Supplementary Figures

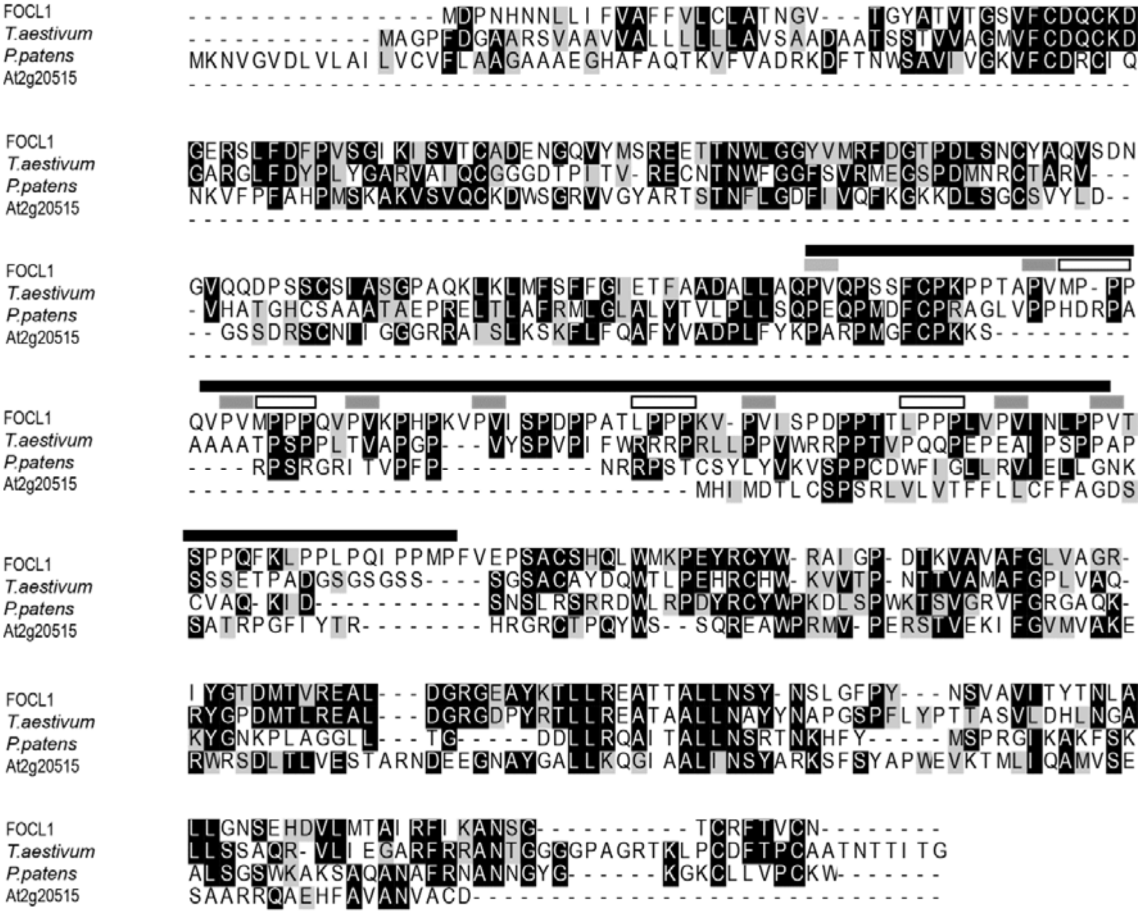

Figure S1 Alignment of FOCL1 amino acid sequence with orthologues from wheat, and Physcomitrella patens and with closest Arabidopsis homologue, At2g20515. Black shading indicates identity, grey shading indicates similarity. Deduced protein sequences were aligned with Multalin (http://multalin.toulouse.inra.fr/multalin) and displayed using Boxshade (http://www.ch.embnet.org/software/BOX_form.html). Potential proline hydroxylation sites PV and PPP are labelled grey and white respectively. Proline rich region is indicated in blue.

