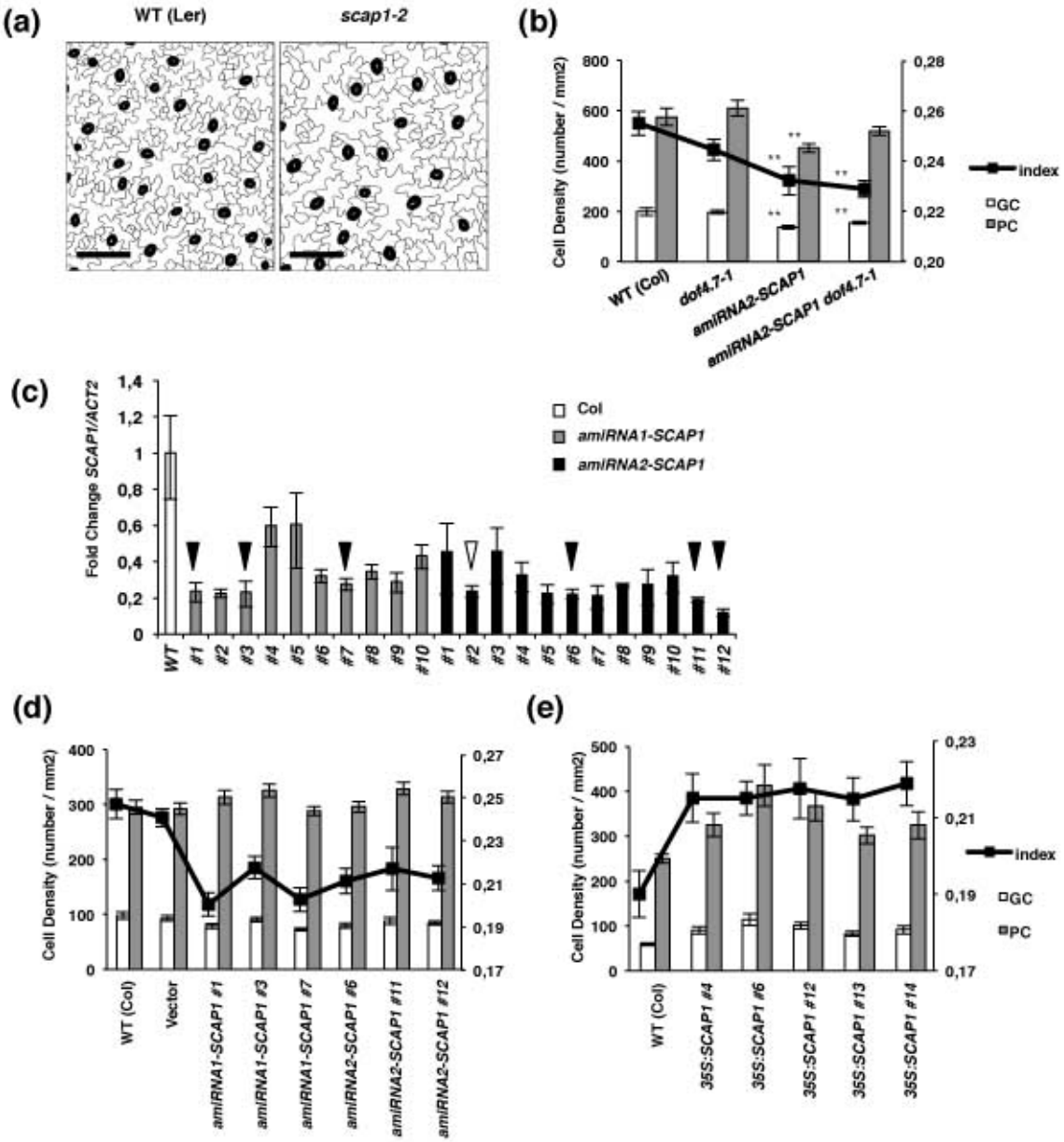

Figure S2. *SCAP1* affects GCs development

(a) Representative abaxial epidermal phenotype of a mature leaf (the 6th leaf) of wild-type (Ler) and *scap1-2* mutants. Guard cells are false coloured in black. Scale bar = 50 µm.

(b) Number of Guard cells (GC), pavement cells (PC) and stomatal index in wild-type (Col), *dof4.7*, *pro35S:amiRNA2-SCAP1* (*amiRNA2-SCAP1*) and *dof4.7 pro35S:amiRNA2-SCAP1* double mutant plants. ** = P<0.01 two tails T Student test. Error bars = Standard Error.

(c) Pattern of *SCAP1* transcript accumulation determined by quantitative PCR in mature leaves in independent T1 *pro35S:amiRNA-SCAP1* (*amiRNA-SCAP1*) transgenic lines, compared with wild-type (Col). *ACTIN* (*ACT2*) was used for normalization. Values represent the mean of two technical replicates. Error bars = standard deviation.

(d) Number of Guard cells (GC), pavement cells (PC) and stomatal index in wild-type (Col) in wild-type (Col) or BASTA selected T2 *pro35S:amiRNA-SCAP1*(*amiRNA-SCAP1*) lines. A transgenic line transformed with empty vector (vector) was used as a further control to account for BASTA treatment. Lines tested in this experiments are labelled in (c) with a filled arrowhead. Line #2, white arrowhead in (c), was not included in this particular experiment. All stomatal index values are significantly different from control ($P < 0.01$), except for line #11 which was not significant.

(e) Number of Guard cells (GC), pavement cells (PC) and stomatal index in wild-type (Col) or BASTA selected T2 *pro35S:SCAP1-YFP* (*35S:SCAP1*) lines. All cells density and stomatal index values are significantly different from control (P<0.01).