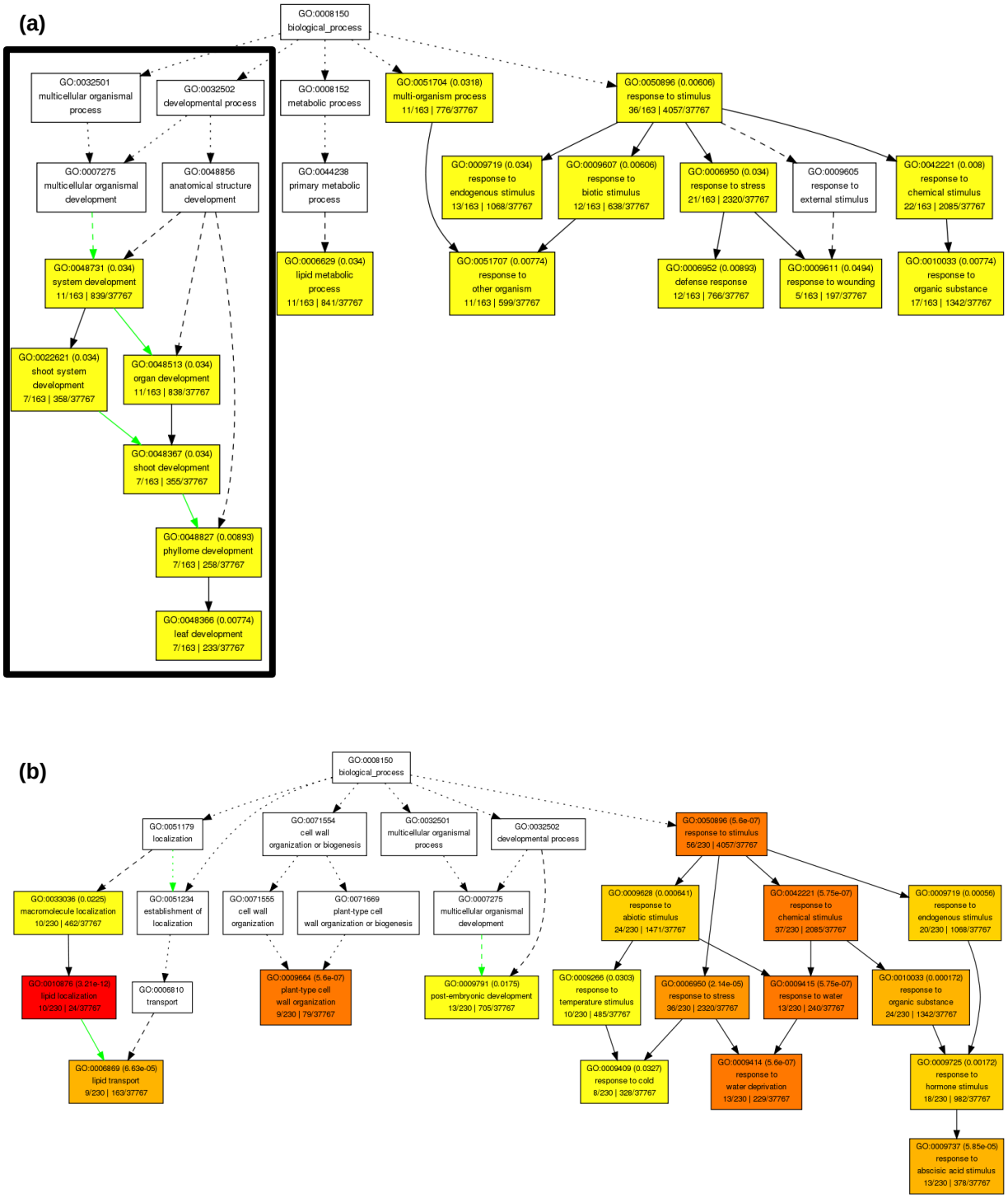


Figure S1. Gene-set enrichment analysis for biological processes of DEGs in *TEM1-OE*.
(a) Enrichment of categories related to plant development (black box) and defense response based on GO analysis of genes down-regulated in *TEM1-OE***.** (b) Enrichment of categories related to stress response and lipid localization based on GO analysis of genes up-regulated in *TEM1-OE***.** Singular Enrichment Analysis (SEA) of ranked gene list (Fold Change >2) was performed using AgriGO tool.

