAACTACT ATGTCAATCCATACCTCAACAAGATCTACAGCCCCGA TGAGTACTCTTCCTTCCTTGTCAGCATCTTCTCAAATT TTGTCAAGGACCTATACGGCCTTGGGGCTCGAAGGAT TGGAGTGACATCACTGCCGCCATTGGGGTGCCTCCCC TTATCCAAAAATATCTTTGGTTACGGTAAAAGTGGCTG TGTTGCGAACTTCAATGCTGATGCCAGAAACTTCAAC AAGAAGGTCACGGCAGCGATCGACTCACTCACTAAG AAGTTTCCAAACCTTAAGATCGCTGCCCTCGACATCTA CACGCCTCTTCTCGAACTAGCCACCAATCCATCAAAAA ACGGTTTCTTTGAGGCGGGGAGAGGCTGCTGCGGGAC AGGGACGGTGGAGACGACATCGTTCCTCTGCAACCCC AAGTCGCTCGGGACATGCTCAAACGCAACCGGCTACG TGTTCTGGGACAGTGTGCACCCATCCCAAGCTGCAAAC CAGTTTATCGCGGATTCGCTCATCCTTGCAGGCATTTCC CTCGTTTCGTGA

Table S2. Primers were used in this study

Primer Name	Primer Sequence
LpGDSLF	ATGGTCAGCACTGGATTT
LpGDSLR	TCACGAAACGAGGGAAAT
*LpGDSL B*amH I *F*	ggatccATGGTCAGCACTGGAT
*LpGDSL X*ho I *R*	ctcgagTCACGAAACGAGGGAA
LpGDSL qPCR *F*	TTAAGATCGCTGCCCTCGAC
LpGDSL qPCR *R*	CACGAAACGAGGGAAATGCC
LpActin F	GCATCACACCTTCTACAACG
LpActin R	GAAGAGCATAACCCTCATAGA
*LpGDSL Eco*R I *F*	gaattcATGGTCAGCACTGGATTT
*LpGDSL Bam*H I *R*	ggatccTCACGAAACGAGGGAAAT
LpBCP F	ATGGCTGGTGCTGTAGT
LpBCP R	TTAGCCAAATAATGCAA
*LpBCP Eco*R I *F*	gaattcATGGCTGGTGCTGTA
*LpBCP Bam*H I *R*	ggatccTTAGCCAAATAATGC

LpGDSL Pro SP1	AAGGTTCTTTCCCGAGGCCTGT
LpGDSL Pro SP2	TTTCCCGTTACAGAACCTCCCG
LpGDSL Pro SP3	GCCAAATGTGATGATGGCCGGA
LpGDSL Pro F	CACATTGATGCCTGACTCAC
LpGDSL Pro R	CTTGGTTCTCTGGCACAAAC
LpGDSL Pro Hind III F	AAGCTTCACATTGATGCCTGACTCAC
LpGDSL Pro Xho I R	CTCGAGCTTGGTTCTCTGGCACAAAC
*LpB3 Bam*H I F	ggatccTCGCAAGTATGCCTGGTT
LpB3 Xho I R	ctcgagATTCGAGACCCTCAACTC
LpGDSL Pro Xho I F	ctcgagGCCTTAATTAACCAACTGCA
*LpGDSL Pro Bam*H I R	ggatccCTTGGTTCTCTGGCACAA
LpGDSL-KpnI-F	ggtaccATGGTCAGCACTGG
LpGDSL-SalI-R	gtcgacTCACGAAACGAGGG
LpBCP-SmaI-F	cccgggATGGCTGGTGCTGT
LpBCP-SpeI-R	actagtTTAGCCAAATAATGC

