# Supporting Information (SI Appendix)

## AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants

**Kentaro Nakaminami, Masanori Okamoto, Mieko Higuchi-Takeuchi, Takeshi Yoshizumi, Yube Yamaguchi, Yoichiro Fukao, Minami Shimizu, Chihiro Ohashi, Maho Tanaka, Minami Matsui, Kazuo Shinozaki, Motoaki Seki and Kousuke Hanada**

## Supporting Text

### Plant material and growth conditions

Arabidopsis thaliana ecotype Columbia-0 was used in the majority of the experiments. Single and double mutants of *pepr* plants were also used from a previously described study (1). Plants were grown on agar plates containing Murashige and Skoog (MS) medium with a final concentration of 1 % sucrose at 22 ºC under long day (16h/8h light/dark) conditions at a light intensity of 50–75 $\mu molm^{-2}s^{-1}$. Ten- to fourteen-day-old Arabidopsis plants were used in the salinity stress assays.

### Generation of AtPROPEP3/AT13-overexpressing and RNAi plant lines

In order to generate transgenic plants overexpressing the various small coding genes, abiotic-stress-related small coding genes were introduced into pMDC32, a vector that possesses a double 35S promoter (2). For the functional studies, knock-down RNAi lines of the AtPROPEP3/AT13 gene was constructed as follows. The RNAi construct was generated using a method described in Higuchi et al (3). The appropriate RNAi fragment was prepared using 2 oligos:5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTTTTATAGTCATTTGTTTCGAA TATGAATTGGATTAATAAAGATCGAATGGCAATGAGTAAAGGAGAA-3' and 5'-GGGGACCACTTTGTACAAGAAAGCTGGGTTTTTTATAGTCATTTGTTTCGAATATGA ATTGGATTAATAAAGATCGATTCTCCTTTACTCATTGCCAT-3' and the fragment was then introduced into pMDC32. The recombinant binary vector was subsequently introduced into Agrobacterium tumefaciens (strain GV3101) and inserted into the Arabidopsis genome using the floral-dip method (4). The level of AtPROPEP3/AT13 mRNA expression in all of the transgenic lines was confirmed by qRT-PCR.

### Salinity stress assay

Salinity tolerant lines among the transgenic lines overexpressing the small coding genes were identified using a plate-based stress test and a root elongation assay. The initial screening utilizing

www.pnas.org/cgi/doi/10.1073/pnas.1719491115

the plate-based test was conducted on T2 generation plants of at least 10 lines for each of the small coding genes. For the assessment of salt tolerance, one-week-old plants were transferred to MS plates containing 200 mM NaCl. The plants were grown at 22 ºC for a period of 10 to 14 days after which the number of surviving plants was counted. P-values were calculated using the chi square test in order to identify lines with significant levels of salt tolerance. Small coding genes where more than two lines of ox plants exhibited a p-value of $< 0.05$ were considered for further screening.

### Liquid culture-based salinity stress test

WT, AtPROPEP3/AT13-ox, or RNAi plants were grown in liquid MS medium for 10 days at 22 ºC under long day conditions. The salinity stress test was performed by replacing the liquid medium with new medium containing 150 mM or 125 mM NaCl. The plants were grown at 22 ºC for a period of 10 to 14 days and survivorship was subsequently evaluated by measuring the chlorophyll content in the plants.

### Measurements of chlorophyll content

Chlorophyll content was measured using a method as previously described in Myouga et al. (5). Whole seedlings of salinity stressed plants growing in liquid culture were used for the measurements. Chlorophyll was extracted with dimethylformamide and the absorbance of the extracted solution was measured at A646.8 and A663.8 with a SmartSpec Plus (Bio-Rad, Hercules, CA, USA). Chlorophyll content was calculated using the following formula: ($\text{Chl a + b} = 17.67A646.8 + 7.12A663.8$).

### Peptide design and treatment assay

Synthetic AT13 peptide fragments were purchased from Eurofins (Ebersberg, Germany) and the designs of the peptide fragments are summarized in Table S3. The synthetic peptides were dissolved in dimethyl sulfoxide (DMSO) and peptide treatments were conducted using the liquid culture-based salinity stress assay. WT or RNAi seedlings were grown in liquid MS medium for 7 days and the medium was then replaced with MS medium containing each peptide fragment and grown for an additional 3 days to serve as a peptide pre-treatment. The salinity stress test was performed by replacing the peptide-containing medium with MS medium containing NaCl and the peptide after the pre-treatment. The plants were grown at 22 ºC for a period of 10 to 14 days and survivorship was evaluated by measuring the chlorophyll content in the plants.

### Microarray analysis

Total RNA was extracted from two biological replicates of eleven-day-old AtPROPEP3/AT13-ox plants, plants treated with AtPEP3/AT13 peptide, and non-treated WT plants with Plant RNA Reagent (Thermo Fisher Scientific, Waltham, MA, USA). Approximately 500 ng of total RNA was used for cRNA labeling using a Quick Amp labeling kit (Agilent Technologies, Palo Alto, CA, USA) and the labeled cRNA was then hybridized to a 44K custom array (Agilent Technologies) as previously described (6). Arrays were scanned with a microarray scanner (G2505B, Agilent Technologies). The microarray data are available on the GEO website (GEO ID: GSE78515). The array intensities were processed using the Bioconductor (www.bioconductor.org) package in the R software environment (www.r-project.org). Hybridization intensities in the arrays were normalized among different arrays by quantile normalization. Normalized intensities of two replicates were compared with LIMMA in the R software environment (www.r-project.org). Up- and down-regulated genes were defined as genes with significantly higher and lower intensities, respectively, in AtPROPEP3/AT13-ox plants vs. non-treated WT plants or in AtPEP3/AT13 peptide treated plants vs. non-treated WT plants (False Discovery Rate <0.05). GO assignments for Arabidopsis genes were obtained from TAIR (www.arabidopsis.org) and used for determining statistically overrepresented GO Categories in either AtPROPEP3/AT13-ox plants or plants treated with AtPEP3/AT13 peptide. Only GO categories belonging to biological processes were analyzed among the top three GO categories. The number of regulated genes in either AtPROPEP3/AT13-ox plants or plants treated with AtPEP3/AT13 peptide was obtained in each of the GO categories. In each GO category, the expected values were then compared with the observed values using the $\chi2$ test to determine whether the ratio of observed numbers of regulated genes to those of non-regulated genes was significantly higher than the expected ratio. To correct for multiple testing, a moderated P value (q) was estimated from raw $\chi2$ test P-values using Q-VALUE software (7). The null hypothesis was rejected if q values were < 0.05.

### Sample preparation for MS/MS analysis

Two-week-old wild-type seedlings were treated with or without application of 200mM NaCl. Total protein was extracted with Lysis Buffer (150 mM NaCl, 1% Triton X-100, 50 mM Tris-HCl (pH 8.0) containing cOmplete protease inhibitor cocktail (Roche, Basel, Switzerland)). Sample preparation was performed as previously described (8). The same amount of total protein samples was separated using SuperSep Ace 15 % (Wako, Osaka, Japan) precast gels and stained using SilverSNAP for a Mass Spectrometry kit (Thermo Fisher Scientific, Waltham, MA, USA). The lower area of gels (below approximately 20 kDa) was cut out and destained using the same SilverSNAP kit. Protein samples were partially digested by trypsin at 37 ºC for 1 h after reduction with dithiothreitol and alkylation with iodoacetamide.

### LC-MS/MS analysis and database searching

Purified peptide samples were analyzed using a HTC-PAL/Paradigm MS4 system coupled to a LTQ-Orbitrap XL (Thermo Fisher Scientific) mass spectrometer. Details of LC-MS/MS analysis and database searching were previously described (8). An amino acid sequence of the AtPEP3/AT13 peptide (EIKARGKNKTKPTPSSGKGGKHN) was searched from obtained spectra using the MASCOT server (version 2.2). The mascot search parameters were as follows: set off the threshold at 0.05 in the ion-score cut-off, peptide tolerance at 10 ppm, MS/MS tolerance at ±0.6 Da, peptide charge of 2+ or 3+, semiTrypsin as the enzyme allowing up to seven missed cleavages.