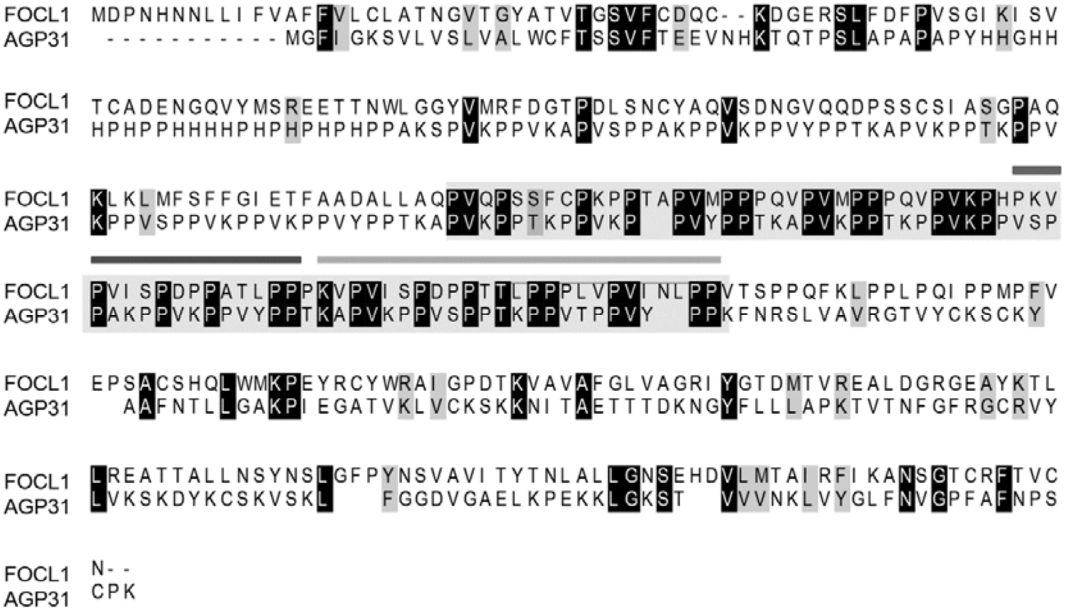

Figure S2

Alignment of deduced amino acid sequences of FOCL1 and AGP31. Conserved residues are shaded. Black shading indicates identity, Grey shading indicates similarity. Background shading indicates proline-rich region. Repeated sequence indicated above sequence. Sequences were aligned as for Figure S1