Table S3 Candidate interacting proteins obtained by yeast two-hybrid screening of *LpGDSL*

serial number	gene name	gene annotation
1	SYP23	Syntaxin of plants, key proteins that regulate vesicle transport (Ibrahim et al., 2020)
2	PHB3	antiproliferative protein Prohibitin3 (Li et al., 2022)
3	CP47	Photosystem II CP47 reaction center protein (Bečková et al., 2022); One of the components of the core complex of photosystem II (PSII). It binds chlorophyll and helps catalyze the primary light- induced photochemical processes of PSII.
4	IGPD	Imidazole glycerol-phosphate dehydratase; Belongs to the imidazole glycerol-phosphate dehydratase family (Qu et al., 2021).
5	HISN6	Histidinol-phosphate aminotransferase (Rutkiewicz et al., 2023)
6	PMM2	Phosphomannomutase (Zhang et al., 2016)
7	BRISC and BRCA1-A	Multifunctional Molecular Machines for Ubiquitin Signaling (Rabl, 2020)
8	EARLI 1	Early Arabidopsis aluminum induced 1, also a member of the lipid transfer protein family (Feng et al., 2014).
9	WVD2	Wave-dampened 2, a novel microtubule-associated protein (Perrin et al., 2007)
10	COBRA	A family of glycosyl-phosphatidyl inositol (GPI) anchoring proteins composed of COBL proteins family of anchoring proteins (Zhang et al., 2023)
11	BAH1	E3 ubiquitin-protein ligase (Xu et al., 2018)
12	GMP	GDP-mannose pyro phosphorylase (Fu et al., 2023)

Table S4 Sequence of *LpGDSL* promoter

name	sequence
LpGDSL promoter sequence	GCCTTAATTAACCAACTGCATACTAGATAGGTAATA TATGGTAAAGTAGATTAGAAACACCTTAGATAATTT CTTTATTATCAATTTTGATTATATACTCTGATTTCAC CTTTTTAGTACTGACCCGTGCGCTGCGGACTAGCCA GCCAACCCCATGCATGCTTTTGTTTGAGAAGGTACC TGGCTTAATCTAACAGGCAACAGCTAATCCACATTA CATCAGTCCATCAACCTGCACAAATTGCTGGCTCGC TGTATAATCTTGTTCACAGAATTGTCTATGTGACCTT TGCCCTTCACCGCTCAAGTCCCGGTACAAGTACCCT TTTCCATCTACCAACAACTACTACATTAATTATATGT TAGAATTGTTTCACTGCCACTTATTTTAGGAGATTAT CGACACAGAAAATTGGAGTACGAAACAATTTTTCTT TCTTTCCGCCTTAACCACGGCTCACTGCTGAATAGCC CTATCCATCTCTCTGGAGTTGGTCCAATCTATATTTA GACTATTAAAATGTAAGCAAGAGGAGAACTACTTA ACCTTCTGTACCACTTTCCCCTTCATATGAGGAACAA TGAGGCAGCTGGAGTTTCCATTTAATGGAAAAGGCA GCCCGGTGTTCCTTGTAATGATATGTCCACTGTATTG CTCTTCCCAACCACCCTGCCATATCAATAAACCTAA TAAAGAGCCACCTTAGTTGTTGTAAGGATTGATGGA CAATGTGGGATGGATCTCTGCTTGTGCTAGCTTTTTA AAAGTTTGCCCACATGTATGCCTTCAATGCTCTTTAA CAAACCCCTTAGACTTTCCTAACAATCACCTCCATAT ATATGGGTCTATCCTCCCAGTAGAGCTTGTACCTGT AAAGCTGGCATTGTTTGTGCCAGAGAACCAAG

Table S5 Analysis of Promoter Region Action Elements in *LpGDSL*

cis-element	Motif (5'-3')	Function	Frequency
CAAT box	CAA	Regulates the transcription initiation of downstream genes and frequency	19
MYC	CATGTG	MYC binding site	1
MRE	AACCTAA	MYB binding sites involved in light response	1
GARE-motif	TCTGTTG	Gibberellin response element	1
Box 4	ATTAAT	Conserved DNA modules involved in light response part of the conserved DNA module involved in light response	1
STRE	AGGGG	Osmotic stress response element	2
RY-element	CATGCATG	Cis-acting elements involved in seed-specific regulation	1
Myb-binding site	CAACAG	Myb binding site	1

