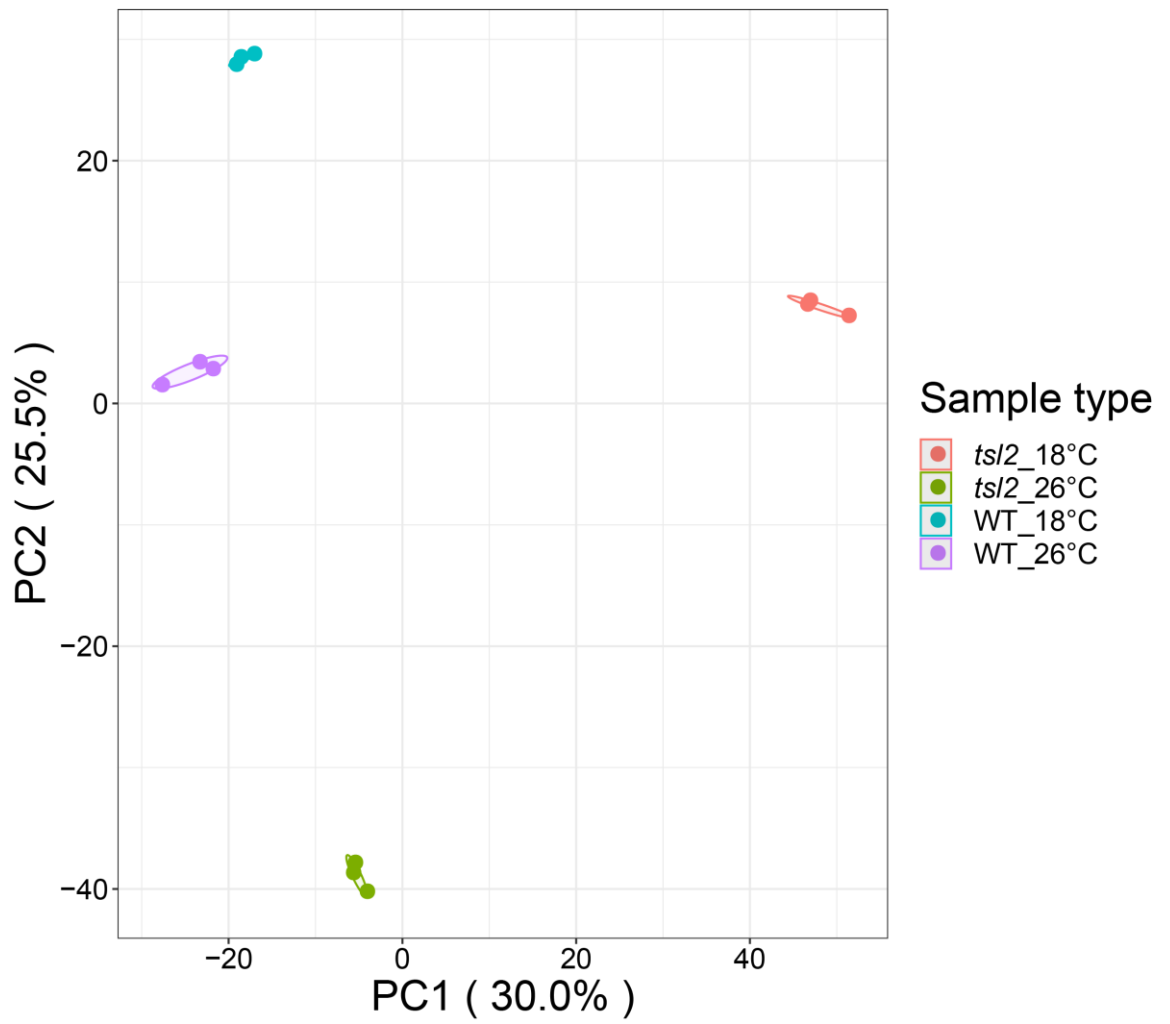
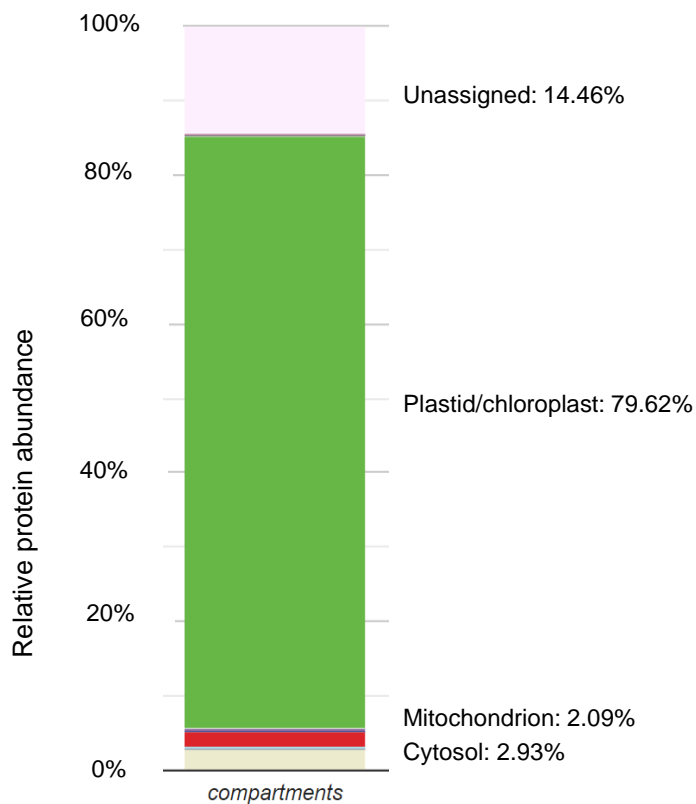


