



**Figure S6.** Comparison of the amino acid sequences of putative HsfA9 proteins from different plants.

In addition to HsfA9 from sunflower (Almoguera et al. 2002) potential HsfA9 homologues encoding transcripts were identified from tomato, potato, maize, barley, rice and coffee from available EST data bases (<http://www.ncbi.nlm.nih.gov/BLAST/>). Shown is the multiple sequence alignment of the translated longest open reading frames performed with Clustal W (version 1.83). For further details see Methods. At, *Arabidopsis thaliana*, Cc, *Coffea canephora*, Ha, *Helianthus annuus*, Hv, *Hordeum vulgare*, Le, *Lycopersicon esculentum*, Os, *Oryza sativa*, St, *Solanum tuberosum*, Zm, *Zea mays*. PLEASE add accession numbers for these sequences. Functional modules are indicated by an open box: DBD, DNA-binding domain, HR-A/B, hydrophobic repeat A/B, NLS, nuclear localization signal, AHA, aromatic and hydrophobic amino acid residues embedded in an acidic surrounding. For further description of the modules, see Nover et al. 2001. Colored boxes mark sequence stretches with homologies, for explanation see the legend below.