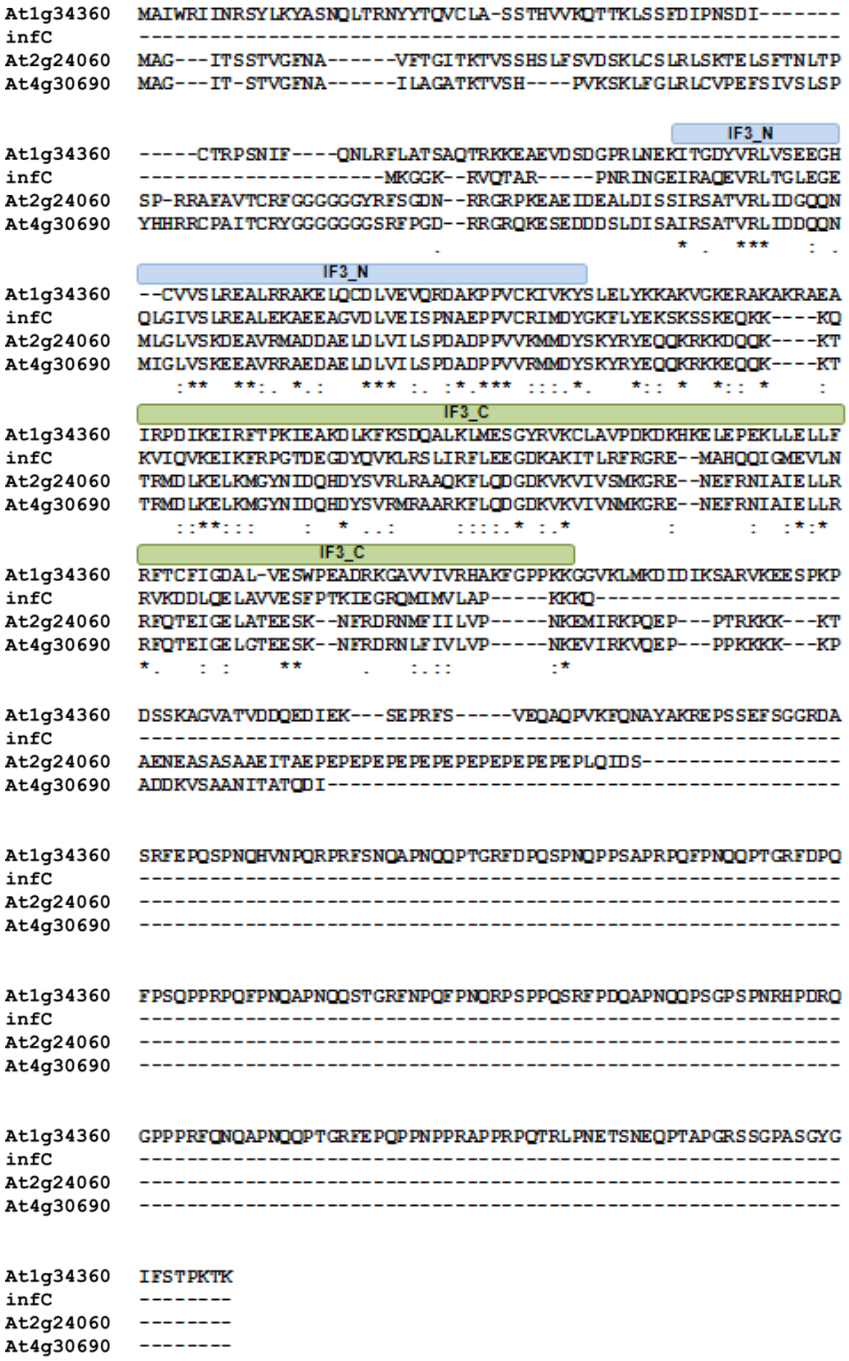
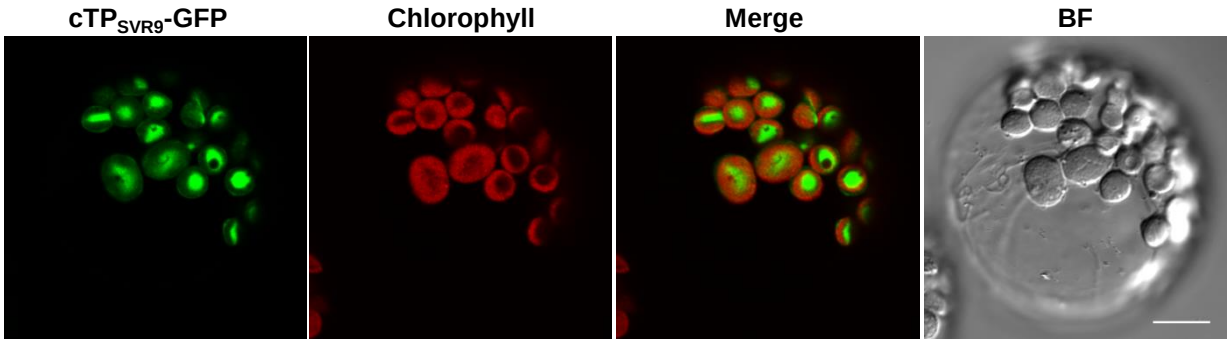
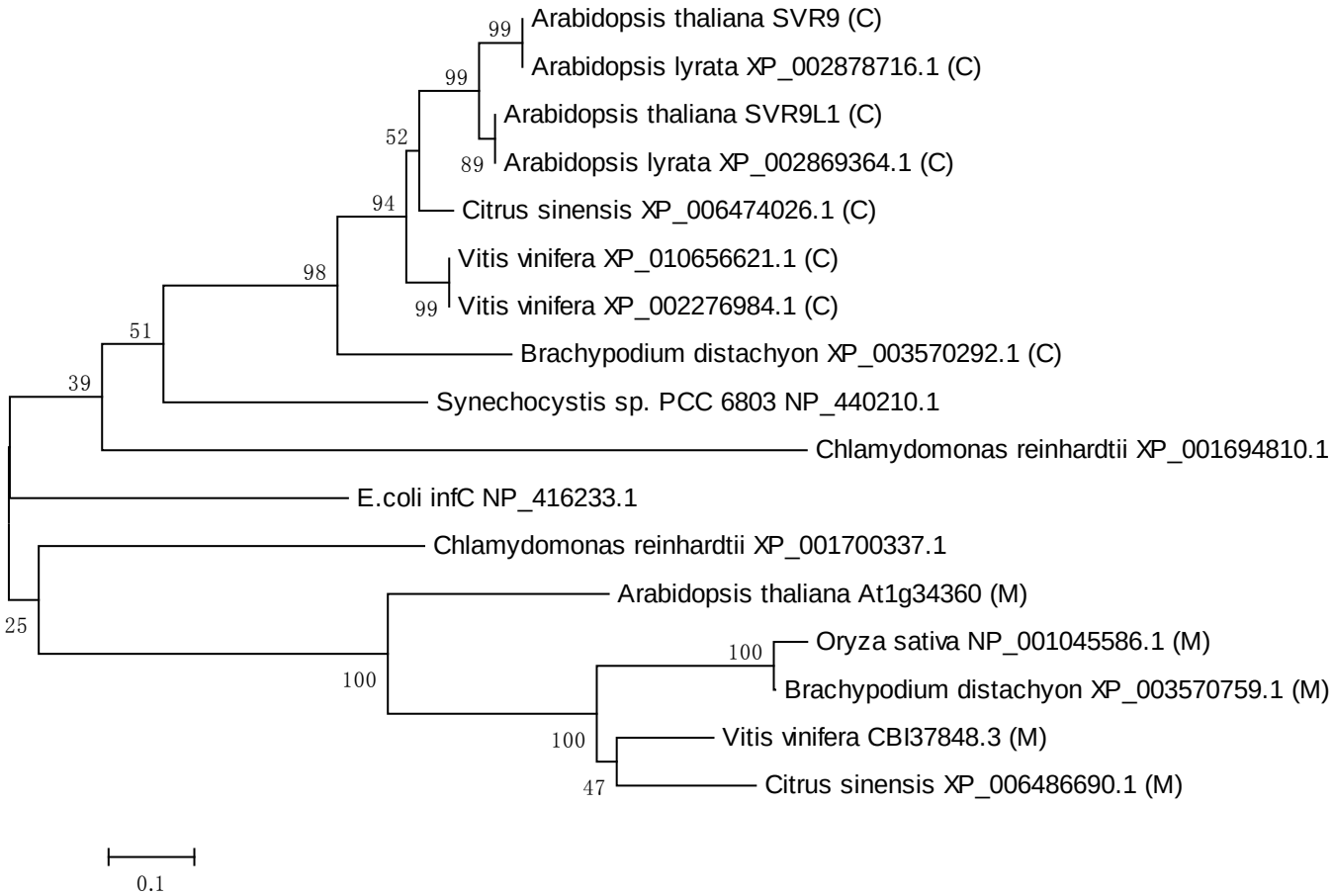


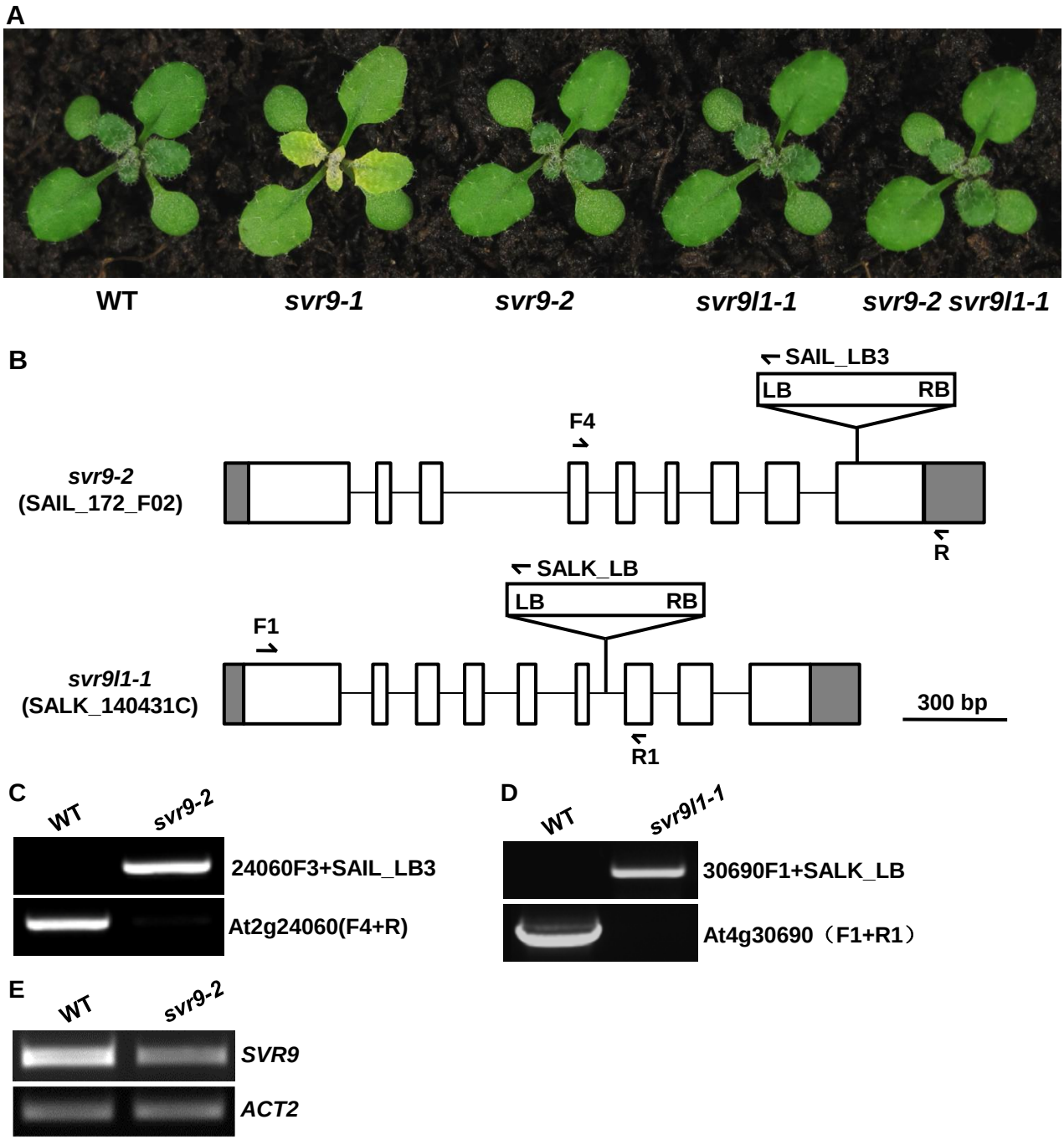
Supplemental Figure S1. Protein sequence alignments of SVR9/At2g24060, SVR9L1/At4g30690, At1g34360 and *E. coli* infC. Protein sequences of SVR9, SVR9L1 and At1g34360 were obtained from The Arabidopsis Information Resource (TAIR) database while infC protein sequence (Accession No.: NP_416233.1) was obtained from National Center for Biotechnology Information (NCBI). Sequences alignments were generated using the ClustalW2 program. Conserved domains of IF3 were marked.