## References

1. Yamaguchi Y, Huffaker A, Bryan AC, Tax FE, & Ryan CA (2010) PEPR2 is a second receptor for the Pep1 and Pep2 peptides and contributes to defense responses in Arabidopsis. *Plant Cell* 22(2):508-522.
2. Curtis MD & Grossniklaus U (2003) A gateway cloning vector set for high-throughput functional analysis of genes in planta. *Plant Physiol* 133(2):462-469.
3. Higuchi M*, et al.* (2009) Simple construction of plant RNAi vectors using long oligonucleotides. *Journal of plant research* 122(4):477-482.
4. Clough SJ & Bent AF (1998) Floral dip: a simplified method for Agrobacterium-mediated transformation of Arabidopsis thaliana. *Plant J* 16(6):735-743.
5. Myouga F, Motohashi R, Kuromori T, Nagata N, & Shinozaki K (2006) An Arabidopsis chloroplast-targeted Hsp101 homologue, APG6, has an essential role in chloroplast development as well as heat-stress response. *Plant J* 48(2):249-260.
6. Hanada K*, et al.* (2013) Small open reading frames associated with morphogenesis are hidden in plant genomes. *Proc Natl Acad Sci U S A* 110(6):2395-2400.
7. Storey JD, Bass AJ, Dabney A, & Robinson D (2015) qvalue: Q-value estimation for false discovery rate control. R package version 2.2.2.
8. Fujiwara M*, et al.* (2014) Interactomics of Qa-SNARE in Arabidopsis thaliana. *Plant Cell Physiol* 55(4):781-789.

## Supporting Figure Legends

**Fig. S1. Homology search and expression analysis of small coding gene candidates.** (A) Box plots of the numbers of homologs in other plant species of small coding genes analyzed in the present study (YES) and not analyzed in the present study (NO). (B) Box plots of fold change of small coding genes analyzed in the present study (YES) and not analyzed in the present study (NO). Gene expression levels and fold change were calculated from our previously published microarray data (6). (C) Summary of peptide candidates containing secreted signal for transgenic Arabidopsis plants.

**Fig. S2. Salinity stress tolerance of overexpressing small coding gene.** Image of salinity stress tolerance of *AT5*, *AT23*, *AT13* and *AT23*-ox plants (T2 generation) by plate-based salinity stress test (top) and survivability (bottom). One-week-old plants were transferred to 200 mM NaCl containing MS plates and grown for 10 to 14 days. Ox plants (red) were compared with WT and T. halophila (positive control). This test revealed that several small coding genes overexpressing plants exhibited salinity stress tolerance and summarized in Table S2. These are the candidates of peptide hormones or -like compounds.

**Fig. S3. Primary root growth of overexpressing small coding gene under salinity stress.** Image of root growth under salinity stress of *AT5*, *AT23*, *AT13* and *AT23*-ox plants (T3 generation) compared with WT (left) and the measurement of primary root (right). One-week-old plants were transferred to 150 mM NaCl containing MS plates and grown on vertical for 14 days. This test revealed that these 4 small coding genes are the candidates of peptide hormones or -like compounds for salinity stress tolerance.

**Fig. S4. Fold change of small coding genes under salinity stress treatment.** Gene expression levels and fold change were calculated from our previously published microarray data (6). Box plots indicated the 4 candidates of salinity stress tolerance related small coding genes, *AT5*, *AT12*, *AT13* and *AT23* (+) compared with the other 11 genes (-) used for screening in this study. Salinity stress tolerance related small coding genes showed higher induction under salinity stress treatment.

**Fig. S5. Specific expression of AT13 mRNA.** Diagrammatic representation of mRNA expression of *AT13* in different tissues, light and environmental stress conditions as determined by microarray analysis. The diagram was obtained from the website, HANADB-AT (http://evolver.psc.riken.jp/seiken). *AT13* mRNA was specifically induced by salinity stress.

**Fig. S6. Expression level of *AtPROPEPs* under salinity stress treatment.** (A) Fold changes of *AtPROPEP* genes were analyzed from our previously published microarray data (6). Two-week-old plants were treated with 200 mM NaCl for 2 (blue) and 6 hours (black). (B) Normalized intensities of *AtPROPEP* genes from microarray data are visualized. The y-axis represents quantile-normalized hybridization intensities from the microarray experiments.

**Fig. S7. AT13 peptide induce salinity stress tolerance.** Whole plant image of peptide treatment test (three replicate) and chlorophyll measurement after test. Seven-day-old plants were pre-treated with 10 μM peptide for 3 days and then 150 mM NaCl was treated with peptides under liquid culture-based salinity stress test. Plants were grown for 10 days and chlorophyll contents were measured to evaluate the salinity stress tolerance. DMSO treatment was as a negative control.

**Fig. S8. Expression levels of the *PEPC1* gene in response to Pep3 treatment and overexpression of *At13*.** In relative comparison to treatment with DMSO (normalized value = 1), a significant up-regulation of *PEPC1* (10.10) was observed in response to the application of Pep3. When relative expression values were compared to wild-type plants (normalized value = 1), the overexpression of *At13* resulted in up-regulation of *PEPC1* (3.02), whereas RNAi suppressed its expression (0.51).

**Fig. S9. AT13RNAi exhibited salt sensitive phenotype.** Whole plant image of *AT13*RNAi plants under liquid culture-based salinity stress test. Ten-day-old plants were treated with 150 mM NaCl and grown on 10 more days. The sensitive phenotype of AT13RNAi plants were complemented with treatment of AT13 peptide. Chlorophyll contents were measured to evaluate tolerance and sensitivity.

**Fig. S10. Treatment with the AT13 peptide does not affect osmotic stress tolerance.** Representative image of plants under a liquid culture-based osmotic stress test. Seven-day-old wild-type plants were pre-treated with 100 nM peptide for 3 days. Subsequently, treatment with 500 mM mannitol was utilized for an osmotic stress with peptides under a liquid culture-based test. Plants were grown for 10 days and fresh weights were determined to evaluate the osmotic stress tolerance.

**Fig. S11. Peptide design of AT13 fragments for treatment assay.** Amino acid sequence of AT13-5 fragment and different length of synthetic peptide fragments used in the salt treatment assay.

**Fig. S12. AT13 peptide induced salinity stress tolerance.** Images of representative plants under liquid culture-based salinity stress test. Seven-day-old plants were pre-treated with different length of 100 nM AT13 peptides for 3 days and then 150 mM NaCl was treated with peptides under liquid culture-based salinity stress test. Chlorophyll contents were measured to evaluate tolerance and sensitivity.

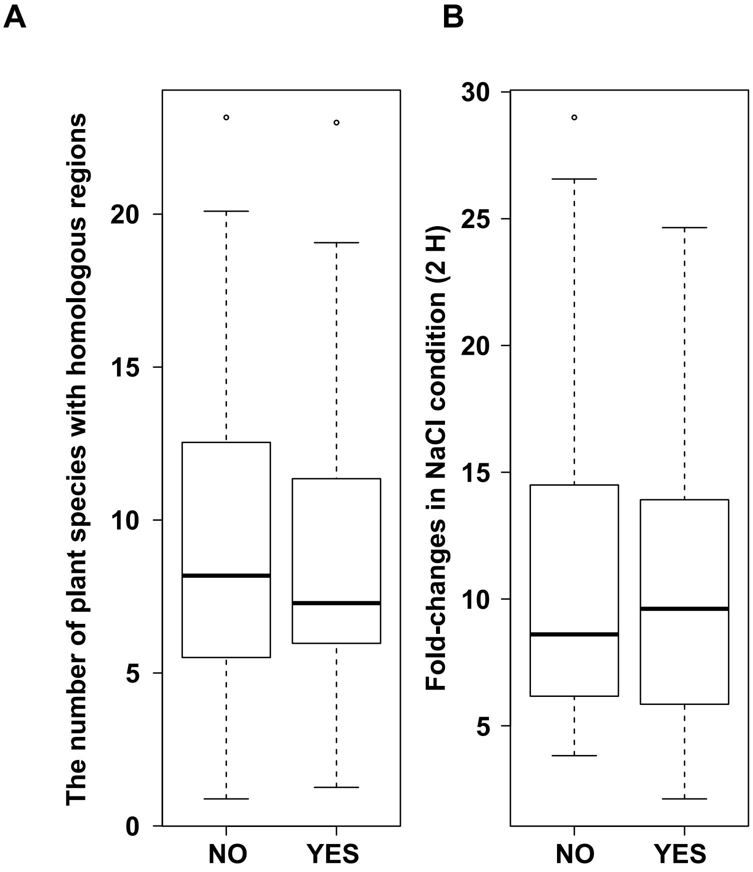
**Fig. S13. High purity AT13 peptide induces salinity stress tolerance.** Images of representative plants under a liquid culture-based salinity stress test. Seven-day-old plants were pre-treated with high purity (>90%) Pep3 or AT13(11-23) peptides for 3 days. Subsequently, 150 mM NaCl was applied with peptides under a liquid culture-based salinity stress test. Chlorophyll contents were measured to evaluate tolerance and sensitivity to the stress treatment.