GCN4_motif	TGAGTCA	Cis-regulatory elements involved in endosperm expression	1
CAT-box	GCCACT	Cis-acting elements associated with phloem tissue expression	1
ABRE	CGCACGTGTC	Cis-actions involved in the abscisic acid reaction component	1
GATA-motif	GATAGGG	Part of a light-responsive element	1
MYB	CAACAGTAACCA CAACCA	MYB binding site	3
P-box	CAACAAACCCCT T	Gibberellin response element and light response element	1
GT1-motif	GGTTAA	Components for Light Response	2
LAMP-element	CTTTATCA	Part of a light-responsive element	1
RAV1AAT	CAACA	The AP2 and B3 sample domains of RAV1 are connected through a highly flexible structure connecting this highly flexible structural linkage, allowing these two domains to interact with the CAACA and CACCTG motifs in a variety of spacings and CAACA and CACCTG motifs in various spacings and orientations. sequences.	1

Figure S1. The conserved domain of LpGDSL protein. Predictive analysis of conserved structural domains of LpGDSL proteins using the Conserved Domain Search function on the NCBI website. The results showed the presence of a highly conserved structural domain SGNH phytolipase at position 300-1165 amino acids, which belongs to the SGNH hydrolase
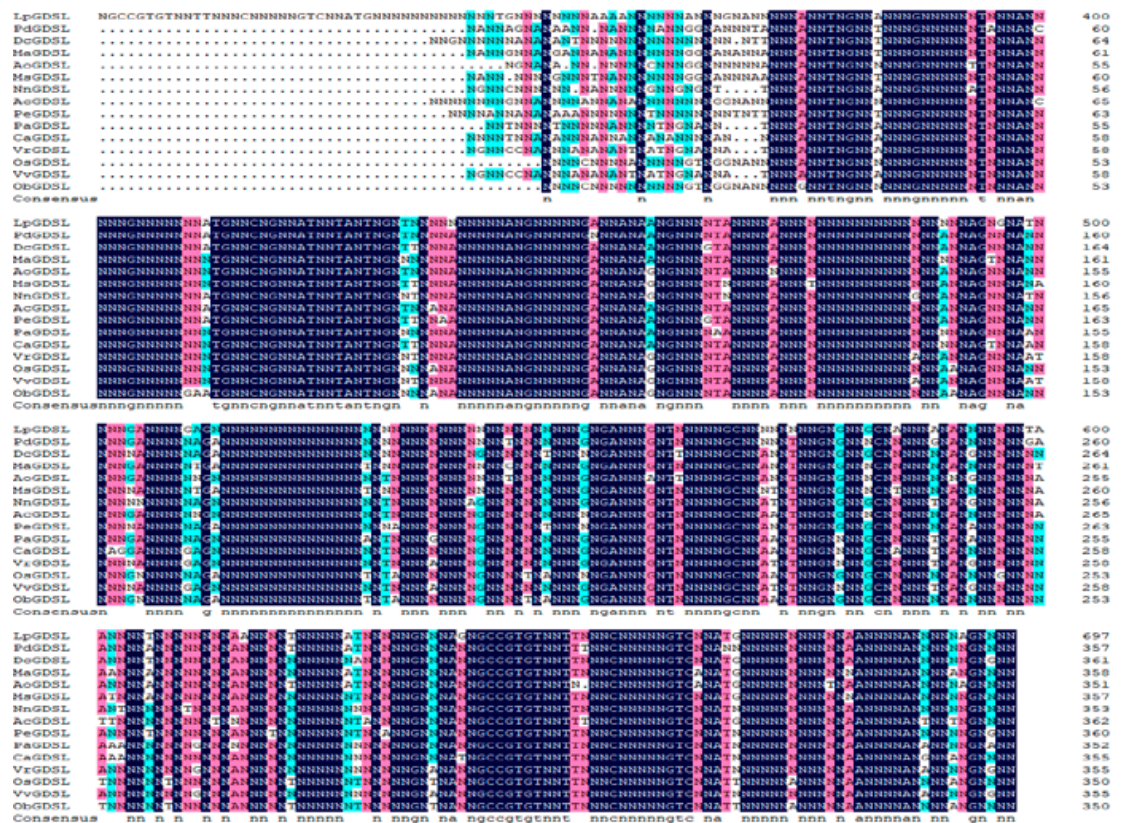
superfamily.