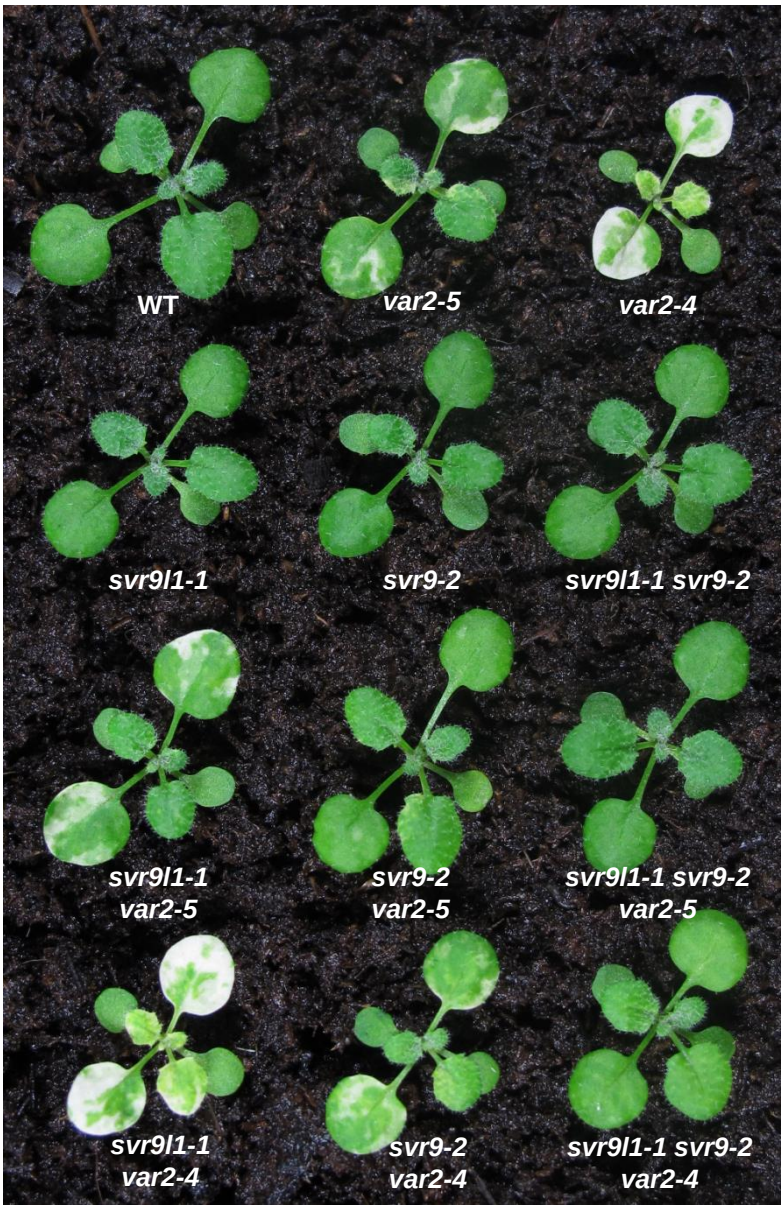
Supplemental Figure S2. Chloroplast localization of cTP$_{SVR9}$-GFP. The N-terminal region of SVR9 (1-70 amino acid residues) was fused with GFP and transiently expressed in wild type leaf protoplasts. GFP and chlorophyll autofluorescence signals were monitored with confocal microscopy. One representative protoplast was shown. BF, Bright Field. Bar: 10 μm.



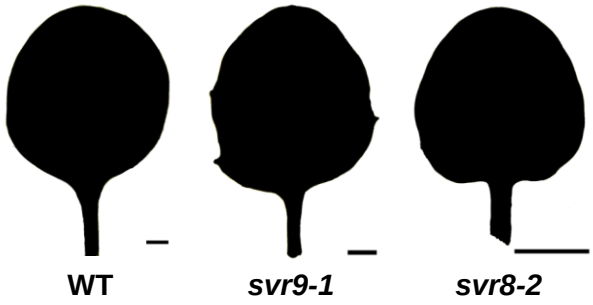
Supplemental Figure S3. Phylogenetic analysis of prokaryotic IF3-like proteins from *E. coli* and representative photosynthetic species. Full length protein sequences of prokaryotic IF3-like proteins from *Arabdiopsis lyrata*, *Vitis vinifera*, *Citrus sinensis*, *Brachypodium distachyon*, *Oryza stativa*, *Chlamydomonas reinhardtii*, *Synechocystis* sp. PCC6803 and *E. coli* were obtained from NCBI. NCBI accession numbers were listed. Full length sequences of SVR9, SVR9L1 and At1g34360 were obtained from TAIR database. The phylogenetic tree was constructed using the boot strap method with 1000 trials by MEGA6. Putative subcellular localizations of these IF3-like proteins were predicted by the TargetP program . M, mitochondrion; C, chloroplast.