**Fig. S14. Detection of the AtPep3 peptide.** (A) C-terminal amino acid sequence of AtPep3. Underline indicates the detected fragment of Pep3 by LC-MS/MS and red characters indicate the minimum size of the Pep3 peptide required to confer tolerance to salinity stress under our experimental conditions. (B) LC-MS/MS spectrum of the AtPep3 fragment. (C, D) Relative abundance of AtPep3 detected from non-treated (C) and NaCl treated samples (D).

**Fig. S15. *pepr* mutants exhibited salt sensitive phenotype.** Representative image of *pepr* mutant plants under liquid culture-based salinity stress test. Ten-day-old plants were treated with 125 mM NaCl and grown on 10 more days. Chlorophyll contents were measured to evaluate tolerance and sensitivity.

**Fig. S16. Phenotype of *pepr* mutants plants subjected to salinity stress.** Images of representative plants after each peptide/salt treatment (top). Chlorophyll content in plants after each peptide/salt treatment (bottom). Seven-day-old single or double receptor mutant plants were pre-treated with 100 nM of a Pep3 peptide fragment for 3 days (peptide pre-treatment) followed by a combined treatment with the peptide plus 150 mM NaCl. All treatments were carried out in liquid culture. Plants were grown for 10 days and chlorophyll content was subsequently assessed

# Fig. S1



C

| | No. of gene with secreted signal | No. of gene without secreted signal | Proportion of genes with secreted signal |
|---|---|---|---|
| **No. of genes analyzed in the present study** | 8 | 9 | 47% |
| **No. of genes not analyzed in the present study** | 11 | 34 | 24% |

**Fig. S2**

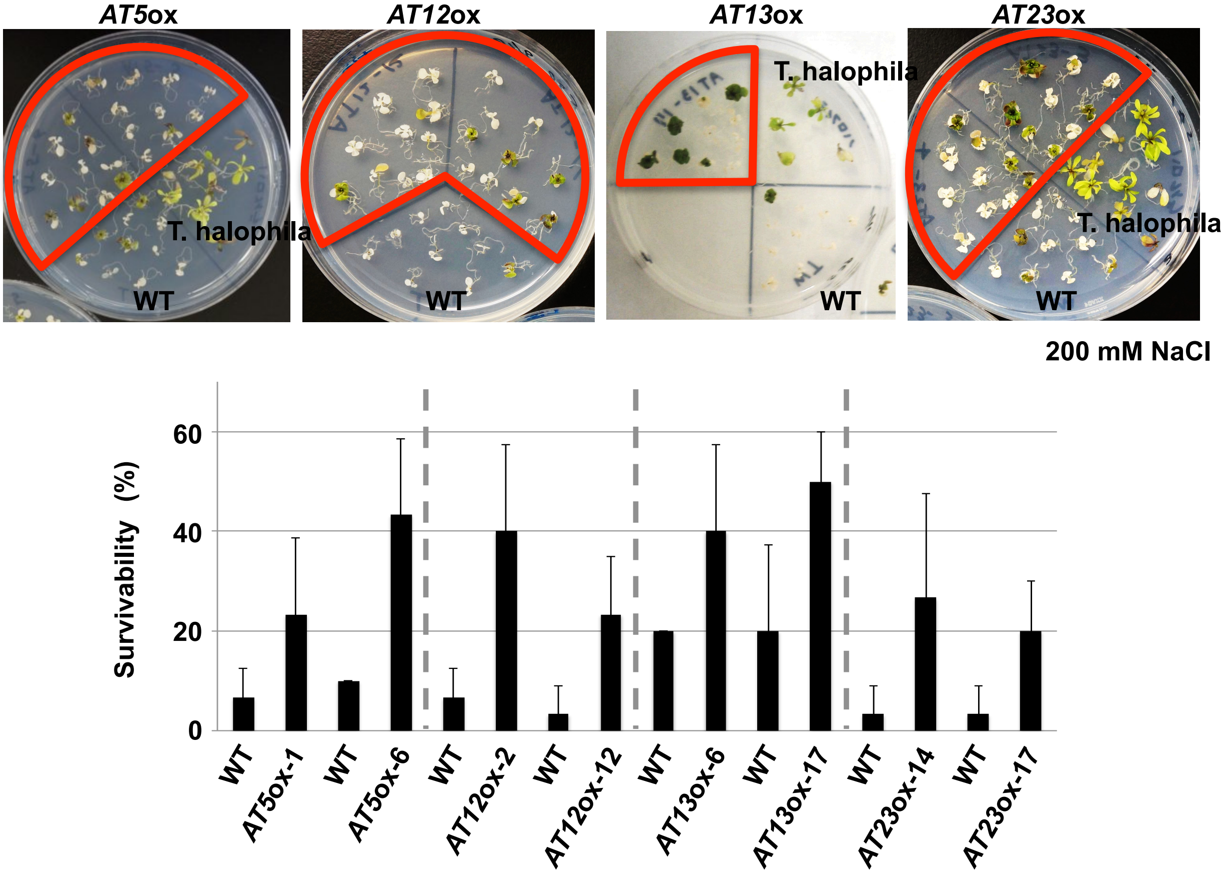

AT5ox
AT12ox
AT13ox
AT23ox
T. halophila
WT
T. halophila
WT
T. halophila
WT
T. halophila
WT
200 mM NaCl
Survivability (%)
0
20
40
60
WT
AT5ox-1
WT
AT5ox-6
WT
AT12ox-2
WT
AT12ox-12
WT
AT13ox-6
WT
AT13ox-17
WT
AT23ox-14
WT
AT23ox-17