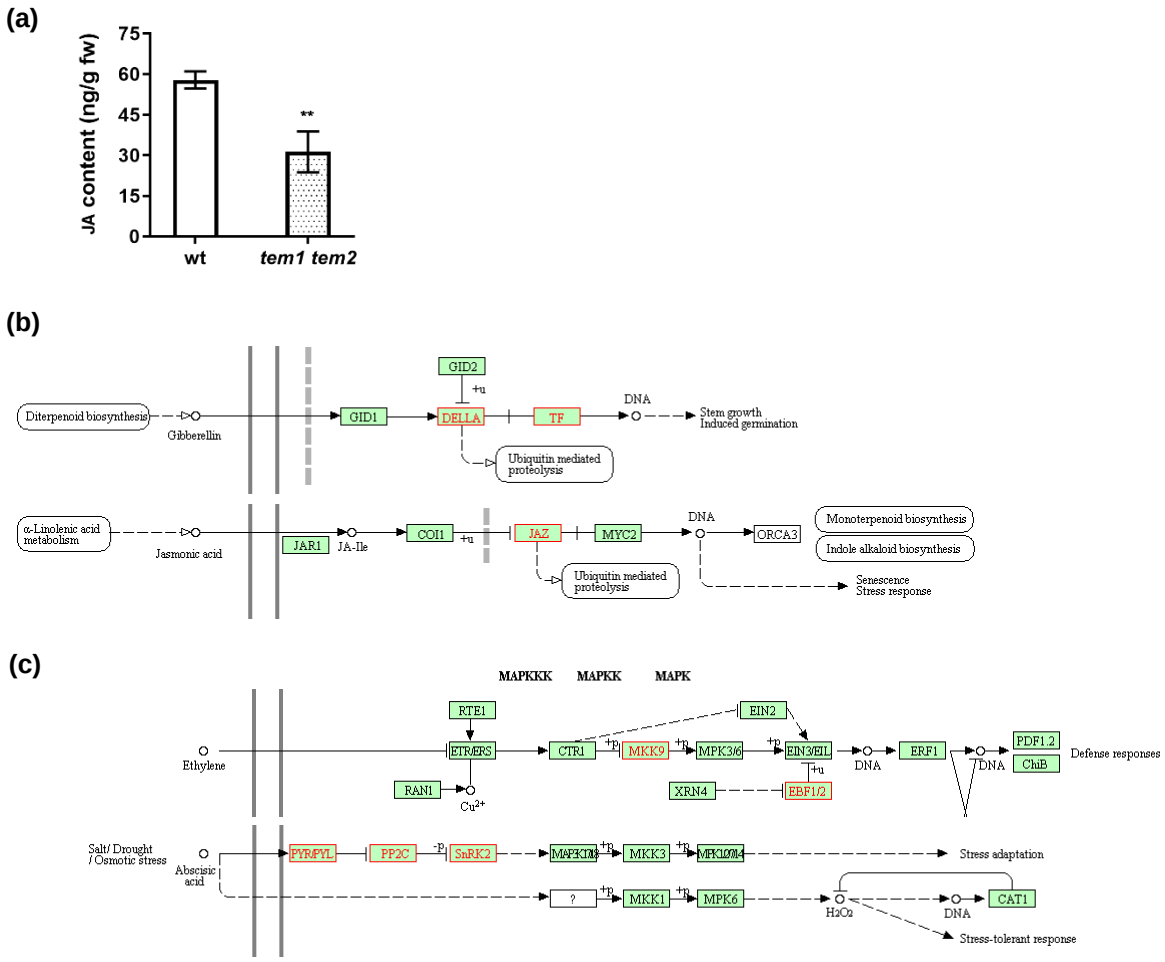


Figure S2. JA content and mapping of DEGs to KEGG Database
(a) Total JA content in wild-type and mutant adult plants. Data represent the Mean value of 3 independent replicates with Standard Deviation, and asterisk statistically significant difference by Student t-test. (b) Enrichment analysis of genes up-regulated in *TEM1-OE* for KEGG pathways related to GA and JA plant hormones signal transduction pathways. (c) Enrichment analysis of genes up-regulated in *TEM1-OE* for KEGG pathways related to MAPK signaling, especially involved in the response to abiotic stresses. KEGG Pathway Enrichment Analysis of DEGs was performed using KEGG mapper.