**Fig. S1. Phenotype of the *ts/2* mutant at 18°C and 26°C.**

(**A-B**) Phenotypes of the mutant plants. The wild-type (WT) and *ts/2* mutant grown under normal growth temperature (22°C) conditions for 4 days were transferred to 18°C or 26°C for 12 days and photographed (A), chlorophyll contents of plant leaves were measured (B). The data represents the average of samples and the error bars indicate the standard error (n = 3).

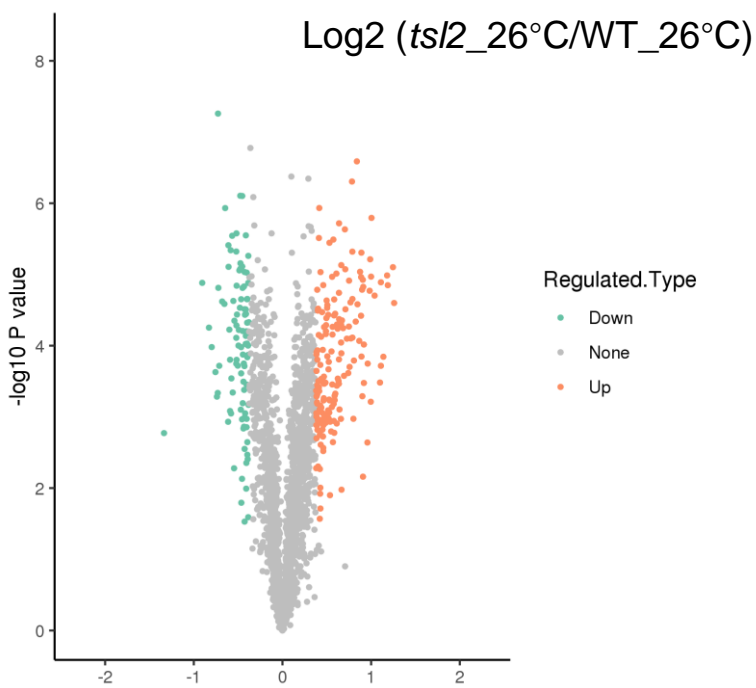
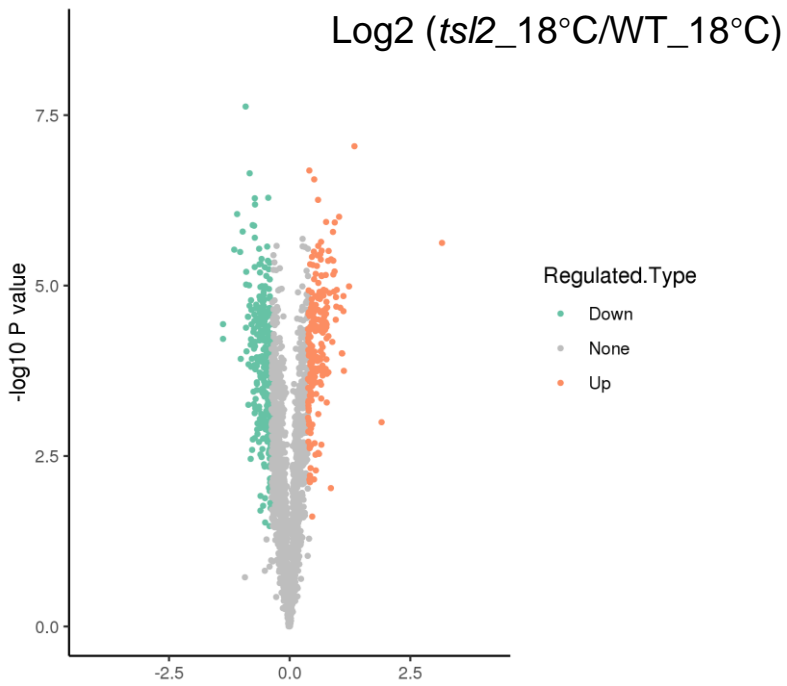


