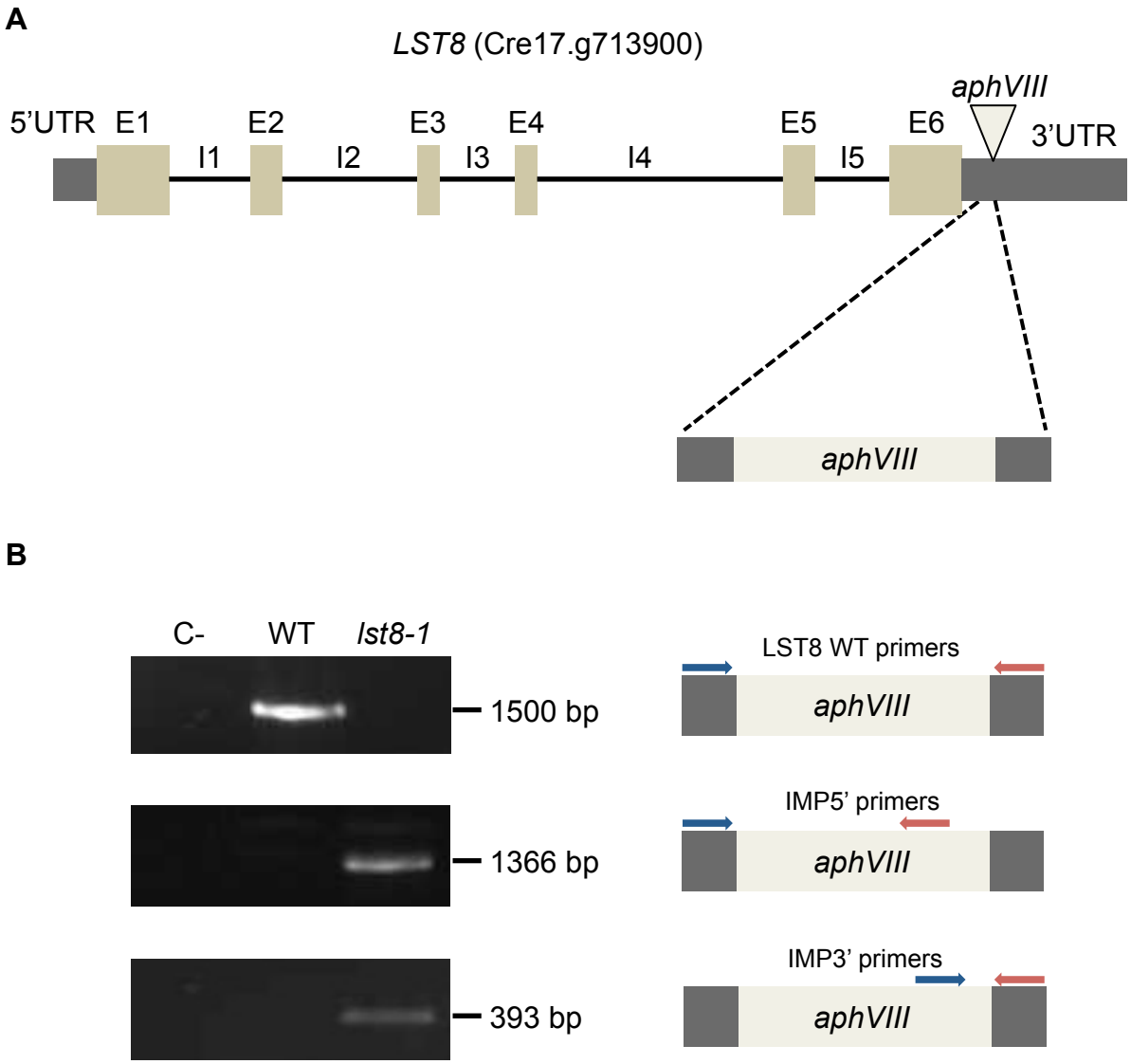
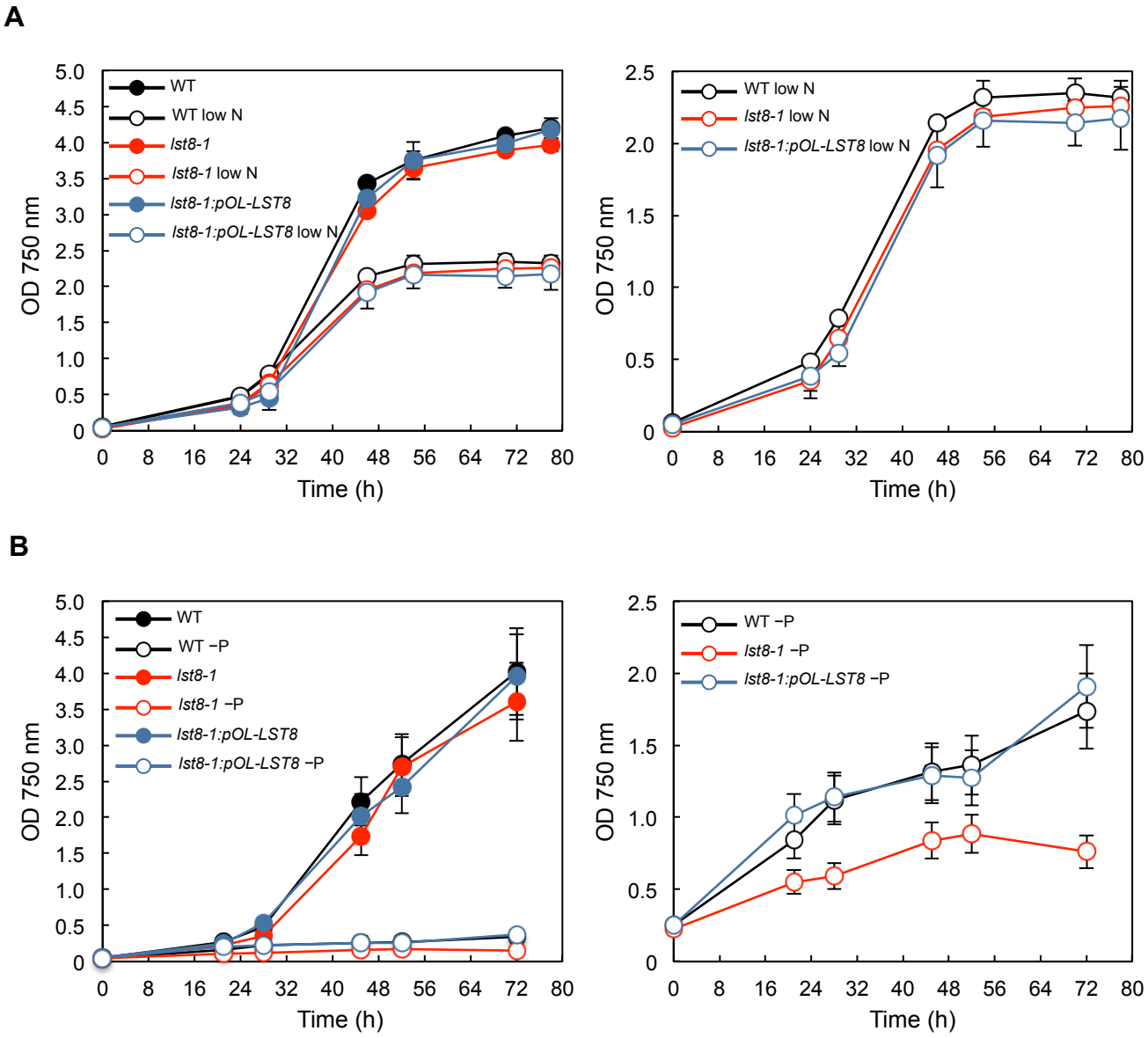
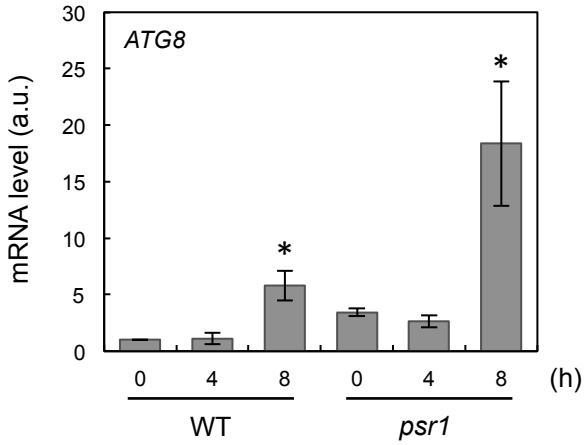