**Fig. S3**

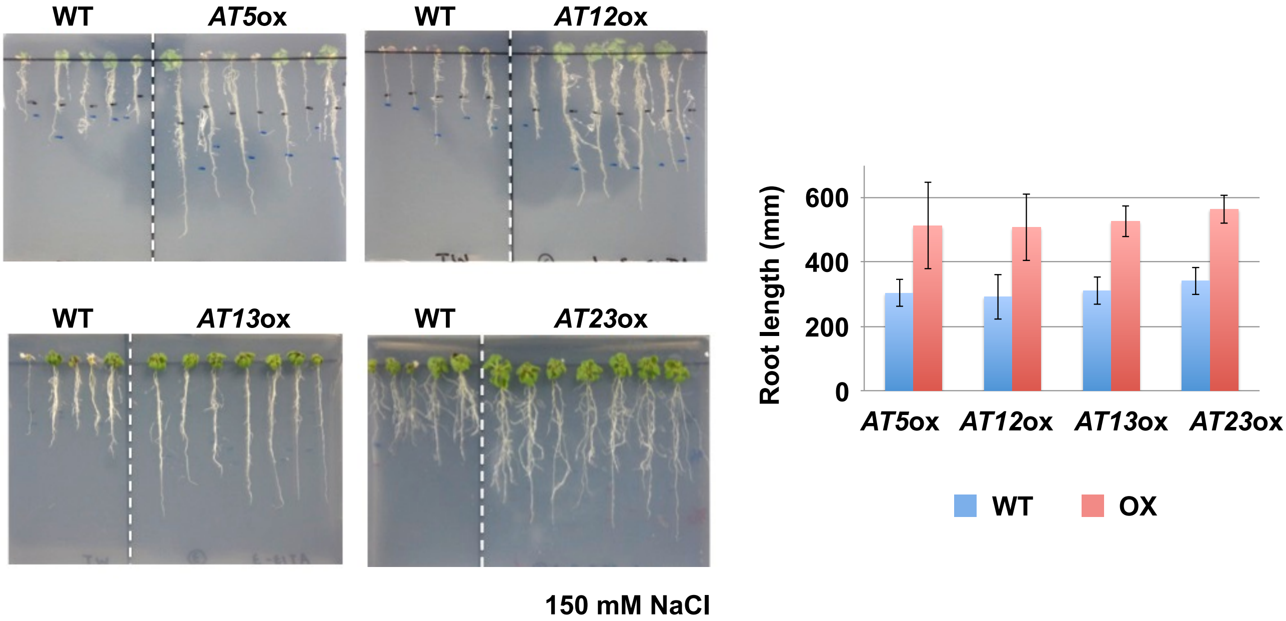
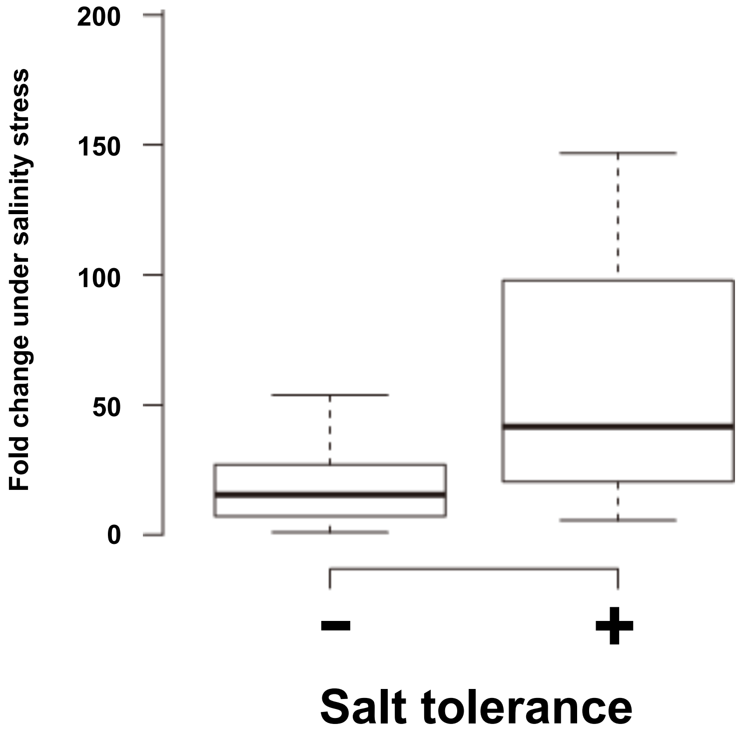

WT
*AT5*ox
WT
*AT12*ox
WT
*AT13*ox
WT
*AT23*ox
150 mM NaCl
Root length (mm)
600
400
200
0
*AT5*ox
*AT12*ox
*AT13*ox
*AT23*ox
WT
OX

**Fig. S4**



200
150
100
50
0
Fold change under salinity stress
-
+
Salt tolerance

# Fig. S5

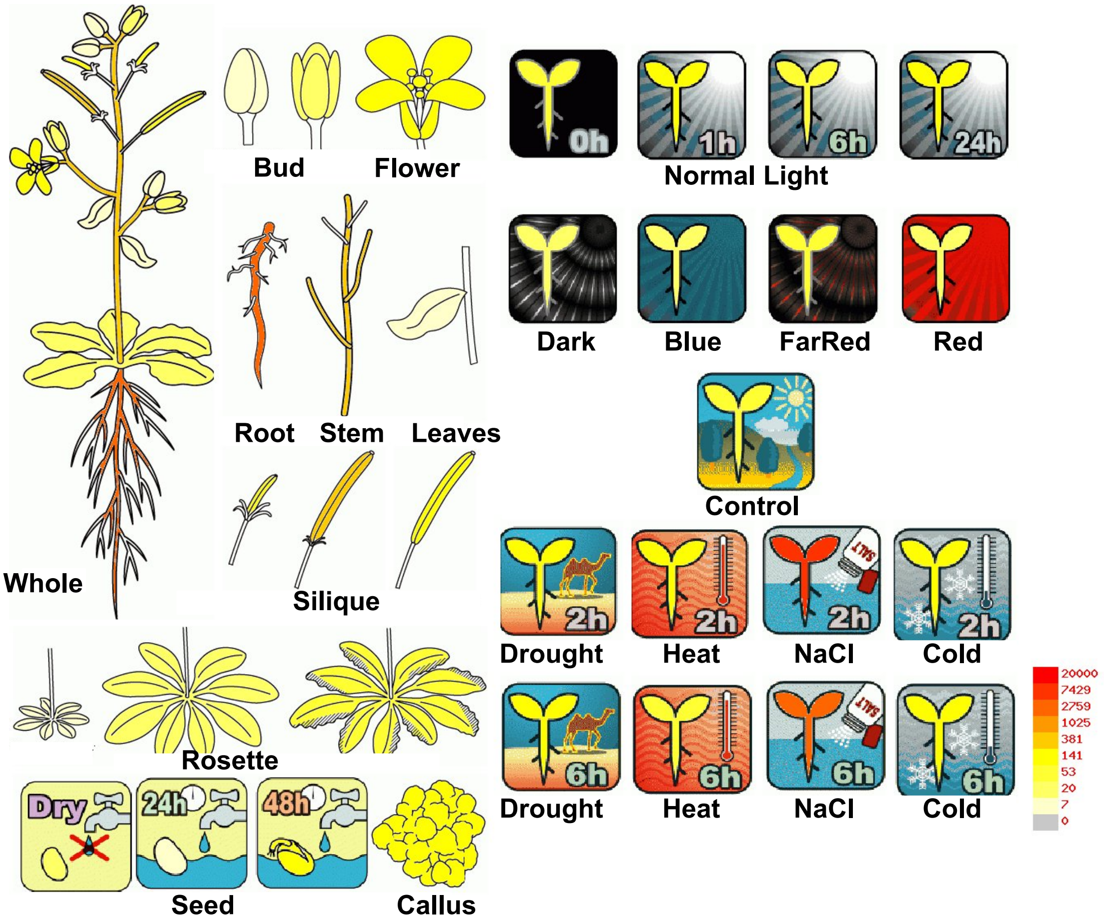

Whole
Bud
Flower
Root
Stem
Leaves
Silique
Rosette
Dry
24h
48h
Seed
Callus
0h
1h
6h
24h
Normal Light
Dark
Blue
FarRed
Red
Control
2h
Drought
2h
Heat
SALT
2h
NaCl
2h
Cold
6h
Drought
6h
Heat
SALT
6h
NaCl
6h
Cold
20000
7429
2759
1025
381
141
53
20
7
0