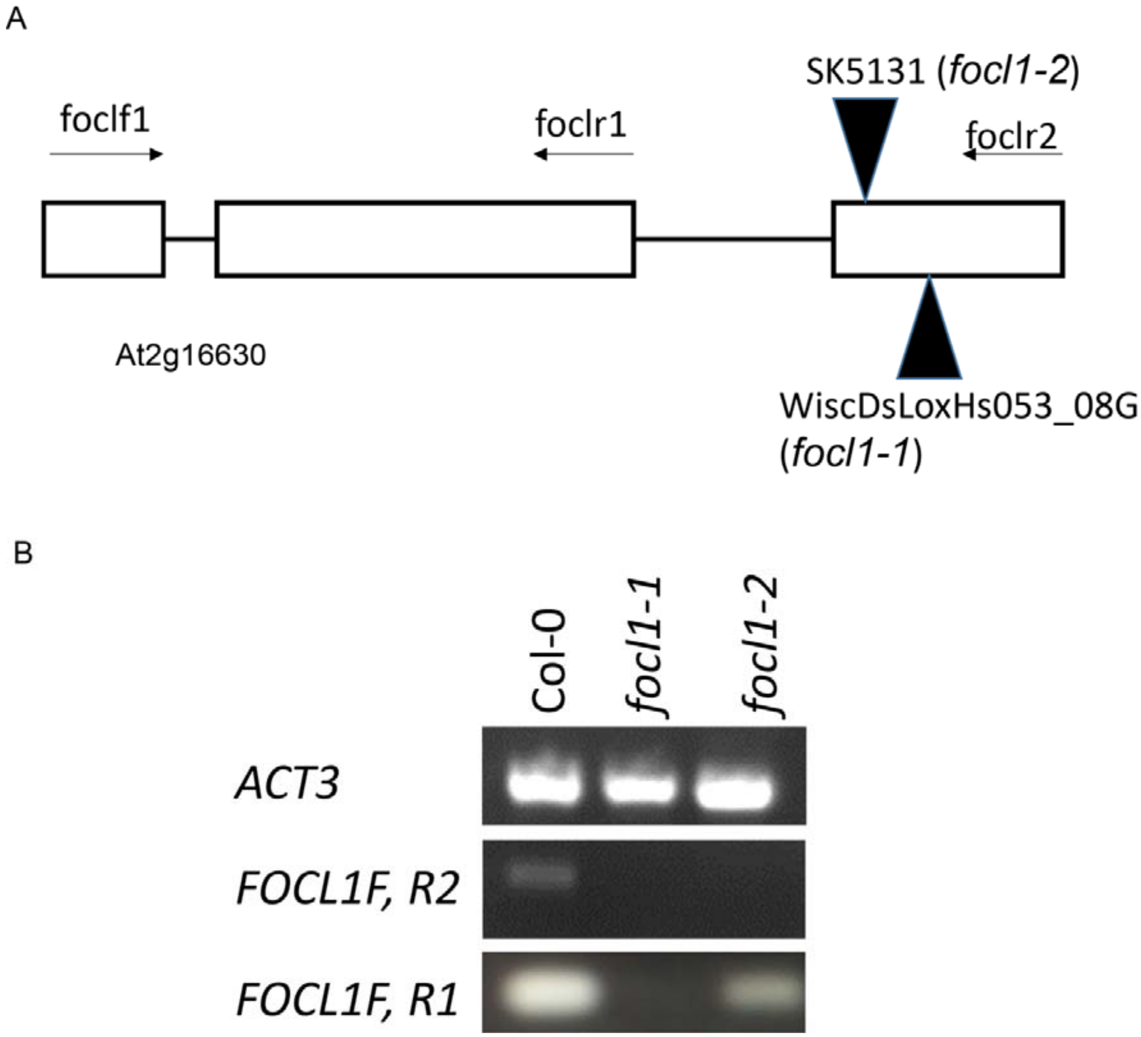

Figure S3. Insertion positions and expression of *focl1-1* and *focl1-2*
focl1-1 and *focl1-2* are null alleles. cDNA was synthesised from two week old MS plate grown seedlings RNA and amplified for 30 cycles with primers indicated.

