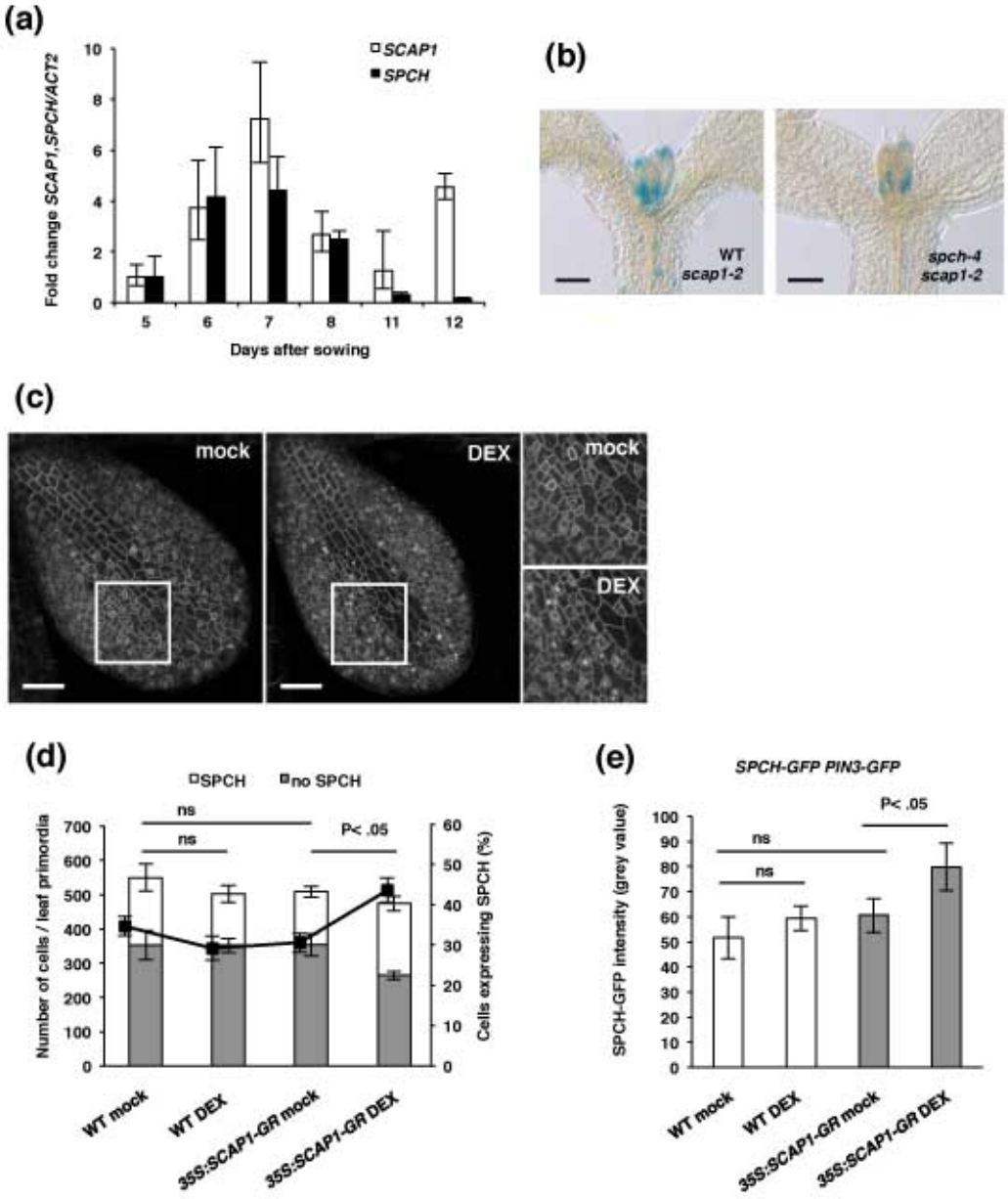

Figure 4. *SCAP1* promotes SPCH protein but not transcript accumulations

(a) Pattern of *SCAP1* and *SPCH* transcript accumulations determined by quantitative PCR in manually dissected first two leaf primordia of wild-type (Col) seedlings at different days after germination. *ACTIN* (*ACT2*) was used for normalization. Values represent the mean of three biological replicates (30 leaves / replica). Error bars = standard deviation.

(b) GUS staining of *scap1-2* in wild-type or *spch-4* mutant background in 5 day old seedlings. Bar = 100 µm

(c) Confocal images of hemizygous *proPIN3:PIN3-GFP proSPCH:SPCH-GFP pro35S:SCAP1-GR* transgenic plants. Shown is the first leaf of plants treated with DEX or mock-treated. Insets show a portion of leaf at higher magnification. Scale bar = 500 µm.

(d) Quantification of epidermal cells accumulating SPCH-GFP proteins in control (mock) or DEX-treated plants. Shown is the average total number of epidermal cells in 6-8 independent first leaf primordia (5 dag). This experiment was performed twice with similar results. Values were compared with one-way ANOVA. NS = not significant.

(e) Mean fluorescence intensity of SPCH-GFP protein nuclear accumulation in control (mock) or DEX treated plants described in (d).