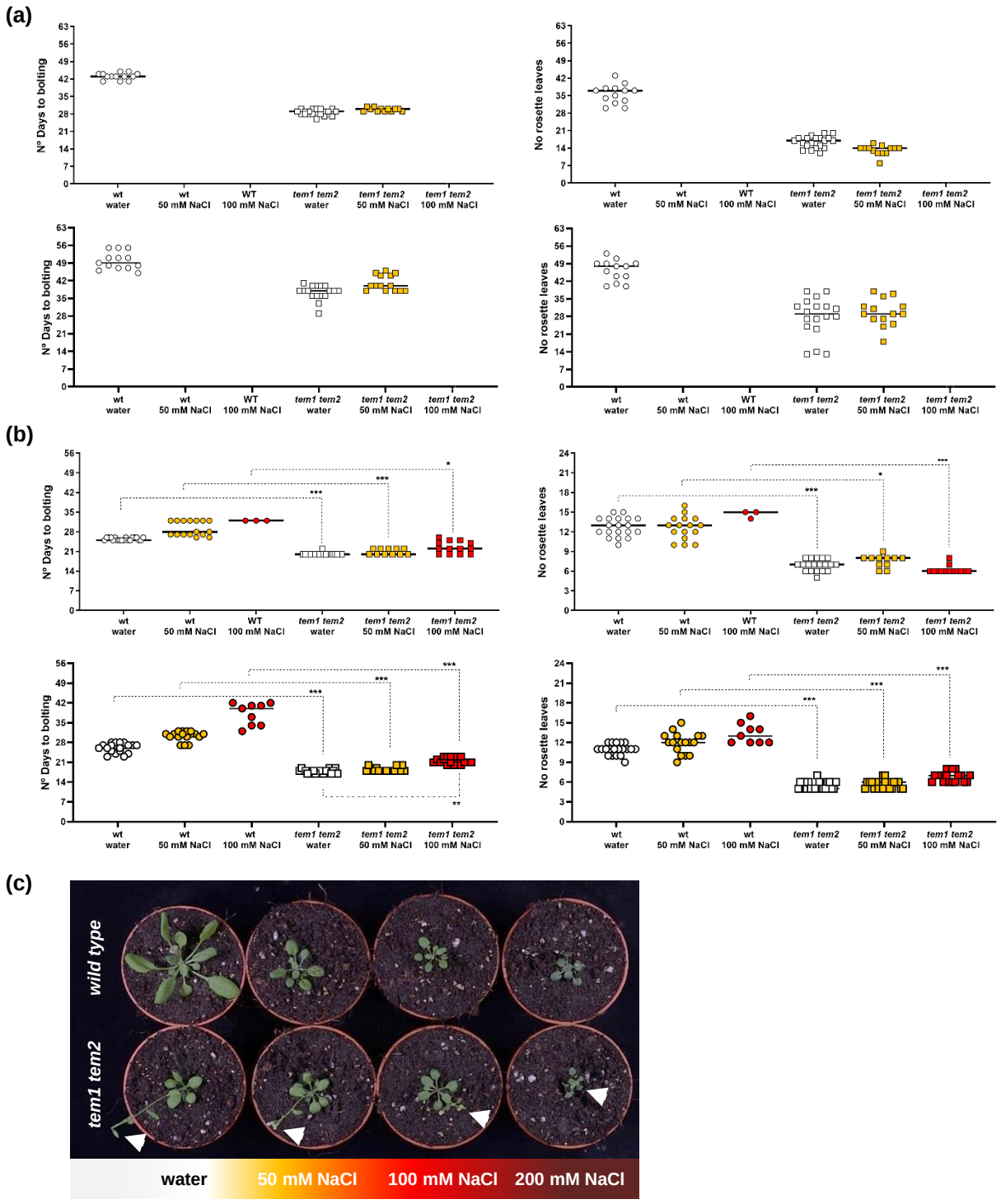


Figure S3. Effect of salinity on the floral transition under SD and LD conditions.
(a) and (b) Biological replicates of flowering time under SD and LD, measured as number of days to bolting and number of rosette leaves formed in wild-type and *tem1 tem2* plants subjected to increasing salinity. Kruskal Wallis one-way ANOVA followed by Dunn's multiple comparisons test was used to assess the statistical significance of differences between treatments and genotypes with $P < 0.005$. (c) Inhibitory effect of increasing salt concentration on leaf and flower development in wild-type and *tem* plants grown for 3 weeks under LD. White arrowheads indicate developing flowers in the mutant.

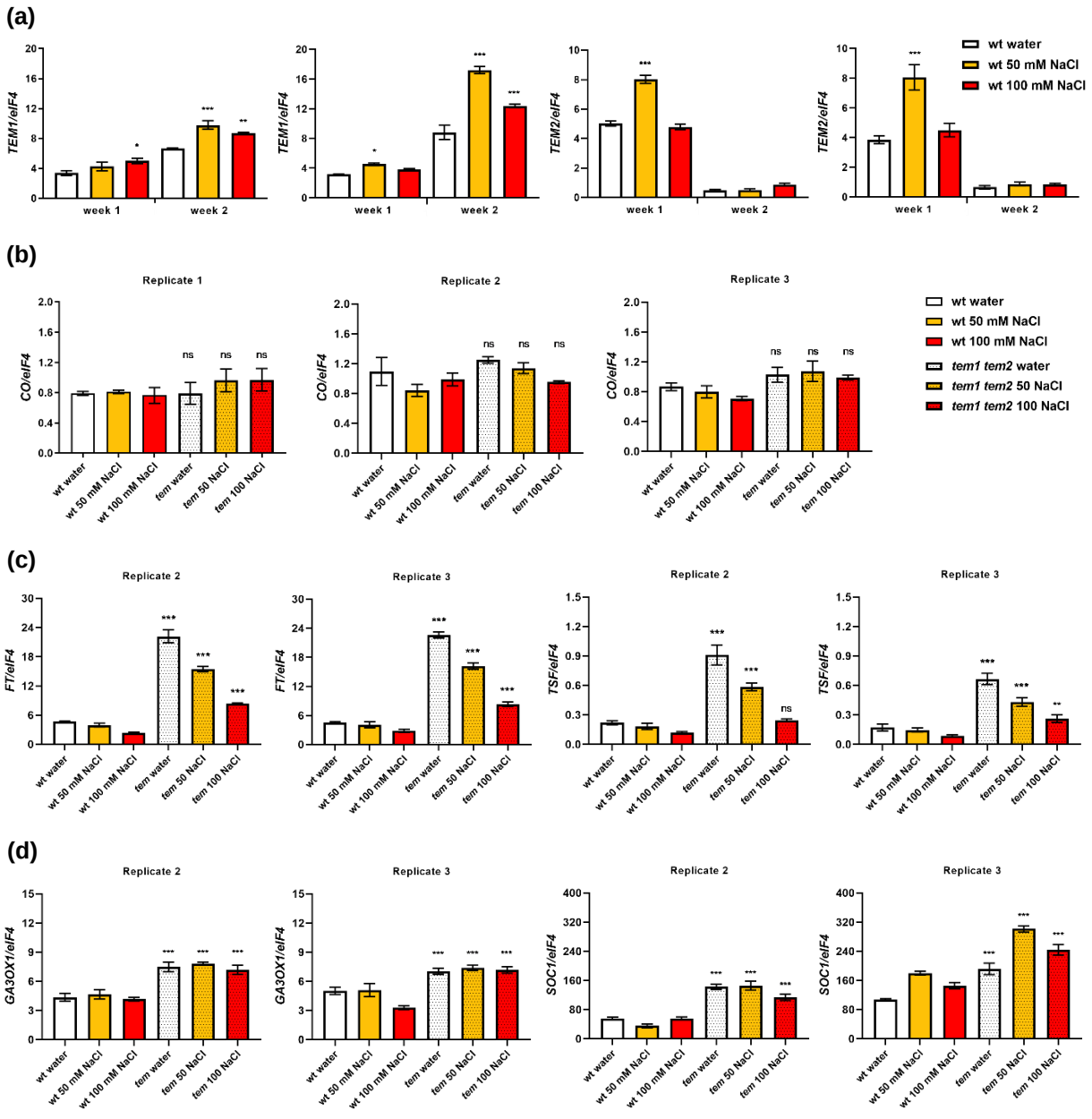
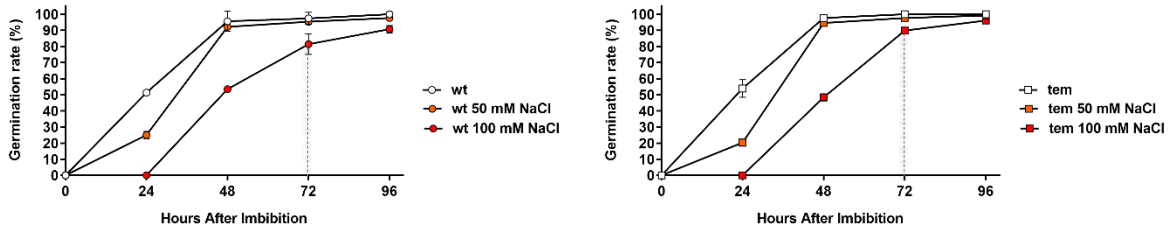