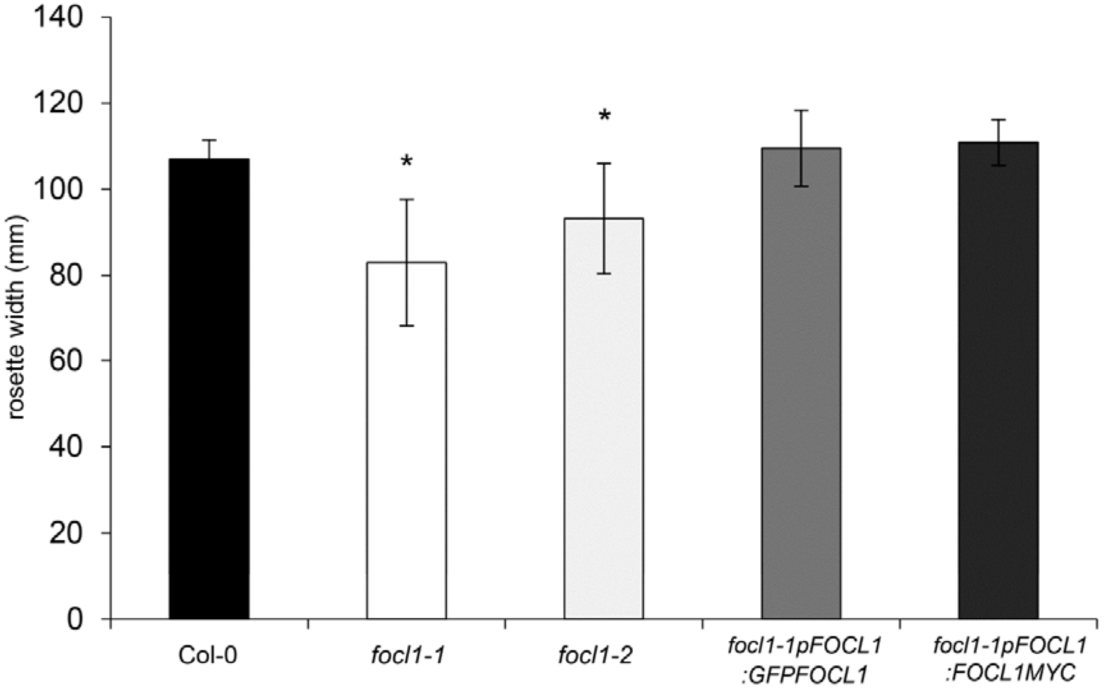

Figure S4 Rosette widths of *focl1-1* and *focl1-2*

Rosette width at bolting of indicated genotypes (n=4-7 plants) *= significantly different from Col-0 p<0.05

