CHARACTERISTICS OF HERBIVORY/WOUND-ELICITED ELECTRICAL SIGNAL TRANSDUCTION IN TOMATO

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SUPPLEMENTARY MATERIALS

Table S1 Primers used for qRT-PCR

Gene	Accession number	Primer sequence(5′–3′)
LOXD	Solyc03g122340	F: TGAATTTCGGGCAGTACCCT
		R: GGATCGTTCTCGTCAGGGAT
AOC	Solyc02g085730	F: TACTTCGGCGATTACGGTCA
		R: TGCAAATATGCCGGATCCAC
OPR3	Solyc07g007870	F: ATAGGAGCTGATCGCGTAGG
		R: TAGGCAAGCTTGGAACCAGA
JAZ10	Solyc08g036620	F: GTGTAATTTGGAACTCACTC
		R: CTGAGTAACATGAGAAGCAAC
ACTIN2	Solyc11g005330	F: GGTGTGATGGTGGGTATGG
		R: GCTGACAATTCCGTGCTC
UBI3	Solyc01g056940	F: AGTCCACTCTCCATCTCGTG
		R: CTCAGCATTAGGGCACTCCT

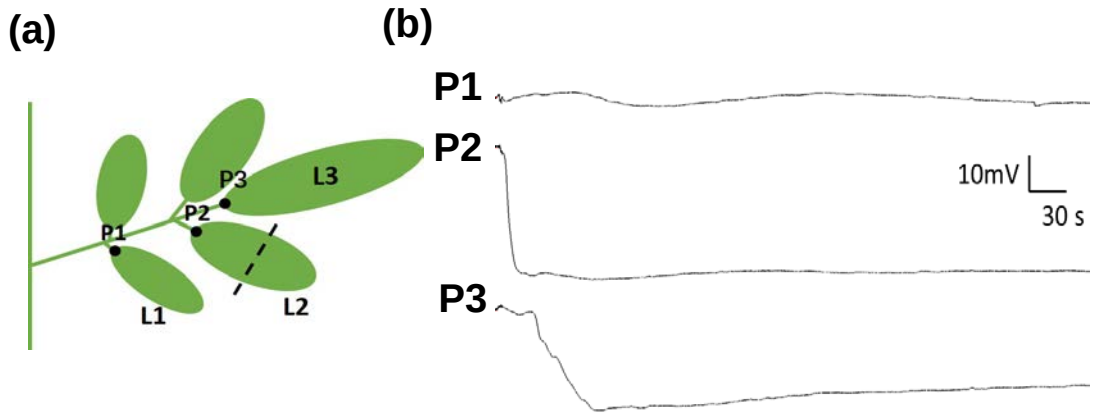

Fig. S1 Electrical signal transduction between leaflets. (a) Experimental design for measuring electrical signals within a compound leaf. Measuring electrodes: P1, junction of the petiole and leaflet 1; P2, junction of the petiole and leaflet 2; P3, junction of the petiole and leaflet 3. Dashed line, position of the mechanical wound at the center of leaflet 2. L1, leaflet 1; L2, leaflet 2; L3, leaflet 3. (b) Electrical signals measured at P1, P2 and P3 of (a). Typical surface potential changes are shown (n = 6).

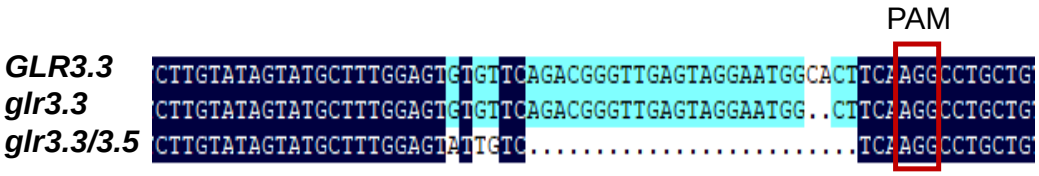

Fig. S2 Schematic of the *glr3.3* mutant and *glr3.3/3.5* double mutant plants among the CRISPR/Cas9 T2 mutant lines. The *glr3.3* mutants have a 2-bp deletion, and *glr3.3/3.5* double mutants have a 25-bp deletion, with a 3-bp change in the open reading frame (ORF), resulting in the premature termination of the translated protein. The red box presents the protospacer-adjacent motif (PAM) sequence.