Figure S4. Expression analysis of regulators of the floral transition

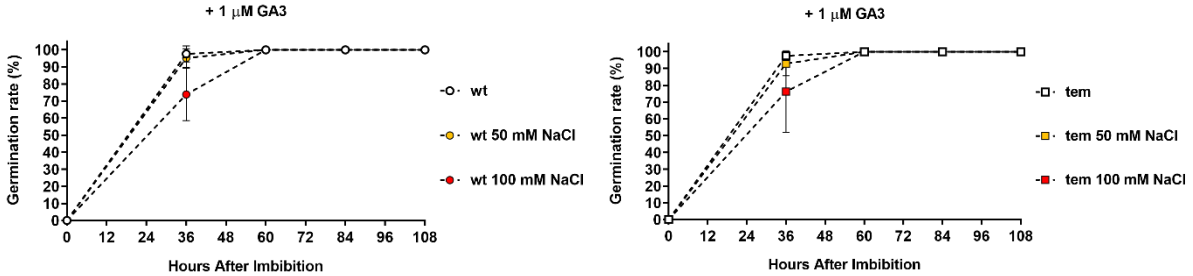
(a) Independent replicates of expression analyses of *TEM1* and *TEM2* genes in wild-type plants grown for one and two weeks under LD and subjected to increasing salt concentration. (b) to (d) Expression analyses of floral promoters in one-week-old wild-type and *tem* seedlings grown under LD in controlled versus salt stress conditions. Biological replicates of RT-qPCR of the floral activator CO (b), the florigens *FT* and *TSF1* (c)**,** *GA3OX1* and the floral integrator *SOC1* (d). One-way ANOVA followed by Tukey's multiple comparisons test was used to assess the statistical significance of differences between treatments and genotypes with *P < 0.005.

(a)



hours	Wild-type 100 mM NaCl		*tem1 tem2* 100 mM NaCl		P value
	%	SD	%	SD	
0	0	0	0	0	ns
24	0	0	0	0	ns
48	53,5	1,68	48,44	2,21	ns
72	81,43	1,97	89,84	1,1	0,03
96	90,69	2,29	96,09	1,1	ns

(b)



(c) **(d)**

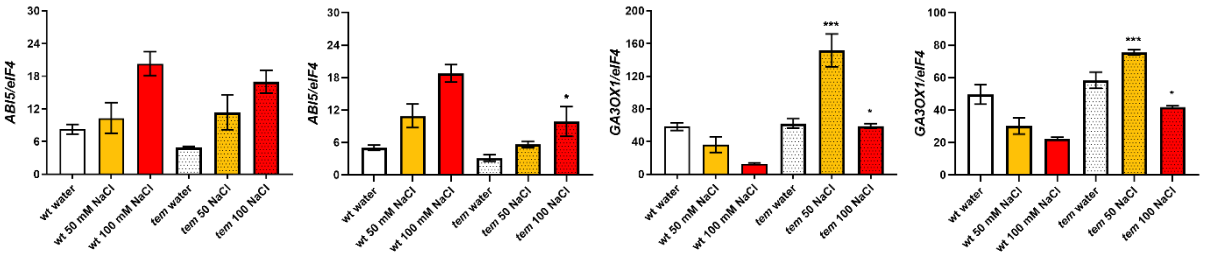


Figure S5. Effect of salinity on wild-type and *tem* seed germination

(a) Germination rate of wild type and *tem* seeds sown on MS medium containing increasing salt concentration, measured every day from imbibition as percentage of seeds showing radicle protrusion. Details of significant difference between genotypes treated with 100 mM NaCl are reported in the table. (b) Germination rate of wild-type and *tem* seeds sown on MS medium containing increasing concentration of NaCl and supplemented with 1 mM GA3, compared to control. (c) and (d) Independent replicates of RT-qPCR of *ABI5* and *GA3ox1* in wild-type and *tem* germinating seeds, collected 48 hours after imbibition under LD.

For germination assays, data represent mean values with SD of 100 seeds for three independent replicates each time-point. Unpaired t-test with Welch's correction was used to assess significant differences between the two genotypes, with $P < 0.005$. For expression analysis, one-way ANOVA followed by Tukey's multiple comparisons test was used to assess the statistical significance of differences between treatments and genotypes with $P < 0.005$.

