

Supplementary Material

Figure S1. Nucleotide and deduced amino acid sequence of OpsHSP18. The canonical TATA-box (boxed), the +1 transcription start site (circled), and 5' and 3'-UTR region (underlined) are indicated.

Figure S2. Clustal W alignment of the OpsHSP18 protein and other plant Class CI sHSP: *Citrullus lanatus* ClHSP18.1A (GenBank Accession No. ADU55789), *Eucalyptus grandis* EgHSP18 (Phytozome Accession EucgrB02376), *Populus trichocarpa* PtHSP17.8 (GenBank Accession No. Pt_XP002298362), *Vitis vinifera* VvHSP18.2 (GenBank Accession No. XP_002280935), *Medicago sativa* MsHSP18.2 (GenBank Accession No. P27880), *A. lyrata* AlHSP18 (GenBank Accession No. XP_002864649) and *A. thaliana* AtHSP17.6C (GenBank Accession No. NP_175759). Characteristic domains are indicated with lines: *N*-terminal, α -crystalline and *C*-terminal domains. Two consensus regions I and II (boxed) and a conserved sequence motif, basic-X-Ile/Val-X-Ile/Val (double underlined). Identical residues (asterisk) and conserved amino acid substitutions (dots) are indicated.

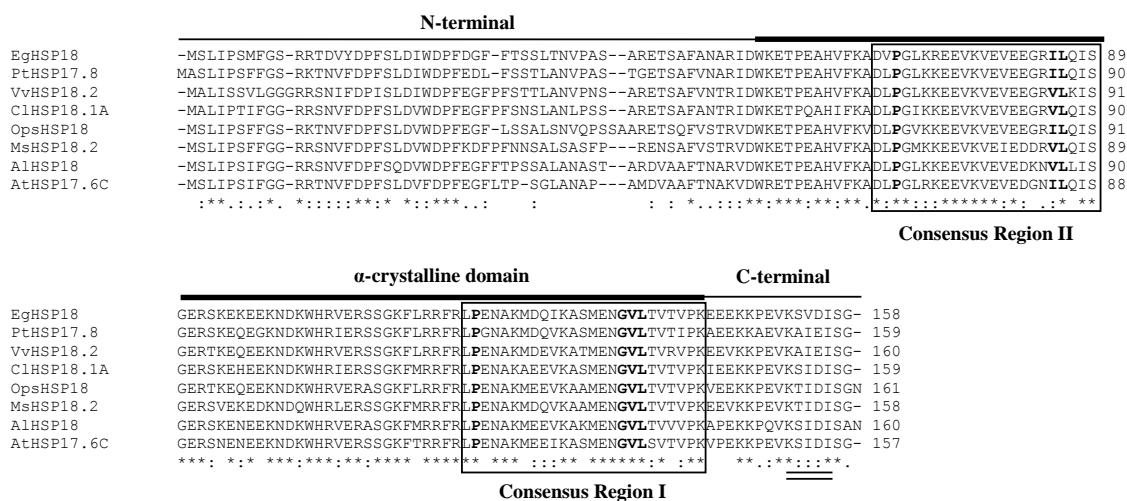
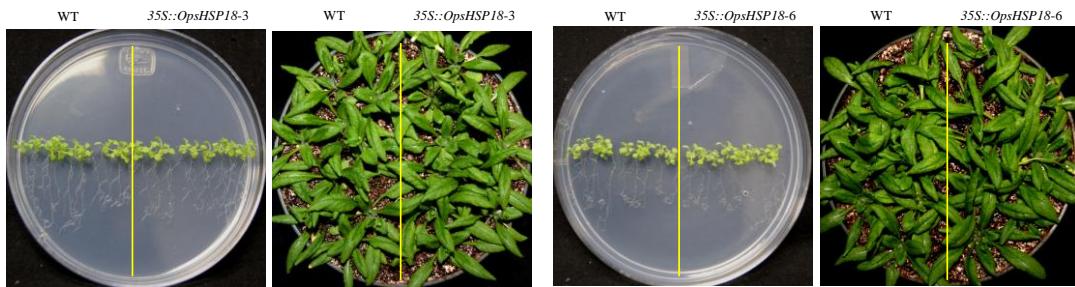
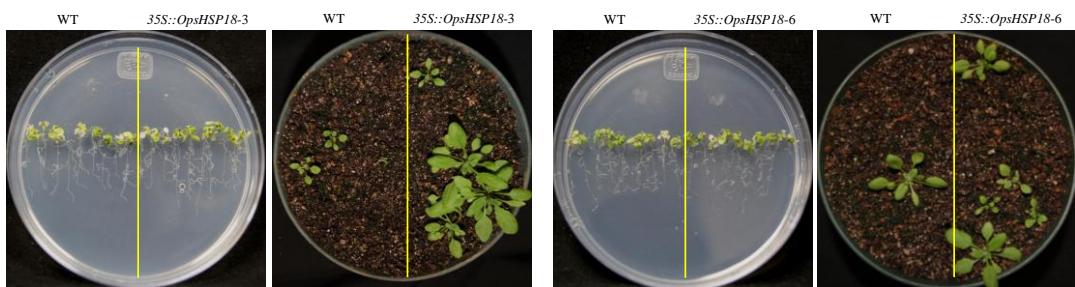


Figure S3. Survival of seedlings of *Arabidopsis thaliana* Col-0 and *35S::OpsHSP18-3* and -6 transgenic lines after salt (NaCl) and osmotic (glucose and mannitol) treatments. Ten day-old seedlings were grown under: (A) control conditions in MS medium for 21 days and, transferred to pots for 21 days, (B) in MS medium with 150 mM of NaCl for 14 days, (C) in MS medium with 7% (388 mM) glucose, and (D) with 5% (274 mM) mannitol during 21 days. After these stress periods, plants were transferred to pots, and survival rates of seedlings were evaluated at 21 days.

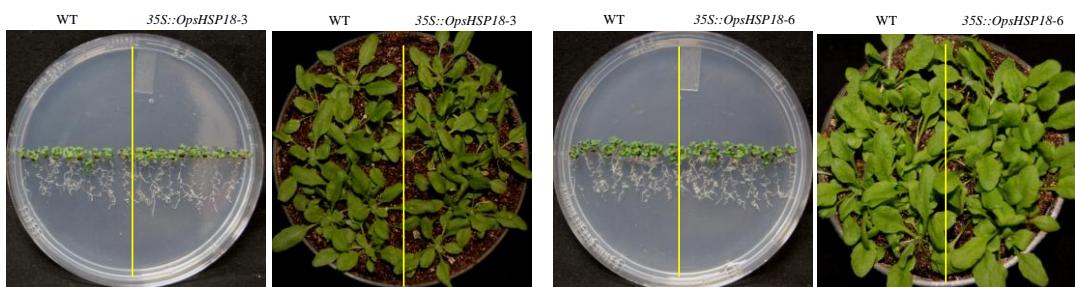
A) Control



B) NaCl



C) Glucose



D) Mannitol