Figure S2. Amino acid sequence alignment of LpGDSL with homologous proteins. The amino acid sequences of GDSL cloned from lily of the valley were compared with those of GDSL proteins from other species by using DNA Man software. The dark blue indicates the highly conserved region of the sequence, the light blue indicates the similar region of the sequence, and the pink indicates the more similar region of the sequence.
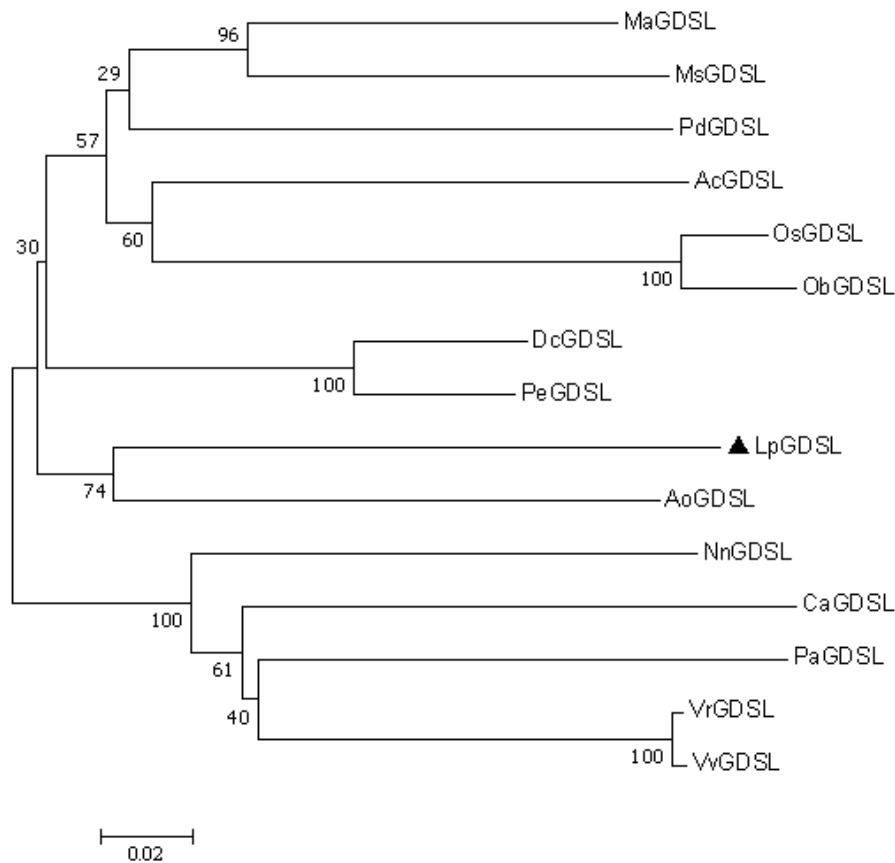
Figure S3. Phylogenetic tree analysis of LpGDSL. The MEGA7 program was used for the construction of phylogenetic trees.

Figure S4. Identification of *L. pumilum* overexpressing *LpGDSL*. Leaf tissues of wild-type and transgenic *L. pumilum* were selected, and their cDNAs were used as templates for real-time

fluorescence quantitative PCR assay to observe the expression levels of *LpGDSL* in wild-type and four transgenic plants. "*" indicates significant difference, Student's *t* test (P < 0.05, ± SEM); "**" indicates extremely significant difference, Student's *t* test (0.01 < P < 0.05, ± SEM); "***" indicates extremely significant difference, Student's *t* test (P < 0.01, ± SEM).