Supplemental Figure 1. The *lst8-1* Mutant Carries an Insertion at the *LST8* 3´UTR. (Supports Figure 1).
(A) Schematic representation of the *aphVIII* insertion in the *LST8* gene. **(B)** Insertional mutagenesis PCR test using LST8 WT primers (top panel), IMP5´ insertional mutagenesis primers (middle panel) and IMP3´ insertional mutagenesis primers (bottom panel). E: exon; I: intron; UTR: untranslated region.

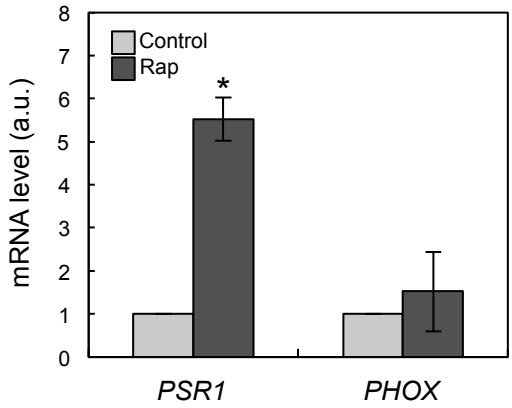


Supplemental Figure 2. Growth of Wild-Type and *lst8-1* Strains under N or P Limitation. (Supports Figure 1).

(A) Left: Wild-type, *lst8-1* and complemented *lst8-1* strains were grown to early exponential phase in TAP medium. Cells were then washed twice with N free medium and shifted to medium containing 1 mM ammonium chloride (low N) as the N source. Right: Data corresponding to N limitation are presented in a separate graph to show the growth curves in more detail. **(B)** Left: Growth of WT, *lst8-1* and complemented *lst8-1* strains in P-replete or P-free (-P) medium. Cells grown to early exponential phase in TAP medium were washed twice with P-free medium and then shifted to the same medium. Right: Data corresponding to P starvation are presented in a separate graph to show the growth curves of WT and *lst8-1* cells in more detail. For **(A)** and **(B)**, experiments were performed at 25ºC under continuous light. Data correspond to mean values of three independent biological replicates for each strain and condition. Error bars indicate the standard deviations of the mean values.



Supplemental Figure 3. RT-qPCR Analysis of *ATG8* in Wild-Type (WT) and *psr1* Strains. (Supports Figure 3). Data show results of RT-qPCR analyses of relative *ATG8* transcript abundance in WT and *psr1* strains treated with 500 nM rapamycin at different times (0, 4 and 8 h) (a.u., arbitrary units). Three biological replicates with three technical replicates were analyzed for each condition.
*, differences were significant according to Student's *t* test, $P < 0.05$. Error bars indicate standard deviations from the mean values.



Supplemental Figure 4. RT-qPCR Analysis of *PSR1* and *PHOX* following Rapamycin Treatment. (Supports Figure 3).

Data show results of RT-qPCR analyses of relative *PSR1* and *PHOX* transcript abundance in WT cells treated with rapamycin for 8 h (a.u., arbitrary units). Three biological replicates with three technical replicates were analyzed for each condition. *, differences were significant according to Student's *t* test, $P < 0.05$. Error bars indicate standard deviations from the mean values.

Supplemental Table 1. Nucleotide Sequences of Primers Used in this Study.

Name	Sequence (5' to 3')
Primers for Genotyping	
LST8_p5´	GTGCCTCATATCACCCGACT
LST8_p3´	AGGATGTCCGTCGAAGTTTG
IMP5´	GCACCAATCATGTCAAGCCT
IMP3´	GACGTTACAGCACACCCTTG
LST8F1	CAGCCTCCTCGGACGCCACTGCCC
LST8R1	TGTCCTGAACAGCCAGCACGCC
Primers for Tagging with the OLLAS Epitope	
LST8OLLR	ACCATTTCCGTGATTGATAGCGcttgcccatcagcctcgggcccagctcgttgg
LST8OLLF	GGCGCGACGTGGACGGGTAAAgcggcttcgccaacgagctgggcccgaggctga
Primers for RT-qPCR	

Name	Sequence (5' to 3')	Reference
5´PSR1	5´-GCGCAGAGTCCTTTGCAA-3´	1
3´PSR1	5´-CGGCGCTAGTTCGTGAAA-3´	
5´PHOX	5´-TTCCGTTTCCGTTCTCTGAC-3´	1
3´PHOX	5´-CCCTGCATCTTGTTCTCCAG-3´	
5´ATG8	5´-TCCCCGATATCGACAAGAAG-3´	2
3´ATG8	5´-TGCGGATGACGTACACAAAT-3´	
5´CBLP	5´-CTTCTCGCCCATGACCAC-3´	2
3´CBLP	5´-CCCACCAGGTTGTTCTTCAG-3´	

1. Bajhaiya AK, Dean AP, Zeef LA, Webster RE, Pittman JK (2016). Plant Physiol, 170(3):1216-1634.
2. Pérez-Martín M, Pérez-Pérez ME, Lemaire SD, Crespo JL (2014). Plant Physiol, 166 (2):977-1008.