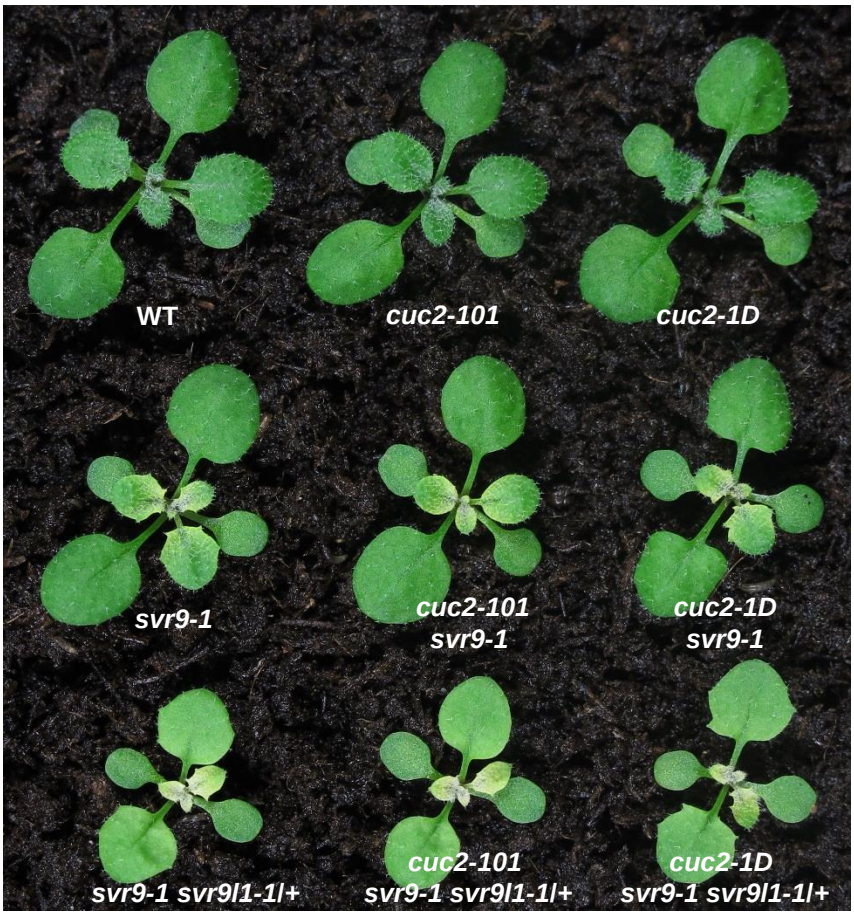
Supplemental Figure S4. Identification of *svr9-2* and *svr9l1-1*. A, Comparison of the overall phenotypes of two-week-old WT, *svr9-1*, *svr9-2*, *svr9l1-1* and the *svr9-2 svr9l1-1* double mutant. B, Schematic representation of the T-DNA insertion sites in *svr9-2* and *svr9l1-1.* Gene models were drawn as in Fig. 2A. Positions of primers used in C were labeled. C-D, Verification of the genotypes of *svr9-2* and *svr9l1-1* plants by genomic DNA PCR using indicated primers. E, Semi-quantitative RT-PCR analyses of the accumulations of *SVR9* transcripts in wild type and *svr9-2*. Expression of *ACT2* was used as an internal control.



Supplemental Figure S5. Whole plant phenotypes of representative 2-week-old plants of the same genotypes shown in Fig. 5A-5D.



Supplemental Figure S6. Comparison of leaf margin development in WT, *svr9-1* and *svr8-2*. Illustrated are silhouettes of the first rosette leaves of 10-day-old seedlings.



Supplemental Figure S7. Whole plant phenotypes of representative 2-week-old plants of the same genotypes shown in Fig. 10A.