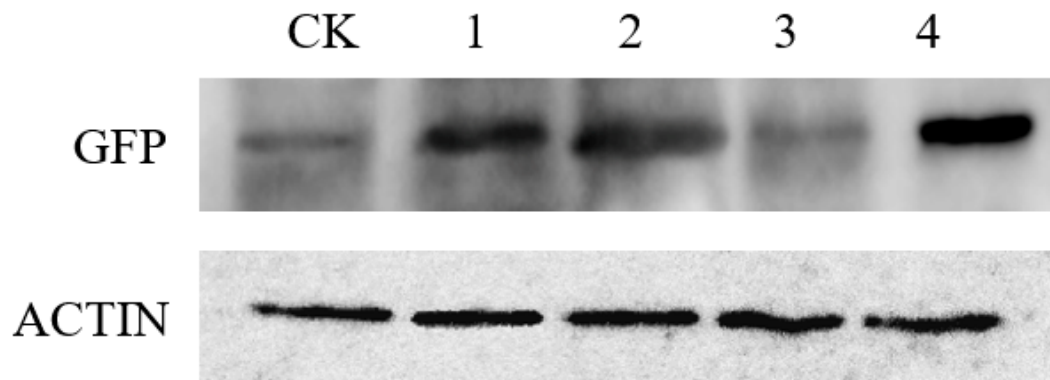Figure S5. Western-blot of *L. pumilum* overexpressing *LpGDSL* under stresses. CK: Wild type control; 1: Under the stress treatment of 2 M H_2O_2; 2: Under the stress treatment of 0.6 M NaCl; 3: Under the stress treatment of 0.5 M Na_2CO_3; 4: Under the stress treatment of 0.5 M $NaHCO_3$.