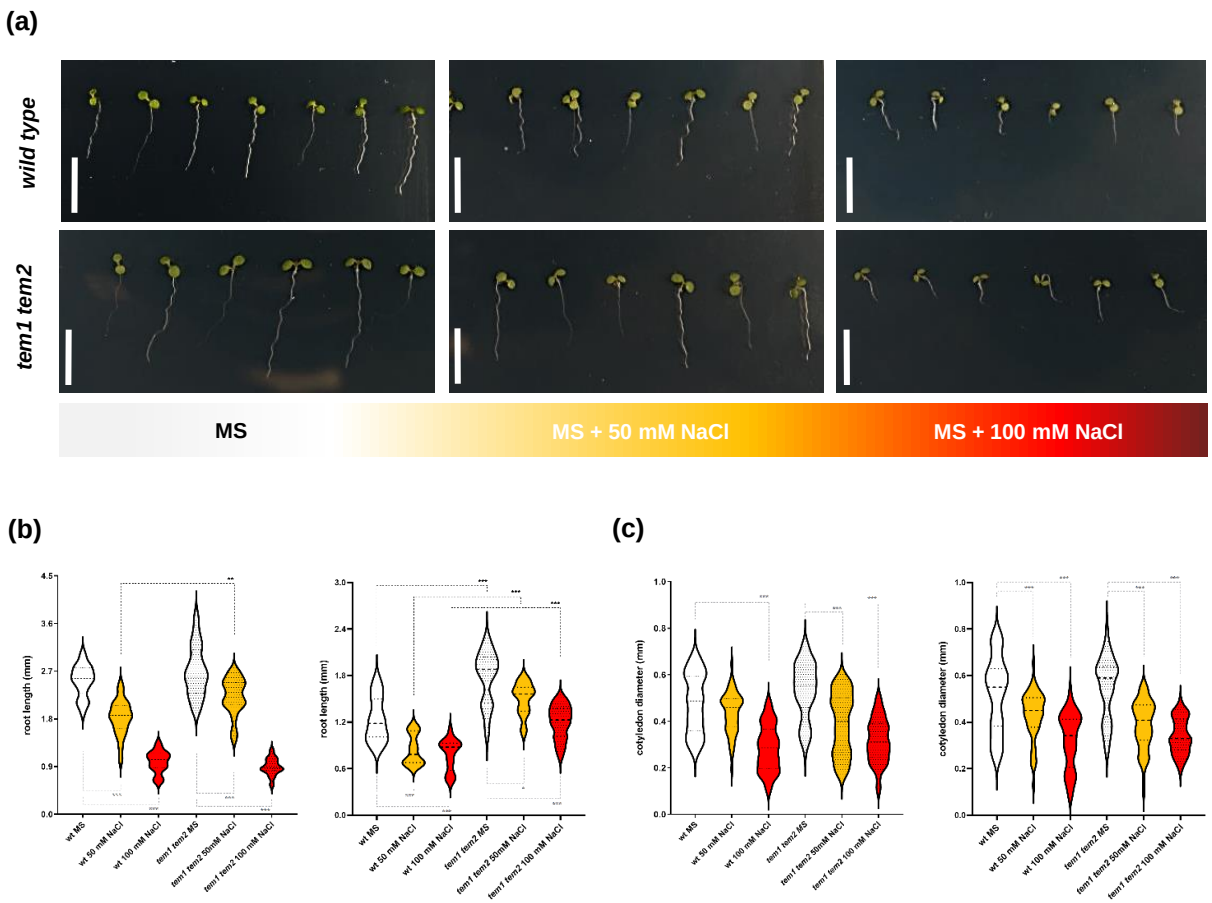


Figure S6. Effect of salinity on wild-type and *tem* seedling growth one week after germination
(a) Inhibitory effect of increasing salt concentration on early stages of vegetative growth. Seeds were sown on MS medium, transferred to different MS plates containing increasing salt concentration upon germination, and seedlings grown for 1 week under LD. (b) Violin plots showing reduction of primary root development in response to salt treatment in seedlings, 7 days after germination. (c) Violin plots showing reduction of cotyledon expansion in seedlings, 7 days after germination. In (b) and (c), two independent replicates are reported. Significant differences between treatments and genotypes were assessed by one-way ANOVA followed by Tukey's multiple comparisons test with $P < 0.005$.