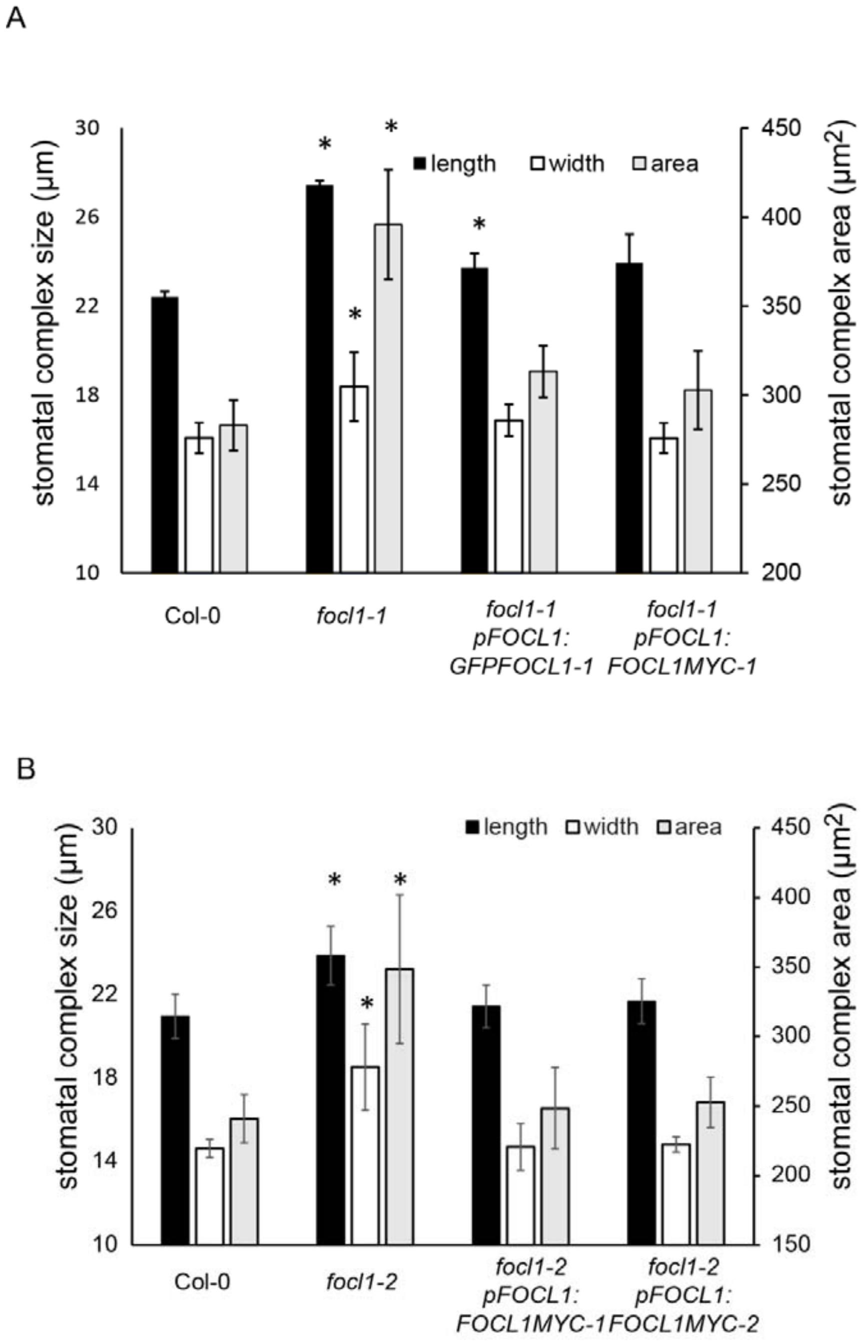

Figure S5 Complementation of *focl1* restores stomatal complex size to wild type

A Complementation of *focl1-1* restores abaxial stomatal complex size to wild type. T1 lines of *focl1-1* transformed with a 3kb genomic construct with either an N-terminal GFP or C-terminal MYC tag reduced stomatal size to wild-type (n=4 plants, 10-20 guard cell pairs from 1 leaf of each) *= significantly different from Col-0 $p<0.05$

B. Complementation of *focl1-2* restores abaxial stomatal complex size to wild type. Two independent T1 lines transformed with a 3kb genomic construct consisting 2kb of upstream sequences and in-frame C-terminal MYC tag restores guard cell pair sizes to wild-type (n=4 plants, 10-20 guard cell pairs from 1 leaf of each) *= significantly different from Col-0 $p<0.05$

