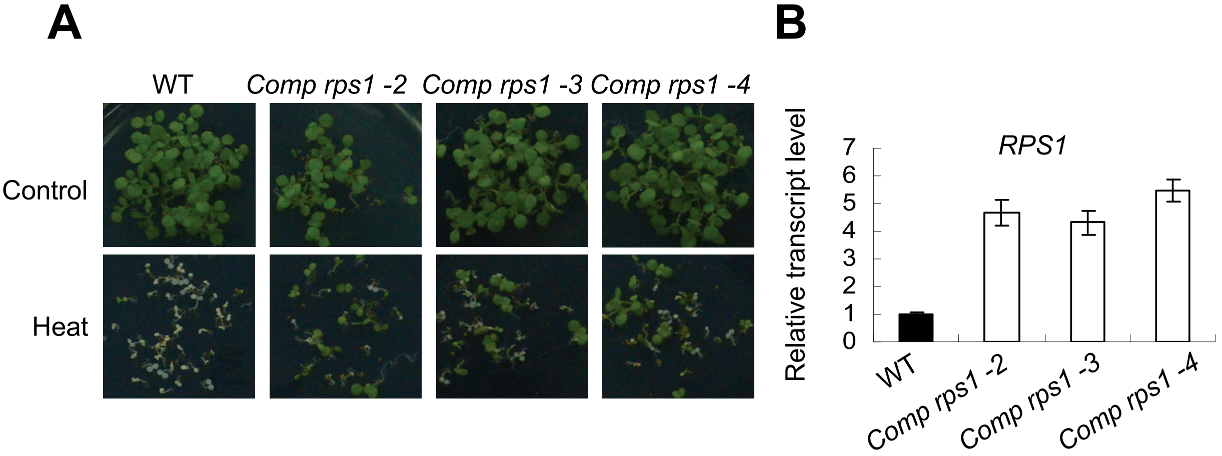

**C**

| **Protein name** | **Gene accession number** | **protein accession number** | **Ratio M/H Control** | **Ratio M/H Heat stress** |
|---|---|---|---|---|
| **D1** | ATCG00020 | gi:44889035 | 1.108 | 1.303 |
| **D2** | ATCG00270 | gi:6685787 | 2.155 | 7.259 |
| **CP43** | ATCG00280 | gi:172045852 | 1.131 | 2.690 |
| **CP47** | ATCG00680 | gi:6685792 | 1.475 | 2.305 |
| **psaA** | ATCG00350 | gi:6685788 | 1.172 | 3.439 |
| **psaB** | ATCG00340 | gi:6685789 | 1.310 | 3.515 |
| **CF1** β | ATCG00480 | gi:6686269 | 2.053 | 3.305 |

**Figure S9.** Overexpression of *RPS1* improves heat tolerance in the genomic complementation lines .

(A) Heat-tolerant phenotypes of the transgenic lines of *rps1* complemented with *RPS1* genomic DNA in comparison with WT seedlings challenged the heat treatment as described in Methods.
(B) qRT-PCR analysis showing expression levels of *RPS1* in the genomic complementation lines as described in (A).
For qRT-PCR analysis, *Actin2* was used as the internal standard. Error bars indicate standard deviations of three technical replicates, and the results were consistent in three biological replicates.
(C) The ratio of peak intensities of M versus H peptides reflects difference between the genomic complementation line *Comp rps1-3* and wild type in translation of the corresponding proteins since the newly synthesized proteins incorporate either the M or H amino acids. Samples were extracted from 7-d-old seedlings of wild type and the transgenic line of *Comp rps1-3* pulse-labeled with “heavy” (H) and “medium heavy” (M) stable isotope amino acids, respectively, as described in Methods.