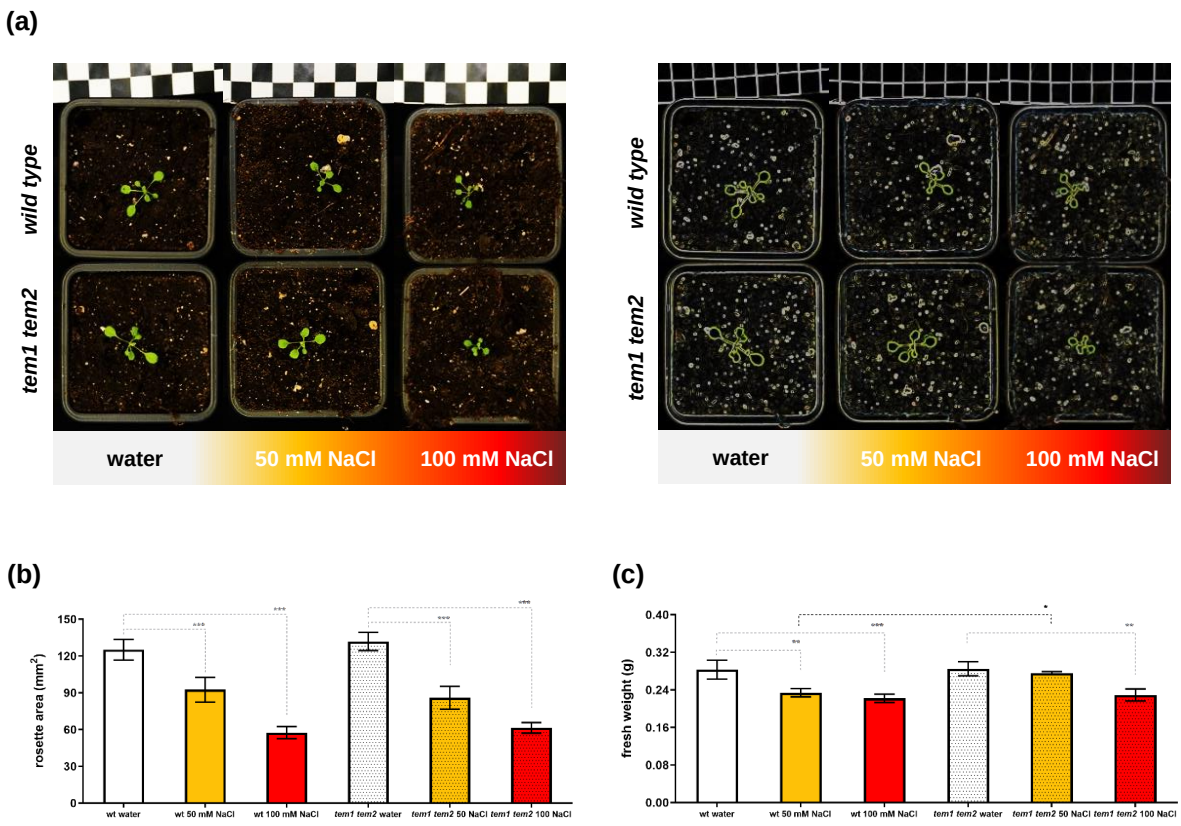


Figure S7. Effect of salinity on wild-type and *tem* seedling growth two weeks after germination.
(a) Inhibitory effect of increasing salt concentration on seedlings grown under LD, 14 days after germination on soil. Images of plants before (left) and after (right) processing with Image J. (b) Bar plot showing rosette area in 2-week-old seedlings grown under LD in soil and irrigated with increasing salt content. (c) Bar-plot showing biomass accumulation of wild type and *tem* 2-week-old plants grown on soil under LD and treated with increasing salt concentration. Mean values with SD of three independent replicates (N=20) are reported. For phenotypic quantifications, significant differences between treatments and genotypes were assessed by one-way ANOVA followed by Tukey's multiple comparisons test with $P < 0.005$.