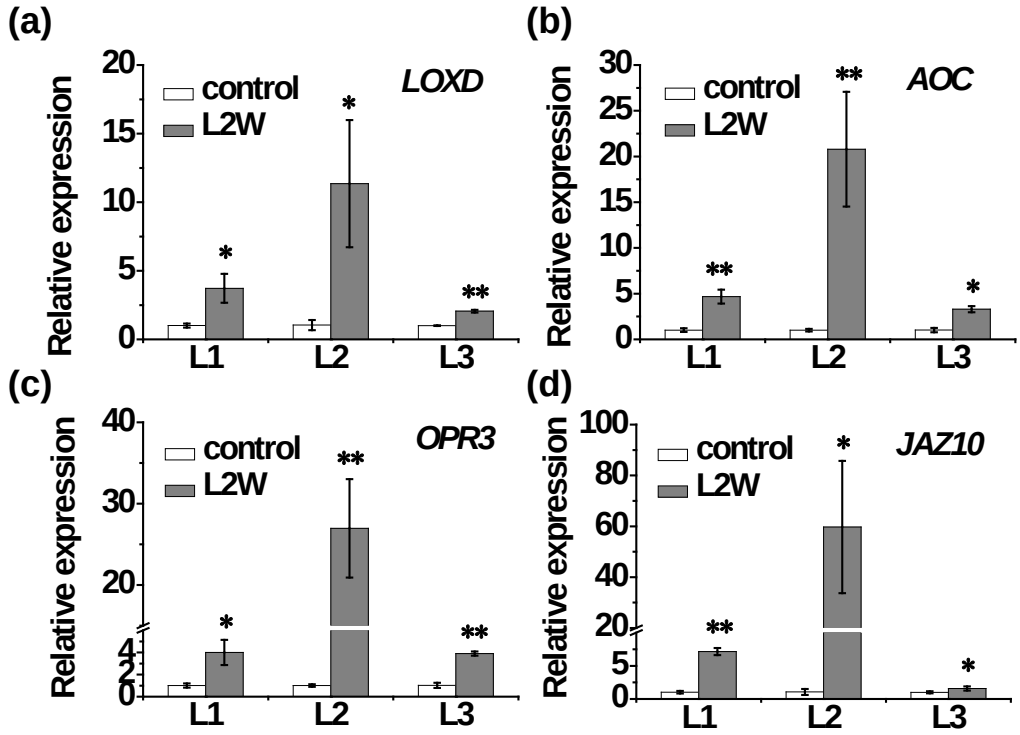

Fig. S3 L2 Wounding induced JA biosynthesis- and signaling-related genes expression within compound leaves. (a) Transcript level of *LOXD* after L2 wounding. (b) Transcript level of *AOC* after L2 wounding. (c) Transcript level of *OPR3* after L2 wounding. (d) Transcript level of *JAZ10* after L2 wounding. Samples were collected 45 min after L2 wounding. Three biological samples were included for qRT-PCR. *ACTIN2* and *UBI3* were used as internal references to calculate the relative expression of target genes, and the gene expression in L1/L2/L3 under control conditions shared with Fig. 4. The data represent the means ± SDs (n = 3). L1, leaflet 1; L2, leaflet 2; L3, leaflet 3. Statistically significant differences are indicated with asterisks (*, $P < 0.05$; **, $P < 0.01$) according to Student's t-test.

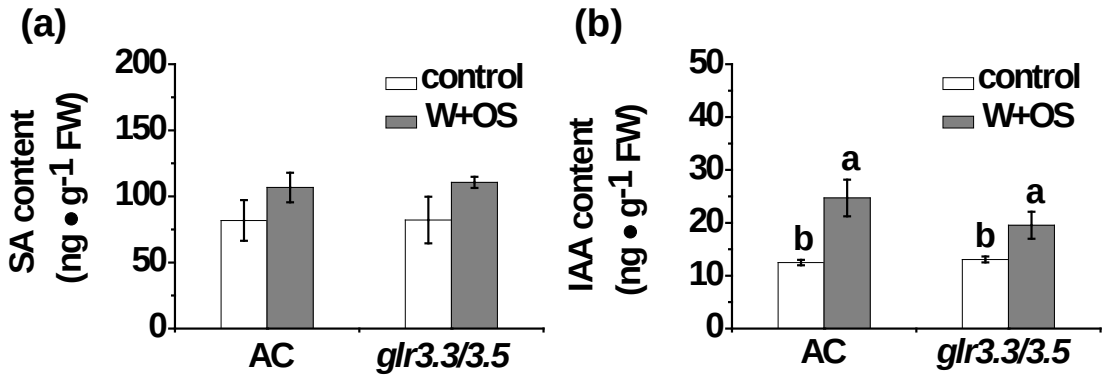

Fig. S4 SA and IAA contents in *glr3.3/3.5* mutants in response to W+OS. (a) SA content in untransformed plants and *glr3.3/3.5* mutants upon W+OS. (b) IAA content in untransformed plants and *glr3.3/3.5* mutants upon W+OS. Samples were collected 1 h after W+OS. Three biological samples were included. The data represent the means ± SDs (n = 3). The means denoted by the same letter do not significantly differ at $P < 0.05$ according to Tukey's test.