**Fig. S6**

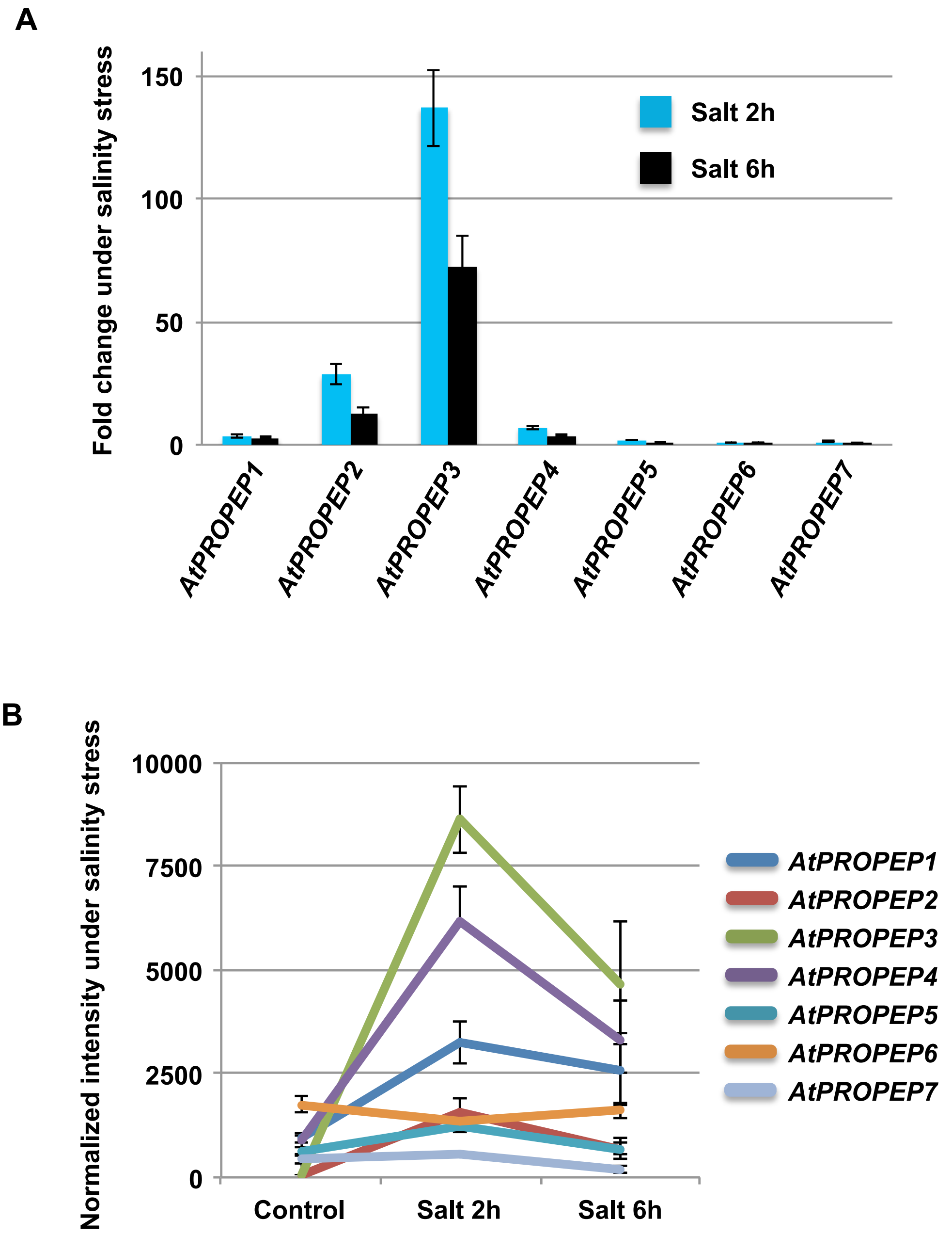
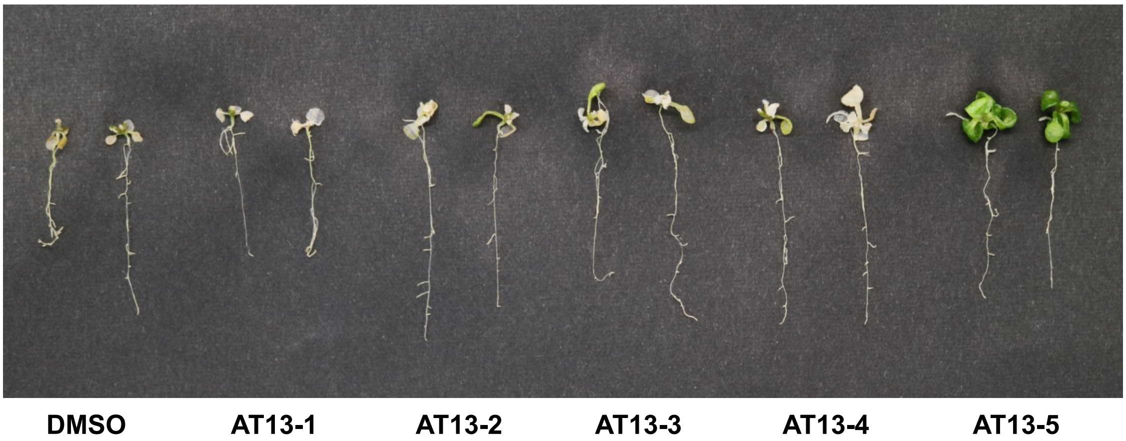
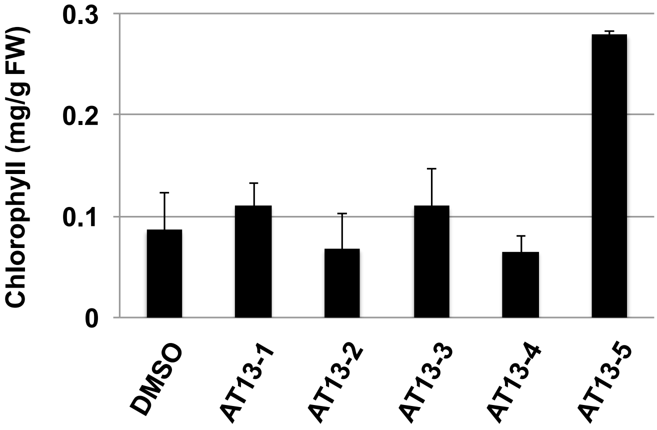
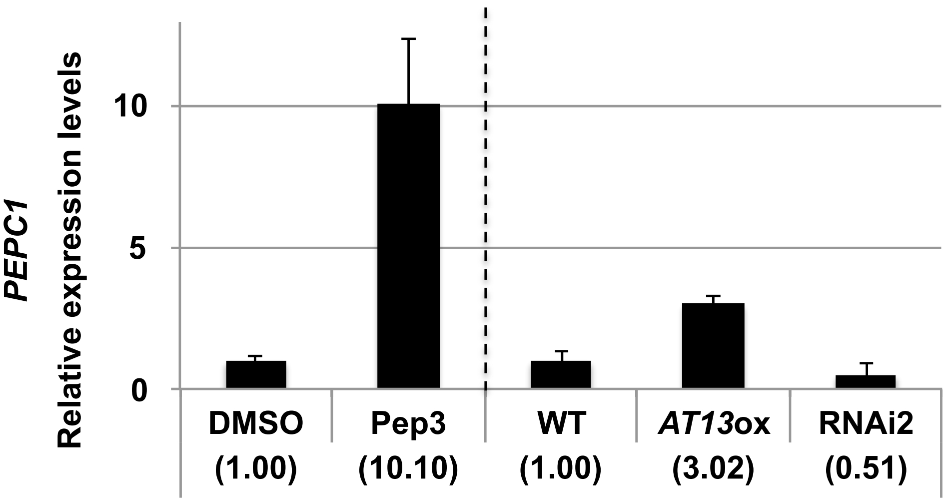

A
Fold change under salinity stress
0
50
100
150
Salt 2h
Salt 6h
AtPROPEP1
AtPROPEP2
AtPROPEP3
AtPROPEP4
AtPROPEP5
AtPROPEP6
AtPROPEP7
B
Normalized intensity under salinity stress
0
2500
5000
7500
10000
Control
Salt 2h
Salt 6h
AtPROPEP1
AtPROPEP2
AtPROPEP3
AtPROPEP4
AtPROPEP5
AtPROPEP6
AtPROPEP7