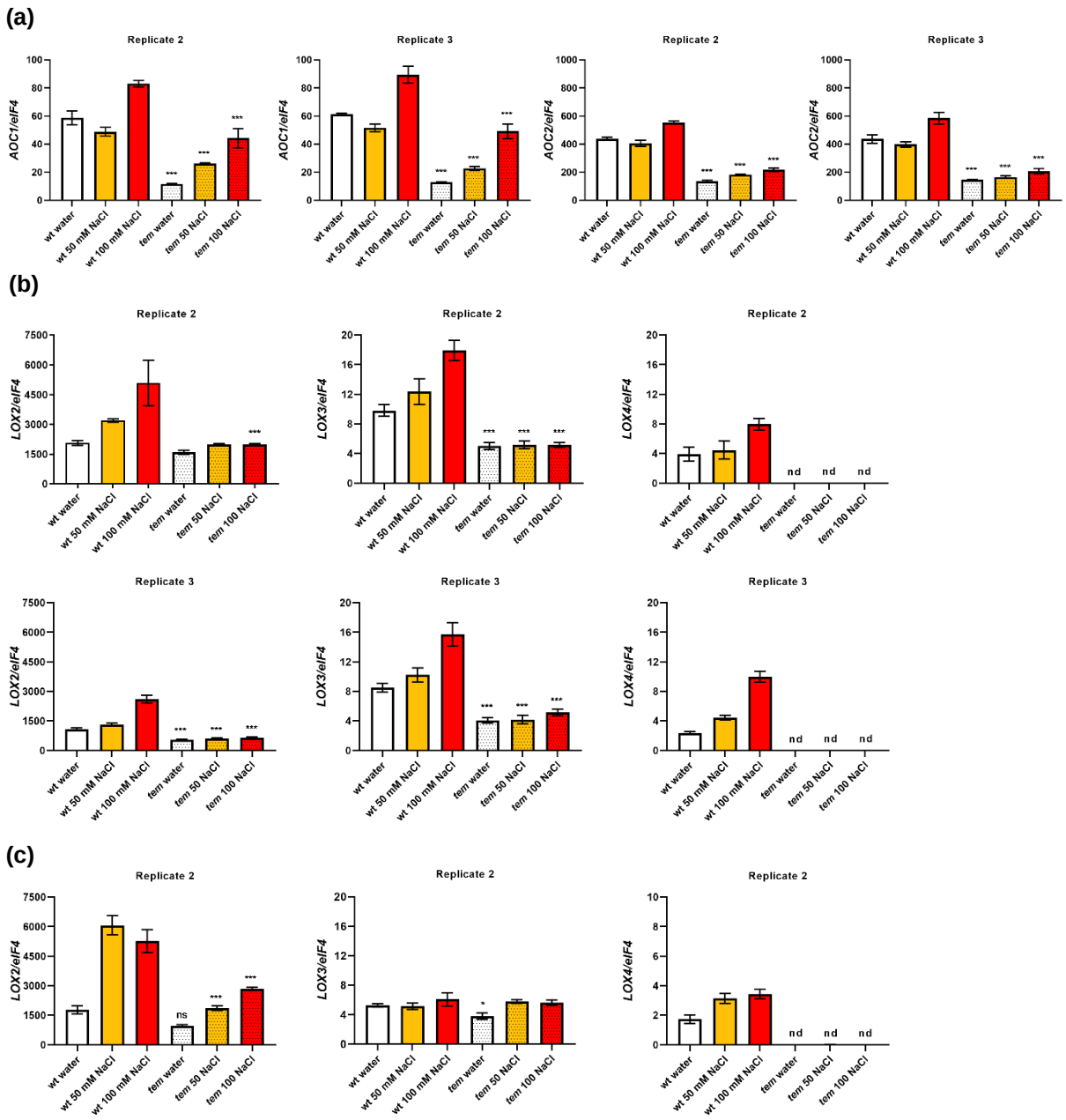


Figure S8. Expression analysis of components of the JA signaling pathway

(a) to (c) Independent replicates of expression analysis of JA biosynthetic genes in wild-type and mutant seedlings grown under LD in controlled versus salt stress conditions. (a) RT-qPCR of *AOC1* and *AOC2* in 1-week-old seedlings. (b) and (c) RT-qPCR of *LOX2, LOX3* and *LOX4* in 1-week-old seedlings and 2-week-old plants, respectively. Significant differences between treatments and genotypes were assessed using one-way ANOVA followed by Tukey's multiple comparisons test with $P < 0.005$.

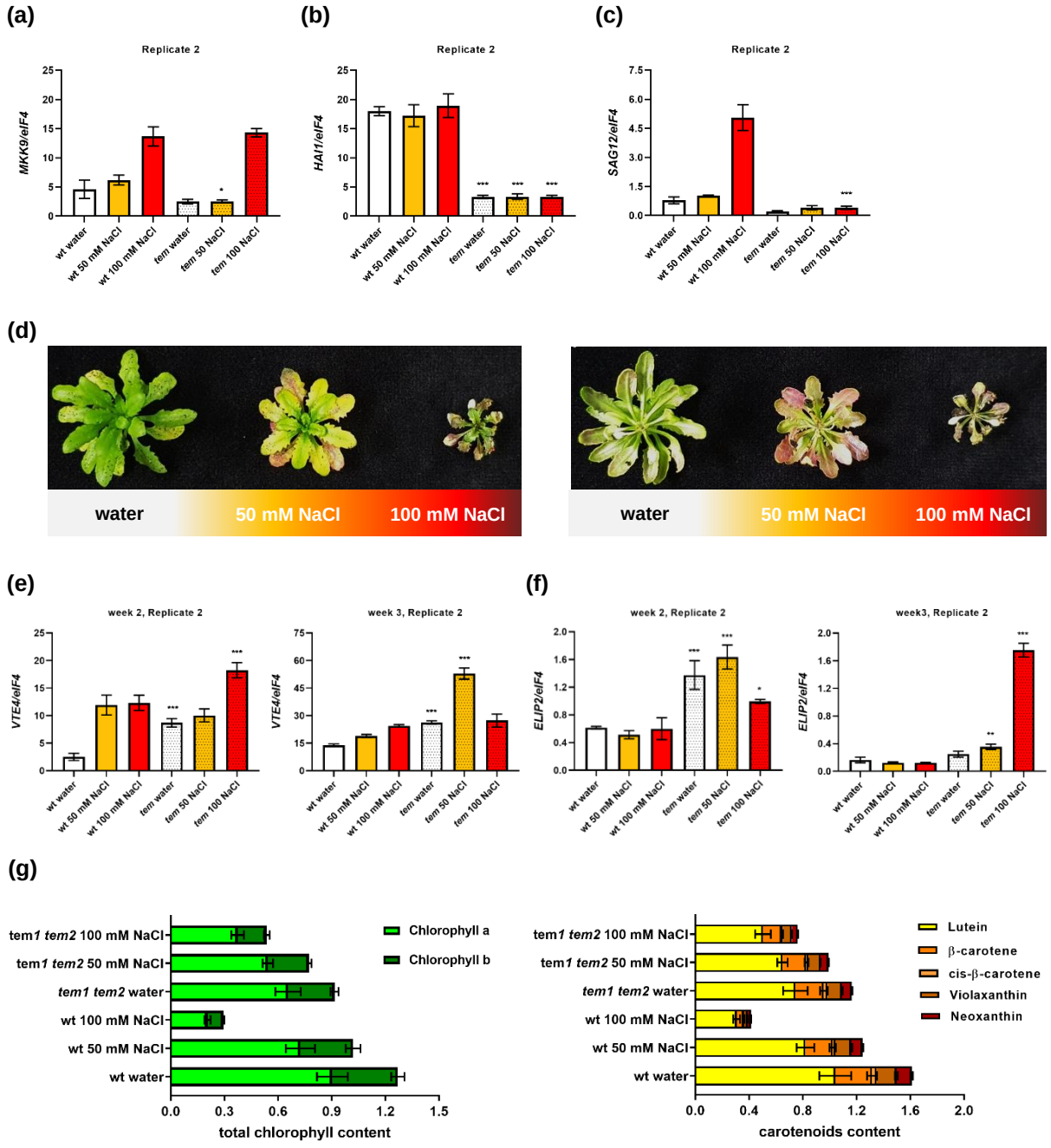


Figure S9. Analysis of photoprotection and senescence in response to salt stress.
(a) and (b) Independent replicates of RT-qPCR of *MKK9* and *HAI1* in 2-week-old plants. (c) Independent replicate of RT-qPCR of *SAG12* in 3-week-old plants. (d) Images of *TEM1-OE* plants showing alterations of rosette leaf size and color after 5 weeks of salt treatment. Left, top view of salinity-induced senescence visible as leaf yellowing and drying; right, bottom view of stress-induced accumulation of anthocyanins. (e) and (f) Independent replicates of RT-qPCR of *G-TMT1/VTE4* and *ELIP2* in 2-week-old and 3-week-old plants. (g) Detailed metabolic analysis of photosynthetic pigments degradation in 4-week-old wild-type and *tem* plants in response to salinity. Left, stacked bar plot showing quantification of chlorophyll a and b in different samples. Right, stacked bar plot showing quantification of lutein, β-carotene, violaxanthin and neoxanthin in different samples.
For expression analysis, significant differences between treatments and genotypes were assessed using one-way ANOVA followed by Tukey's multiple comparisons test with $P < 0.005$.

