



**Figure S3. Role of *SCAP1* on stomatal genes transcript accumulations**

Transcript accumulation of stomatal markers determined by quantitative RT-PCR.

(a, c, e-h) Transcript accumulation of *SPCH*, (a), *EPF2*, (c), *MUTE*, (e), *FAMA*, (f), *EPF1*, (g), and *EPFL9*, (h) in wild-type (Col), *pro35S:amiRNA2-SCAP1* (*amiRNA2-SCAP1*) and *pro35S:SCAP1-YFP* (*35:SCAP1*). Total RNA was extracted from the first two-leaf primordia manually dissected at different developmental stages. Values represent the mean of three biological replicates (30 leaves / replica). Error bars = standard deviation.

(b, d) The mRNA levels of *SPCH*, (b) and *EPF2*, (d) in 10 days-old *pro35S:SCAP1-GR* or wild type plants treated by spraying with DEX or mock-treated and sampled at different time points. Values represent the mean of two biological replicates. Error bars = standard deviation.