**Fig. S7**


DMSO
AT13-1
AT13-2
AT13-3
AT13-4
AT13-5


Chlorophyll (mg/g FW)
0.3
0.2
0.1
0
DMSO
AT13-1
AT13-2
AT13-3
AT13-4
AT13-5

## Fig. S8



*PEPC1*
Relative expression levels
0
5
10
DMSO
(1.00)
Pep3
(10.10)
WT
(1.00)
*AT13*ox
(3.02)
RNAi2
(0.51)

**Fig. S9**

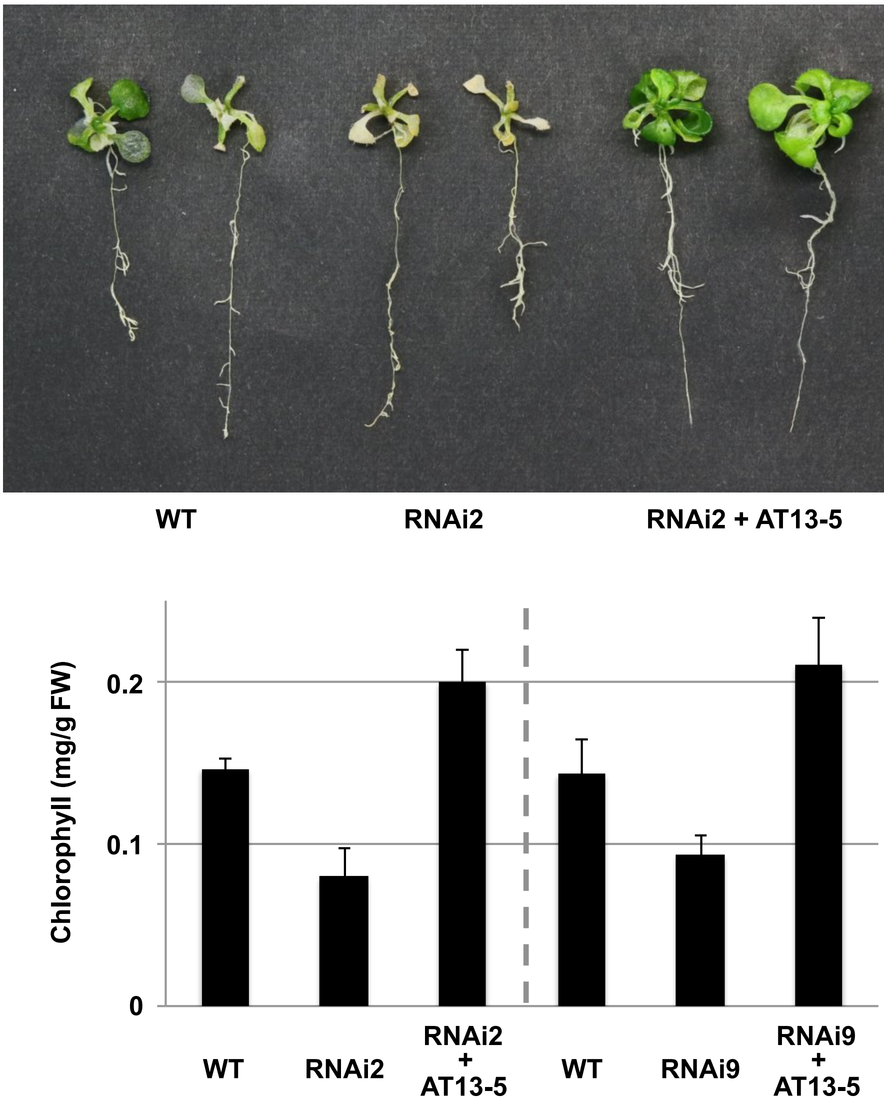

WT
RNAi2
RNAi2 + AT13-5
Chlorophyll (mg/g FW)
0.2
0.1
0
WT
RNAi2
RNAi2 + AT13-5
WT
RNAi9
RNAi9 + AT13-5

Fig. S10

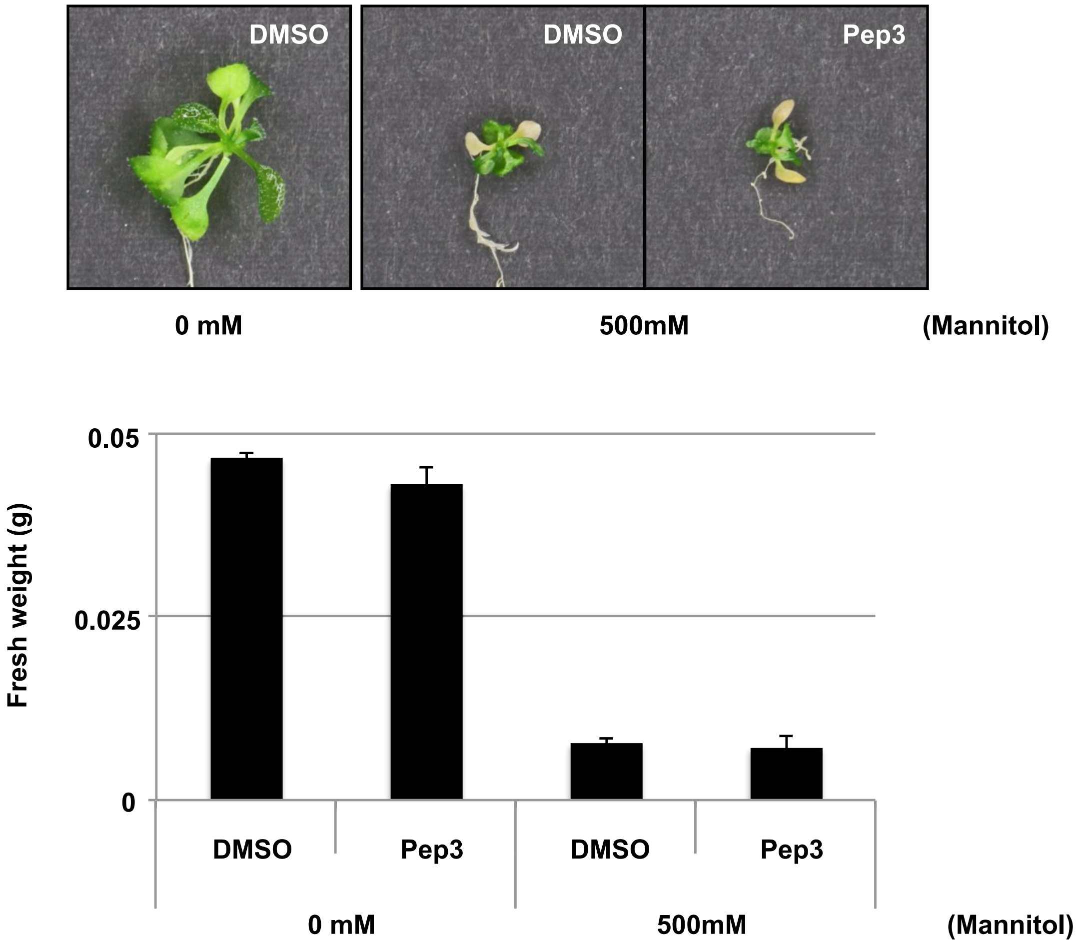
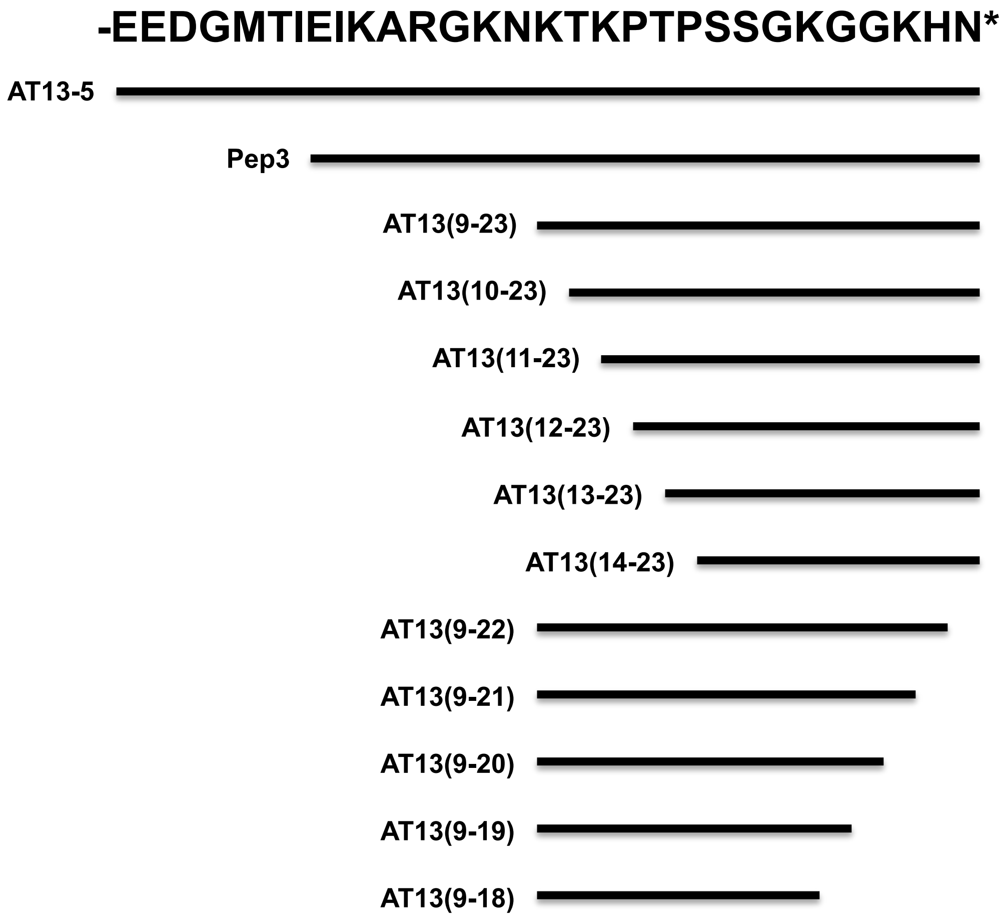