(a)

Name: RAV1(1)
Species: Arabidopsis thaliana
Family: AP2/EREBP
Logo:

Matrix:													
	A |	14	16	7	0	47	62	0	69	9	41	34	27
	C |	17	11	14	62	12	4	69	0	7	4	6	9
	G |	12	10	35	0	9	3	0	0	32	4	10	17
	T |	6	14	1	0	0	0	0	0	21	20	19	16

Max. score: 10.65
Threshold: 5.01

Name: RAV1(2)
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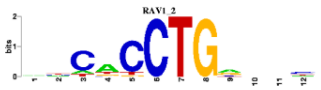
Family: AP2/EREBP
Logo:

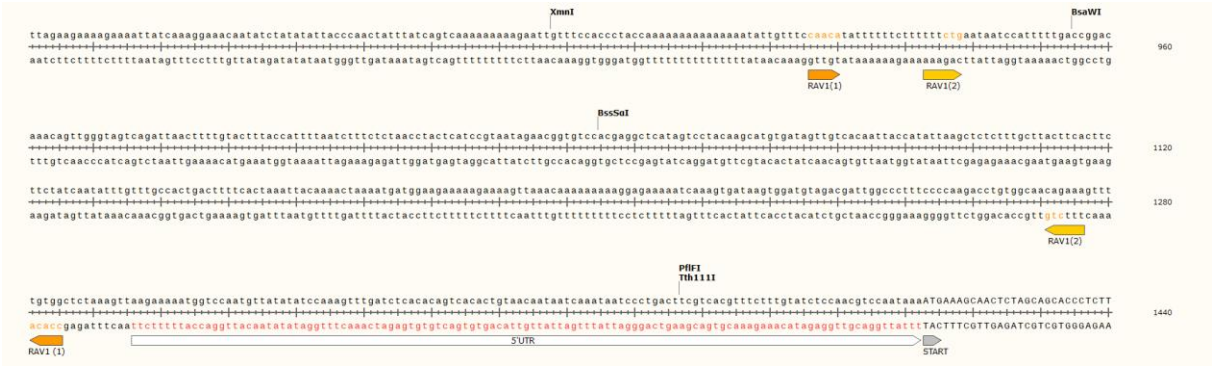


Matrix:													
	A |	22	13	8	40	1	0	0	0	24	12	12	8
	C |	12	15	49	6	56	65	0	0	7	15	14	20
	G |	10	8	1	8	3	0	0	58	19	18	16	5
	T |	18	28	7	11	5	0	65	0	5	9	10	13

Max. score: 11.21
Threshold: 4.98

(b)

>VTE4: 497 bp from ATG; -127 bp form ATG



(c)

>HPCA1: -2080 bp form ATG

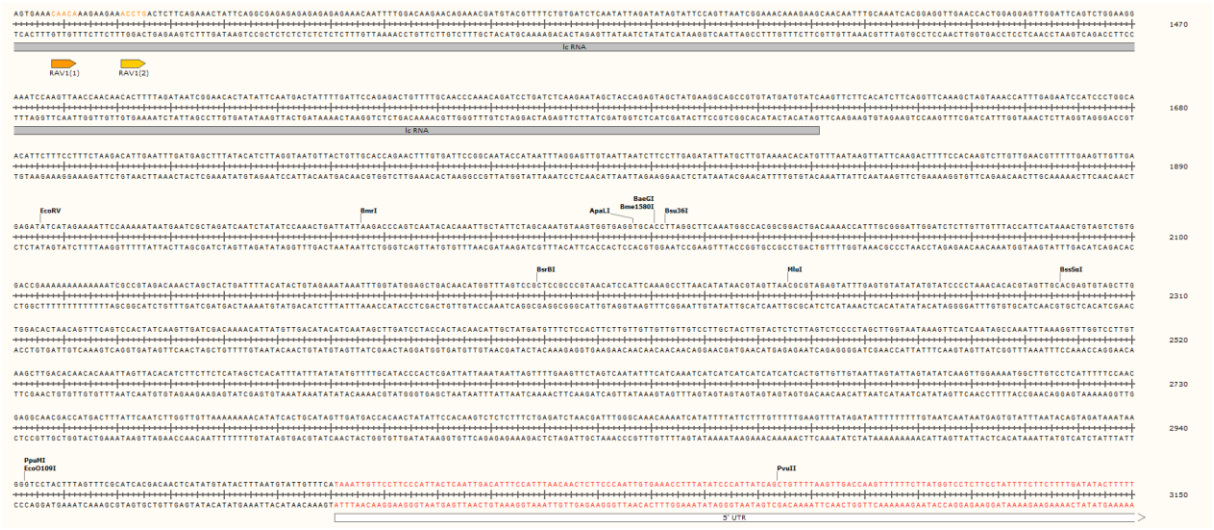


Figure S10. In silico promoter analysis of putative downstream targets of TEMs.
(a) Bipartite Consensus sequences bound by RAV proteins. Left, AP2 binding site; right, B3 binding site. (b) Presence of two putative RAV consensus sequences in forward and reverse orientation in the promoter of *VTE4*. (c) Presence of a putative RAV consensus sequence in a long non-coding RNA sequence located in the promoter of *HPCA1*. Promoter analysis was carried out using Athamap.