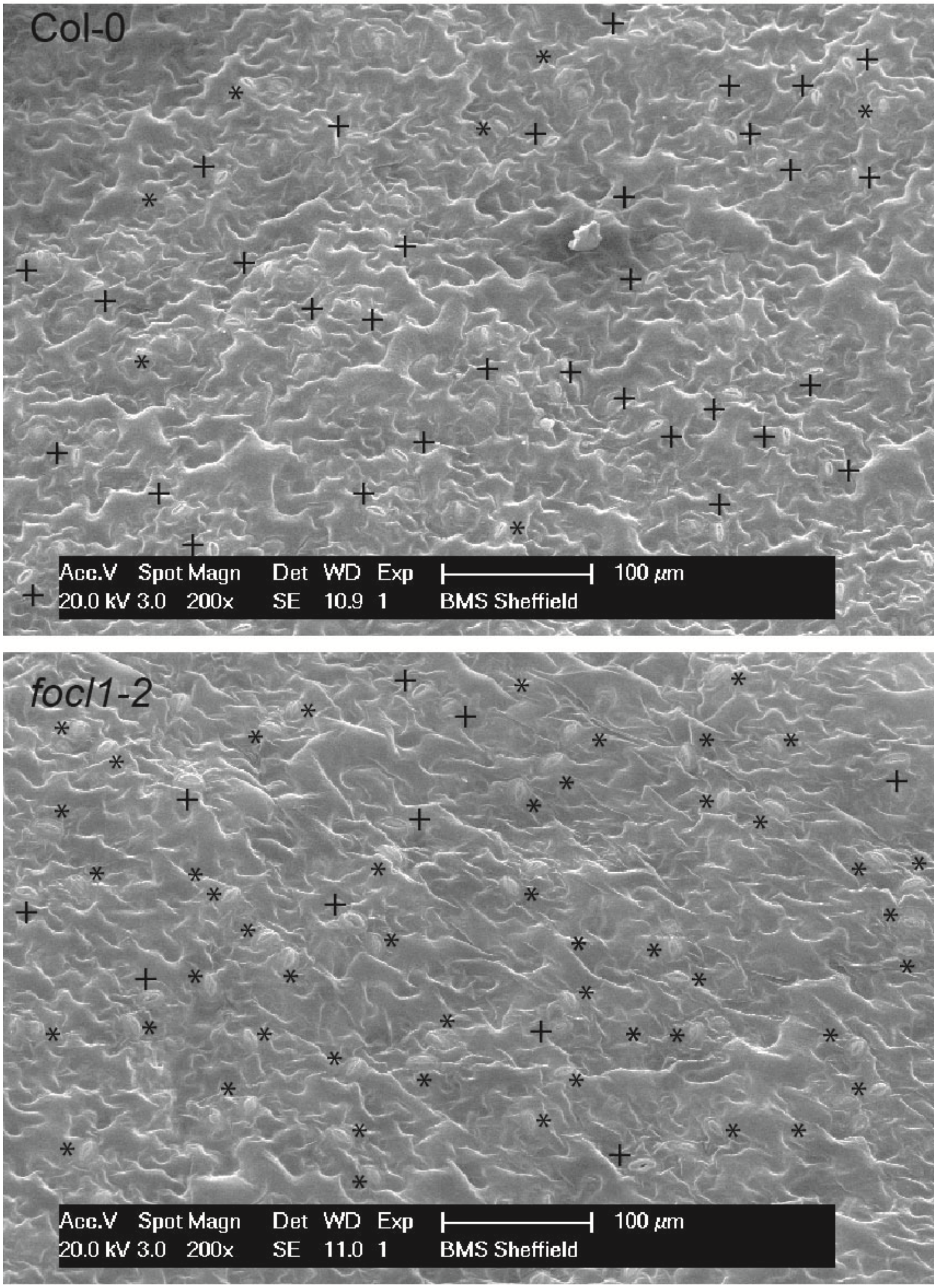

Figure S6 Wide view of abaxial epidermis of mature leaves of Col-0 and *focl1-2*. Stomata that are judged to have a partial or completely open OCL in a low magnification image are indicated with +, closed pores with*.

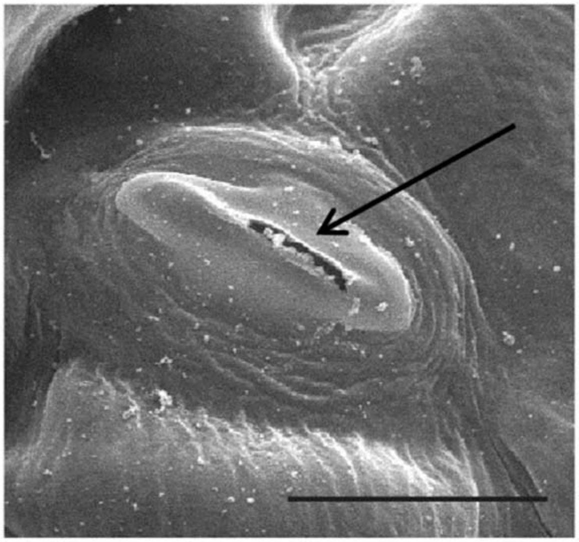

Figure S7 SEM of *focl1-1* stomate showing partial opening (indicated with arrow). Bar =10μm.