DMSO
DMSO
Pep3
0 mM
500mM
(Mannitol)
0.05
0.025
0
Fresh weight (g)
DMSO
Pep3
DMSO
Pep3
0 mM
500mM
(Mannitol)

**Fig. S11**


-EEDGMTIEIKARGKNKTKPTPSSGKGGKHN*
AT13-5
Pep3
AT13(9-23)
AT13(10-23)
AT13(11-23)
AT13(12-23)
AT13(13-23)
AT13(14-23)
AT13(9-22)
AT13(9-21)
AT13(9-20)
AT13(9-19)
AT13(9-18)

## Fig. S12

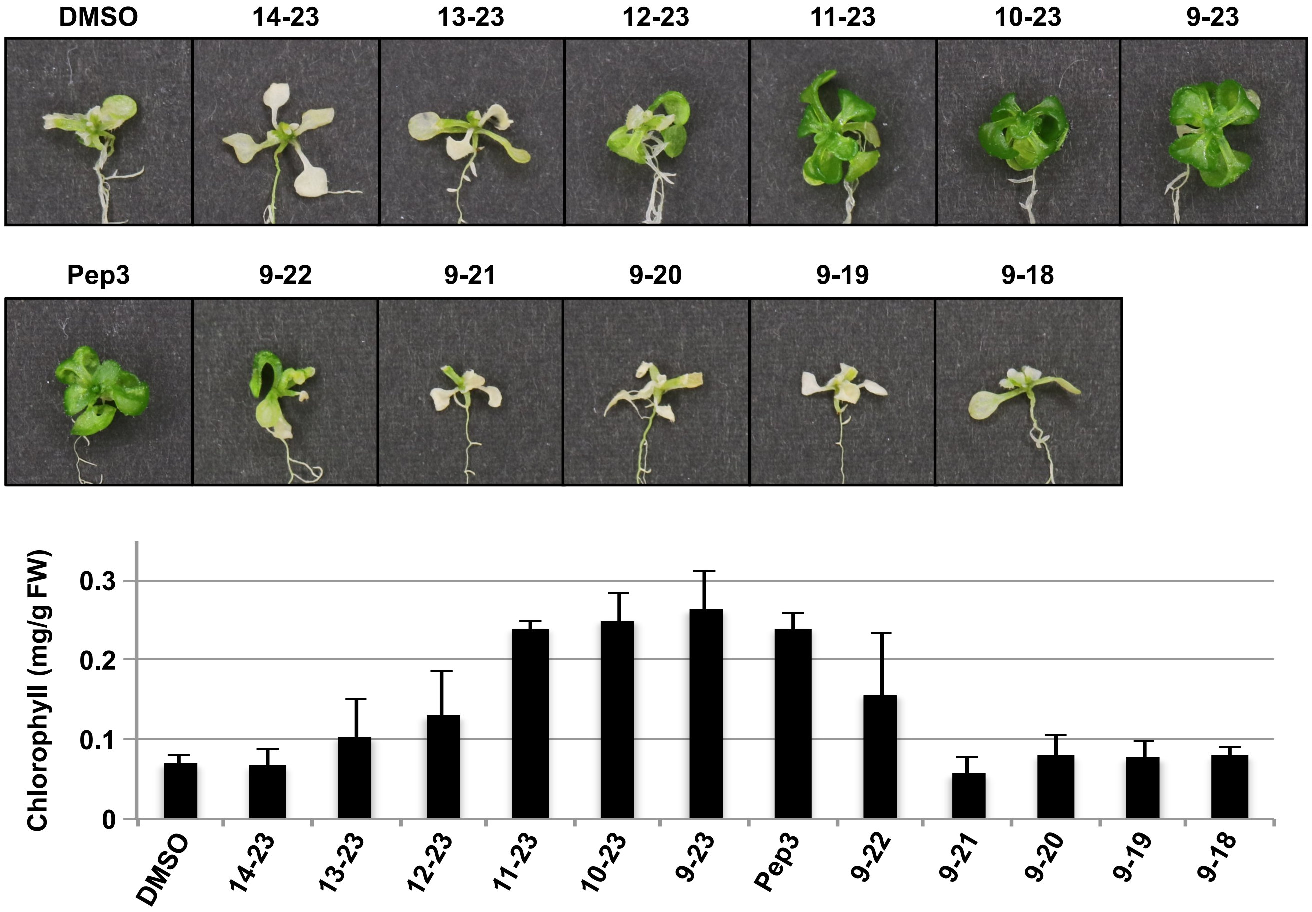
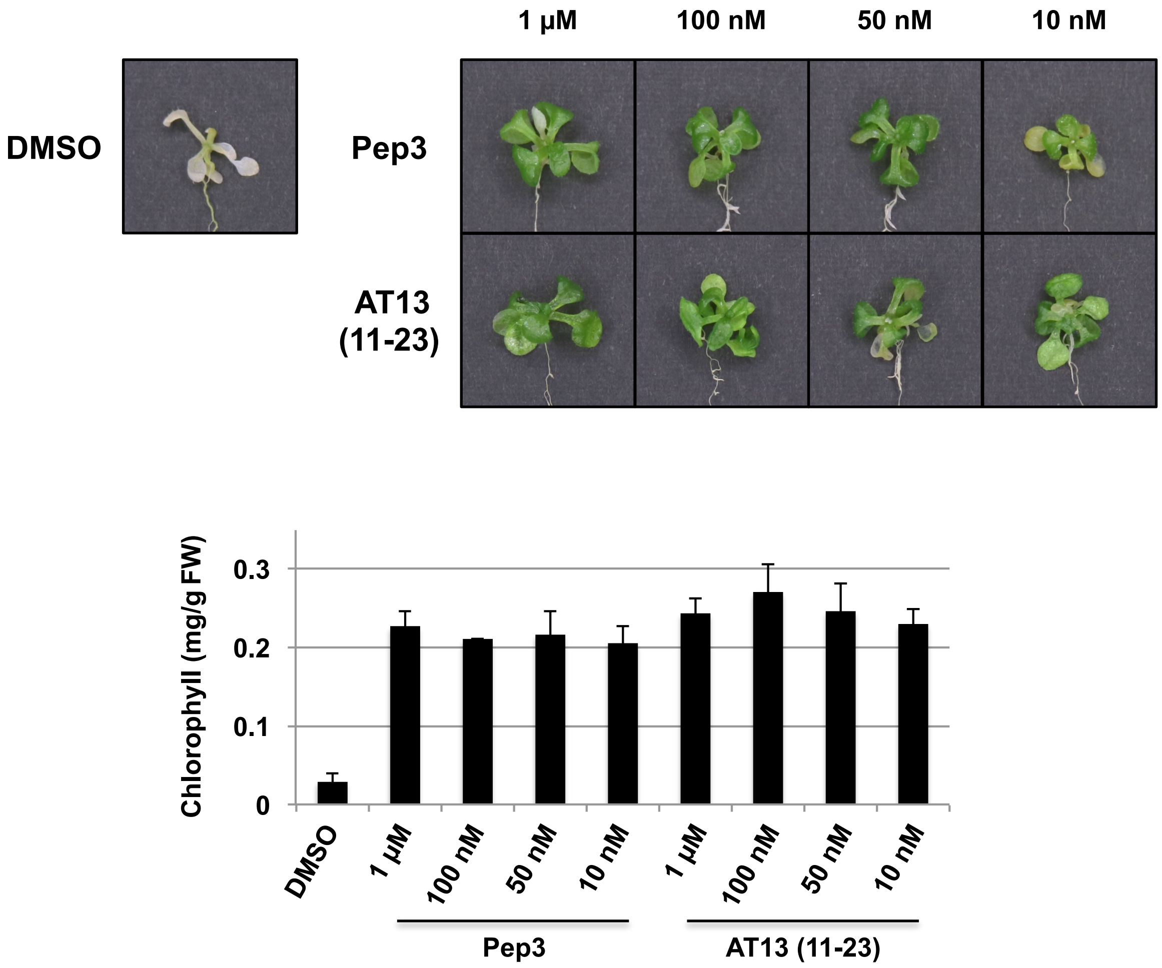

