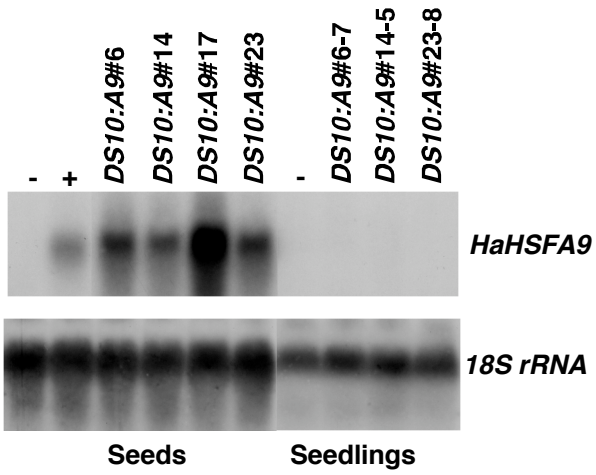

Figure S1. Seed-specific overexpression of *HaHSFA9* mRNAs from the *DS10* promoter in transgenic tobacco. We depict northern hybridization analyses of total RNA from seed samples from the indicated heterozygous T_0 lines. Also shown, similar analyses for 21 dpi seedling samples from the corresponding homozygous daughter lines. Total RNA amount per lane was 15μg. Hybridization controls: (-) RNA from non-transgenic tobacco seeds; (+) RNA from sunflower embryos (21 days post-anthesis). Labeled DNA probes are indicated to the right of the autoradiographs. The *HaHSFA9* probe was prepared by labeling an *Xba*I fragment (1287 bp) from plasmid p35:HSFA9 (Almoguera et al., 2002, cited in the manuscript). The fragment used for the *18S rRNA* probe was described by Almoguera and Jordano (Plant Mol Biol 19: 781-92, 1992). DNA fragments were labeled using the Megaprime DNA Labelling System from Amersham Biosciences and following directions from the manufacturer. Hybridizations were performed overnight at 65ºC in the modified Church and Gilbert buffer (Proc Natl Acad Sci U S A, 81: 1991-5 [1984], 7% [w/v] SDS, 0.5 M NaHPO4 [pH 7.2], 10 mM EDTA).