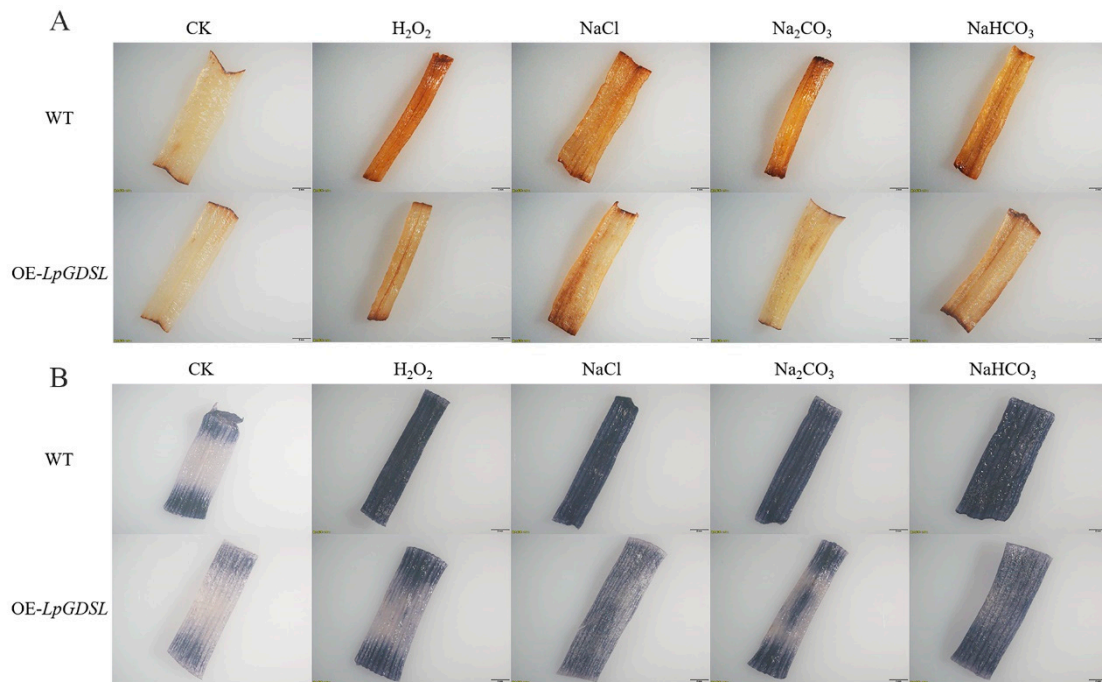Figure S6. DAB and NBT staining of wild-type and overexpression plants under stress. After irrigation stress with 2 M H_2O_2, 0.6 M NaCl, 0.5 M Na_2CO_3, and 0.5 M $NaHCO_3$, the same parts of wild-type (WT) and overexpression *L. pumilum* (OE-*LpGDSL*) leaf were cut and stained with DAB and NBT, respectively. In situ NBT and DAB staining methods were used to detect the accumulation of O_2^- and H_2O_2 in seedling leaves, which reflected the ability of LpGDSL to reduce ROS content in plants. The deeper the blue color is, the more O_2^- accumulated. The darker the brown color is, the more H_2O_2 is accumulated. Under normal culture conditions (CK), both wild-type and overexpression plants were lightly colored. Both wild-type and overexpression plants became darker in color after stress treatment. However, the overexpression plants were significantly lighter in color than the wild-type plants, indicating that the ac-cumulation of O_2^- and H_2O_2 in the overexpression plants was significantly lower than that in the wild-type.CK: No treatment has been done. Scale bar = 200 μm.
