Figure S1: CML43 regulation 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.
Figure S2

*Figure S2:* Trichome morphology of Arabidopsis WT and *cml42* mutant (5-week-old plants).
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 *cmI42* 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 *cmI42* plants were analyzed by unpaired t-test and are statistically significant *P = <0.05.*
Figure S6: Elevation in cytosolic calcium concentration $[\text{Ca}^{2+}]_{\text{cyt}}$ 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).
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  5’- CGAAGAAAGAATCGTCGAGTG -3’
CML42-2-RP  5’- CCATTAAAGCAACCAAGCTTG -3’
LBb1.3       5’- ATTTTGCCGATTTCGGAAC -3’
ACT2-F       5’- GTTGGGATGAACCAGAAGGA-3’
ACT2-R       5’- GAACCACCGATCCAGACACT -3’
CML42-F      5’- ATGGAGAGTAAACAACGAGA-3’
CML42-R      5’- AGAAGAAGGGATGACAACAGTA-3’