

Figure S1: *CML43* regualtion by *S. littoralis* oral secretions. Mean (± SE) *CML43* transcript levels in OS treated leaves of Arabidopsis after 30, and 60 min of treatment; elicitation and calculation as in Fig. 2A.

cml42







Figure S2: Trichome morphology of Arabidopsis WT and *cml42* mutant (5-week-old plants).

A WT+H₀O WT+OS 140cml42+H_O cml42+OS 120-JA-Ile (ng/g FW) 100-60· Time (min) В 2500-JA (ng/g FW) Time (min) С 3000-OPDA (ng/g FW) 0 4 Ò Time (min)

Figure S3: Phytohormone changes upon *S. littoralis*-OS application in *cml42* mutant plants. Levels of (+) JA-Ile (**A**), JA (**B**) and *cis*-OPDA (**C**) in Arabidopsis WT and *cml42* mutant line treated with *S. littoralis* OS (1:1 diluted) for 30, 60, 90 and 120 min. The phytohormone levels were measured from the local leaves.

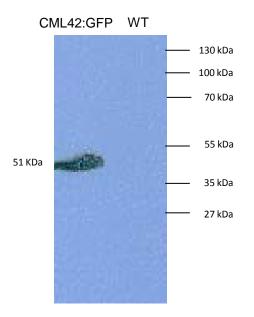


Figure S4: CML42:GFP full length protein expression in transformed Arabidopsis. Protein was extracted from GFP:CML42-transformed stable Arabidopsis lines. Supernatant of crude lysate was analyzed by western blotting using anti-GFP antibodies.

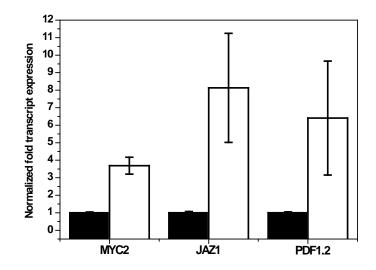


Figure S5: Relative mRNA levels (n=5) of defense-related genes *MYC2*, *JAZ1* and *PDF1.2* in undamaged *cml42* mutants (white) and control WT (black).

Transcript abundance in leaves were determined by real-time PCR analysis and normalized to the plant *RPS18B* mRNA level. Fold change in leaf tissue was calculated by comparative Ct method using an independent WT plant as control. Differences between Col-0 and *cml42* plants were analyzed by unpaired t-test and are statistically significant *P = <0.05.

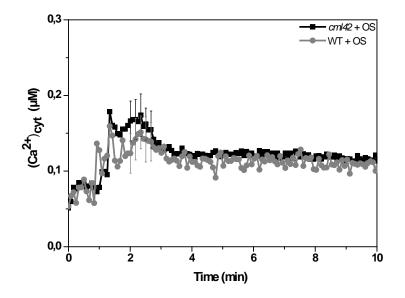
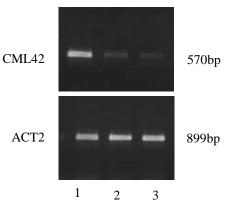


Figure S6: Elevation in cytosolic calcium concentration $[Ca^{2+}]_{cyt}$ induced by *S. littoralis* oral secretions is not altered in *cml42* plants. Application of 40 µL *S. littoralis* oral secretions (1:1 diluted) to 4-week-old Arabidopsis leaf disc of aequorin WT (dark grey), *cml42* x aequorin (black).



WT cml42-2 (SALK_040227)

Figure S7: Verification of SALK_040227 T-DNA lines

Semi-quantitative RT-PCR analysis of *CML42* transcript expression in wild type control (WT,1) and *cml42-2* (SALK_040227) mutant line (2, 3) using total RNA isolated from leaves. Expression of the house-keeping gene *ACT2* (*Actin 2*) was used as quantitative control.

SALK_040227 plants homozygous for T-DNA were identified by PCR, using primer pairs *CML42-2-LP* and *CML42-2-RP* for verification of wild type gene and *LBa1.3* and *CML42-2-RP* for T-DNA insertion. The absence of *CML42* mRNA in the homozygous SALK_040227 was checked by RT-PCR using *CML42* gene specific primers and reduced transcript (knock-down) was detected.

CML42-2-LP CML42-2-RP LBb1.3	5'- CGAAGAAAGAATCGTCGAGTG -3' 5'- CCATTAAAGCAACCAAGCTTG -3' 5'- ATTTTGCCGATTTCGGAAC -3'
ACT2-F	5'- GTTGGGATGAACCAGAAGGA-3'
ACT2-R	5'- GAACCACCGATCCAGACACT -3'
CML42-F	5'- ATGGAGAGTAACAACAACGAGA-3'
CML42-R	5'- AGAAGAAGGGATGACAACAGTA-3'