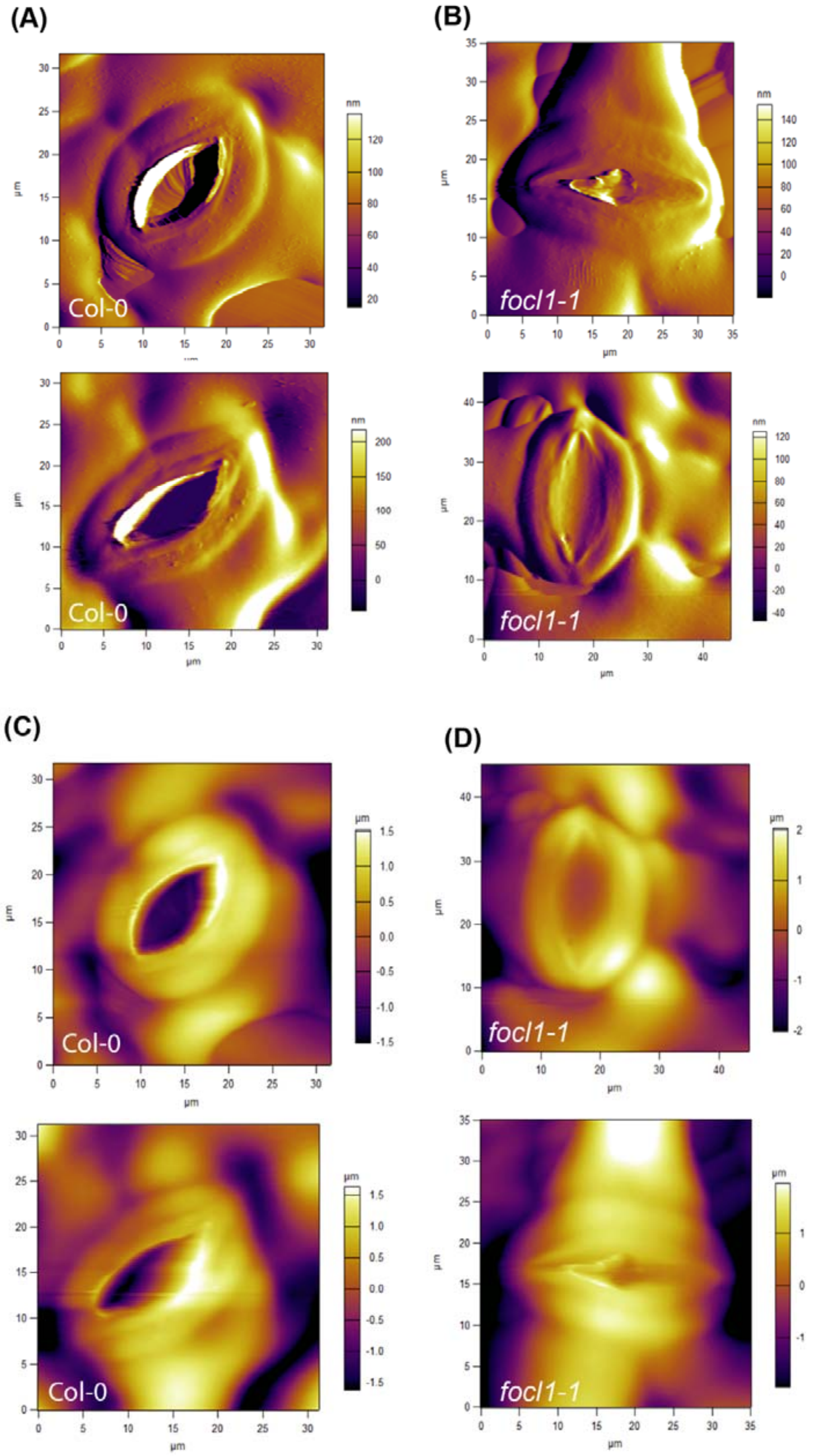

Figure S8

A & B . Deflection images for two stomata from Col and focl1-1**. C & D** Height data for two stomates from Col-0

Figure S9 Complementation of *focl1-1* and *focl1-2* with either and N –terminally located GFP tag or C –terminally located MYC tag restores leaf temperature to wild type. Plants were transferred from high humidity and temperature measured by infra-red thermography (n=3-4 plants, 1 measurement from 3 leaves of each) *= significantly different from Col-0 p<0.05) *