Additional file 2. Primer sequences and qRT-PCR conditions.

	Forward	**Reverse**
18S	TAGATAAAAGGTCGACGCGG	CCCAAAGTCCAACTACGAGC
PSII-W PGSC0003DMG400020141	GGATGAAAGAATGAGCACAGAAGG	AGACCAAACCAAACCGAAGACT
PSAK PGSC0003DMG400020505	TTGTTTGCTGGTAGATTTGGGC	GGTCCCCTGTCTGTAAGCC
PSII 5kDa PGSC0003DMG400010498	ACGTCATCTCCATTTCTAGTCCA	TCTTATTGCTTTTTGAATGCGTGG
HSP70 PGSC0003DMG400030089	GACGAGAAAGCAGCAGAAGAC	CCATGCACACACTAATCTCTGG
PSI-H PGSC0003DMG400016504	TCACCCTACAACTCCCTTCAGA	AGCCACCTCCCAATATCAAGA
EF-1α	ATTGGAAACGGATATGCTCCA	TCCTTACCTGAACGCCTGTCA

18S rRNA gene was used in RT-PCR analysis (standard conditions, Temperature of annealing = 52°C) to control quality of cDNA before qRT-PCR.

qRT-PCR program cycle parameters were set as follows: 50°C for 2 min (stage 1), 95°C for 10 min (stage 2), 95°C for 15 sec and 60°C for 1 min (stage 3 repeated 40 times), 95°C for 15 sec, 60°C for 15 sec and 95°C for 15 sec (stage 4). Melting curve analysis was performed to check specificity of the reactions. The relative expression levels were calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001). EF-1α was used as internal control. Data representing three biological replicates and three technical replicates are expressed as mean ± standard deviation.

Reference

Livak KJ, Schmittgen TD. Analysis of relative gene expression data using real-time quantitative PCR and the $2^{-\Delta\Delta CT}$ method. Methods. 2001;25:402-8.