A

B

Figure S2. qRT-PCR analysis of miR169nm overexpressing lines.

(A) Mature miR169 transcript levels determined by qRT-PCR, miR164 was used as a control. **(B)** Gene expression profile of *NF-YA Arabidopsis* genes in *P35S:miR169nm* lines.

Eight-day-old plants of two independent miR169nm overexpressing lines were used for RNA extraction in **(A)** and **(B)**. Values represent means and error bars indicate SE of three independent amplification reactions.