**Fig. S2. Principle Component Analysis (PCA) of samples for quantitative proteomics.**

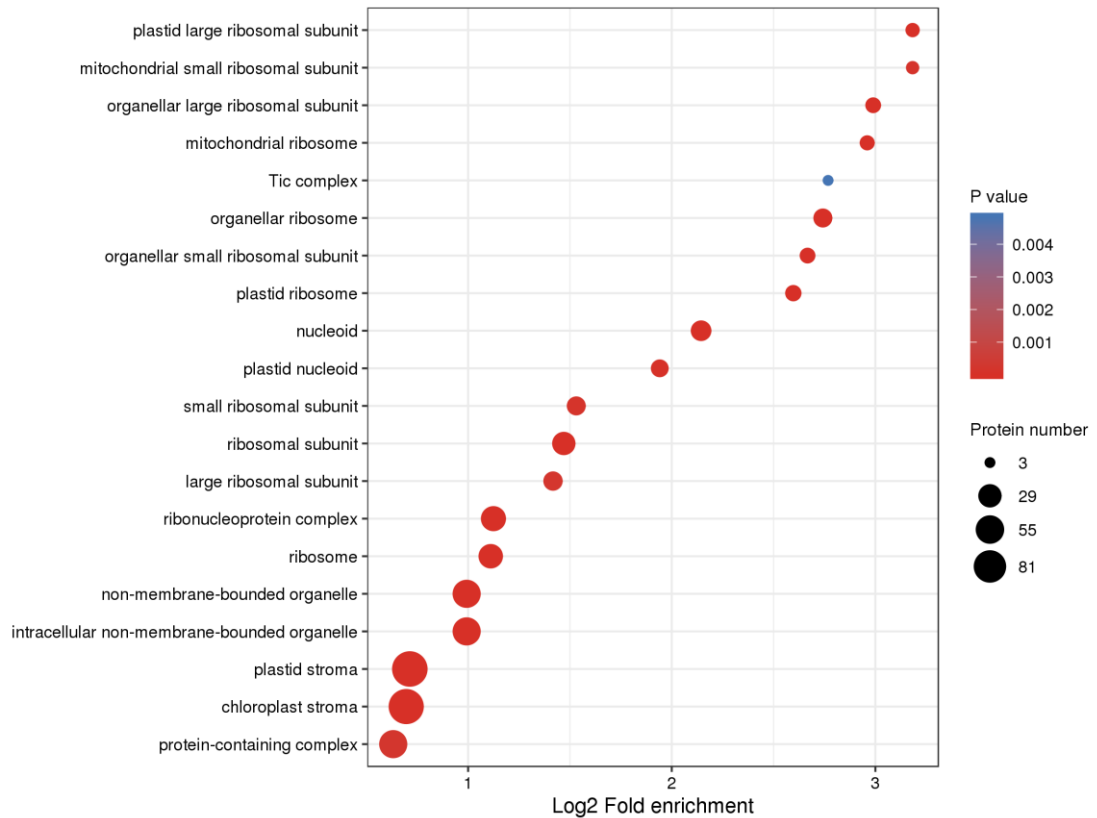


**Fig. S3. Gene Ontology (GO) analysis of subcellular localizations of quantifiable proteins identified in the proteomics study.**

Protein subcellular localizations were predicted by SUBA4 using the multiple marker abundance profiling (MMAP) online tool (<https://suba.live/toolbox-app.html>).



**Fig. S4. Differentially expression proteins between WT and *ts/2* mutant plants under two temperature conditions.**



**Fig. S5. Go analysis of proteins up-regulated in *ts/2* mutant plants at 18°C.**

Criteria for differential expression were set as  $q \leq 0.05$ , fold change (FC)  $\geq 1.3$  for upregulation. Totally 208 up-regulated proteins in *ts/2* mutant at 18°C were used for GO analysis.