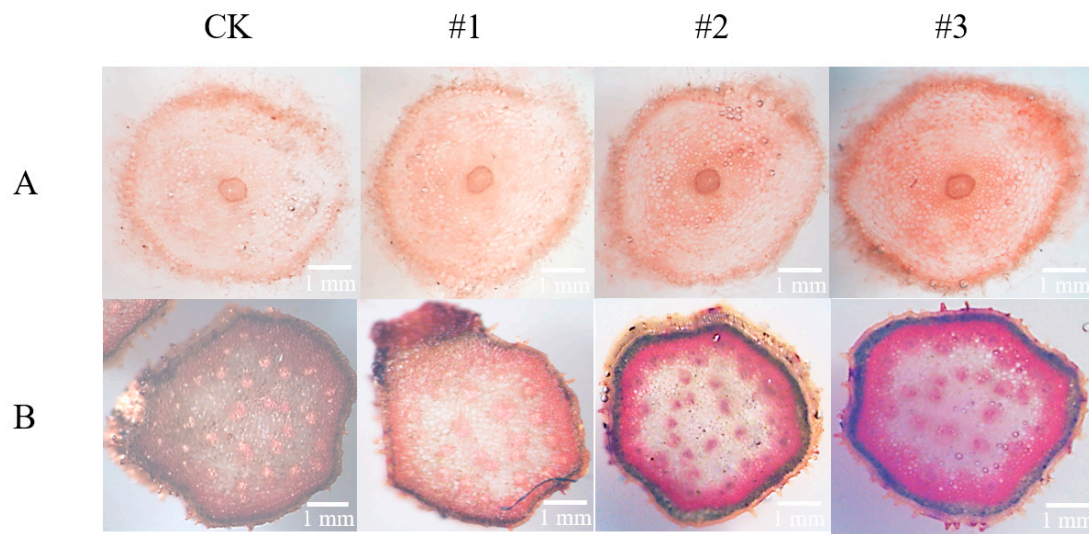
Figure S7. A. Thrombosed staining of *LpGDSL* transgenic *L. pumilum*. Stem corkiness of wild-type and overexpressed *LpGDSL L.Pumilum* stained for Sudan III. B. Lignification of *LpGDSL* transgenic *L. pumilum*. Lignin staining of stems of wild-type and overexpressed *LpGDSL L.Pumilum*. CK: Wild-type. *L.Pumilum*. #1, #2, #3: overexpressed *L. pumilum*. Do 3 repetitions of the over expression. Scale bar = 1 mm.
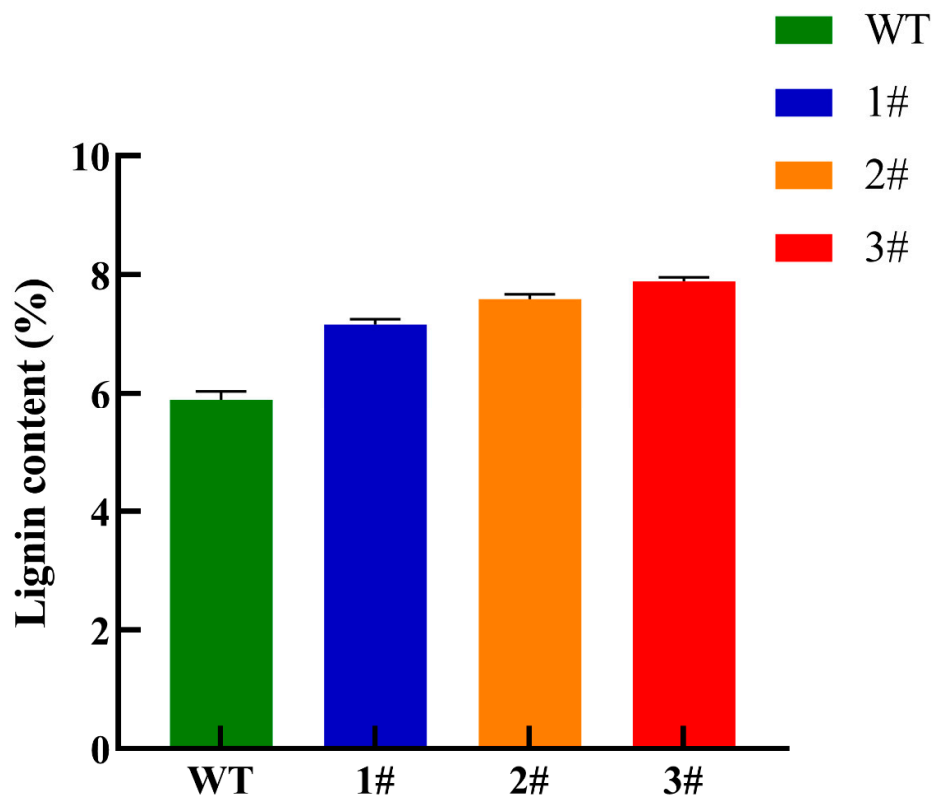
Figure S8. Lignin content in stems of WT and *LpGDSL* overexpressing plants. Lignin content was determined by UV spectrophotometry. Wild-type and overexpression plants with uniform growth were selected as experimental materials. Do three biological replicates. WT: Wild-type. #1, #2, #3: overexpressed *L. pumilum*.
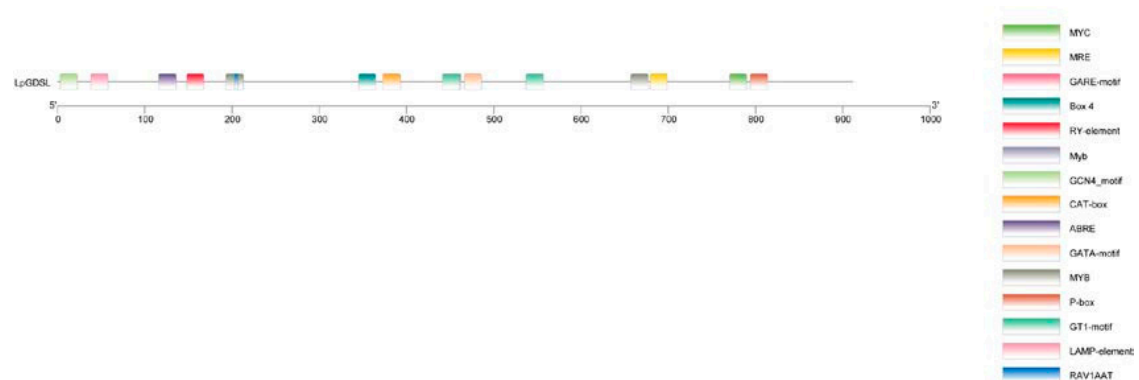

Figure S9. Analysis of Promoter Region Action Elements in *LpGDSL*.

Plant care software was used to analyses the promoter region of *LpGDSL* for its action elements.

TBtools software was used to map the screened actors.