DMSO
14-23
13-23
12-23
11-23
10-23
9-23
Pep3
9-22
9-21
9-20
9-19
9-18
Chlorophyll (mg/g FW)
0.3
0.2
0.1
0
DMSO
14-23
13-23
12-23
11-23
10-23
9-23
Pep3
9-22
9-21
9-20
9-19
9-18

Fig. S13

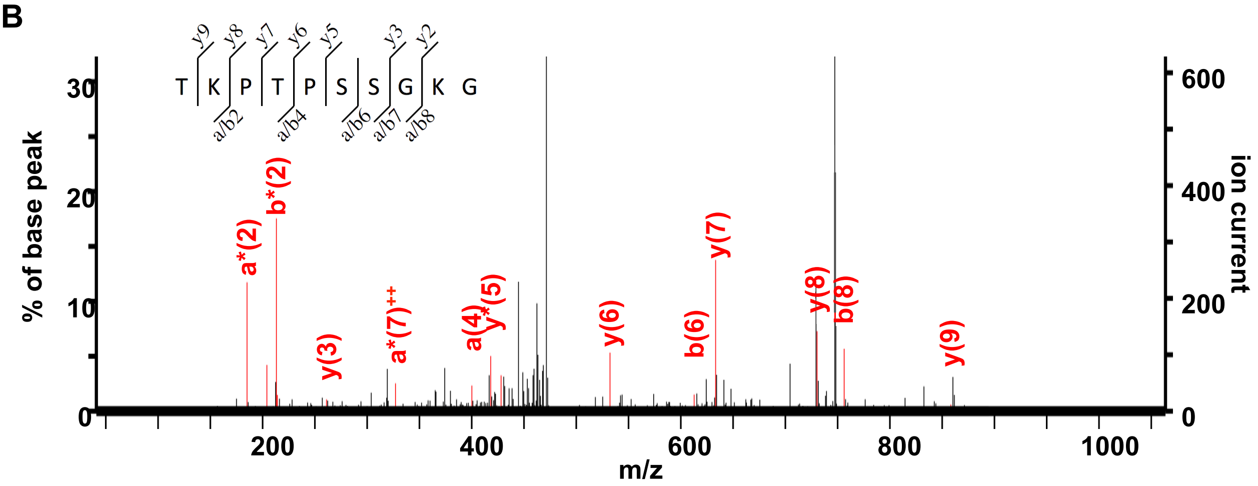

1 µM
100 nM
50 nM
10 nM
DMSO
Pep3
AT13 (11-23)
Chlorophyll (mg/g FW)
0.3
0.2
0.1
0
DMSO
1 µM
100 nM
50 nM
10 nM
1 µM
100 nM
50 nM
10 nM
Pep3
AT13 (11-23)

# Fig. S14

**A**

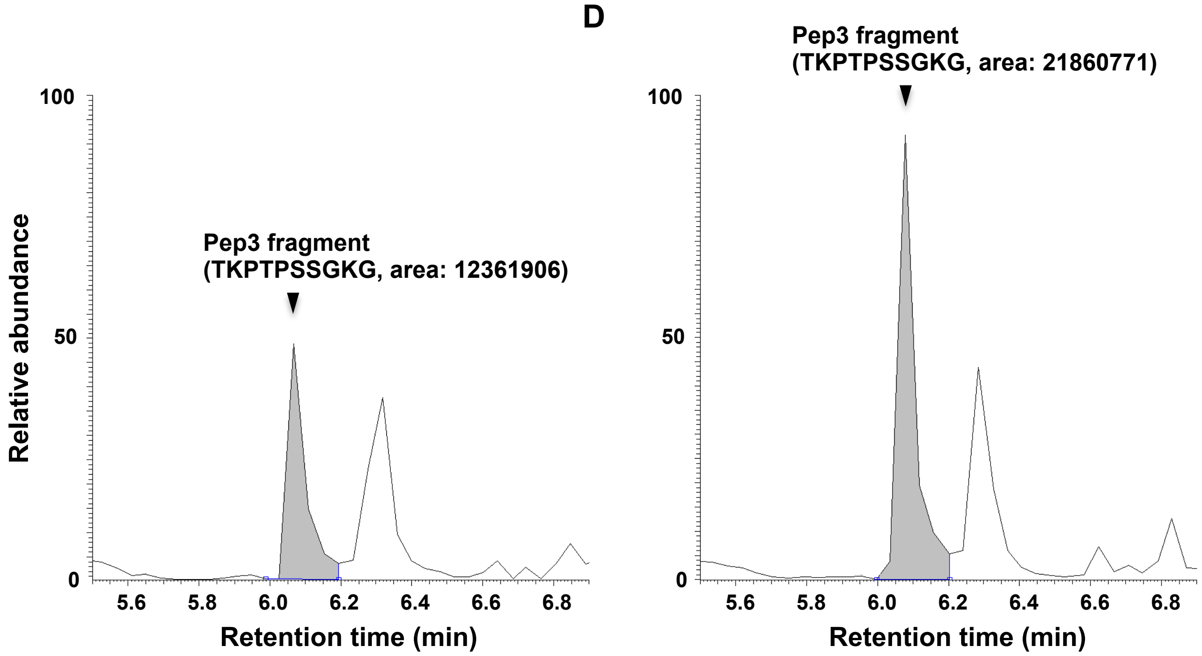
AT13(Pep3)      EIKARGKNKTKPTPSSGKGGKHN*

**B**



```
00072     Mass: 2419     Score: 19     Matches: 1(1)   Sequences: 1(1)   emPAI: 2.63
AT13(Pep3)
Query  Observed  Mr(expt)  Mr(calc)   ppm   Miss  Score  Expect  Rank  Unique   Peptide
  475  480.2611  958.5077  958.5084  -0.67    1     19    0.011    1      U     K.TKPTPSSGKG.G
```

**C** **D**



# Fig. S15

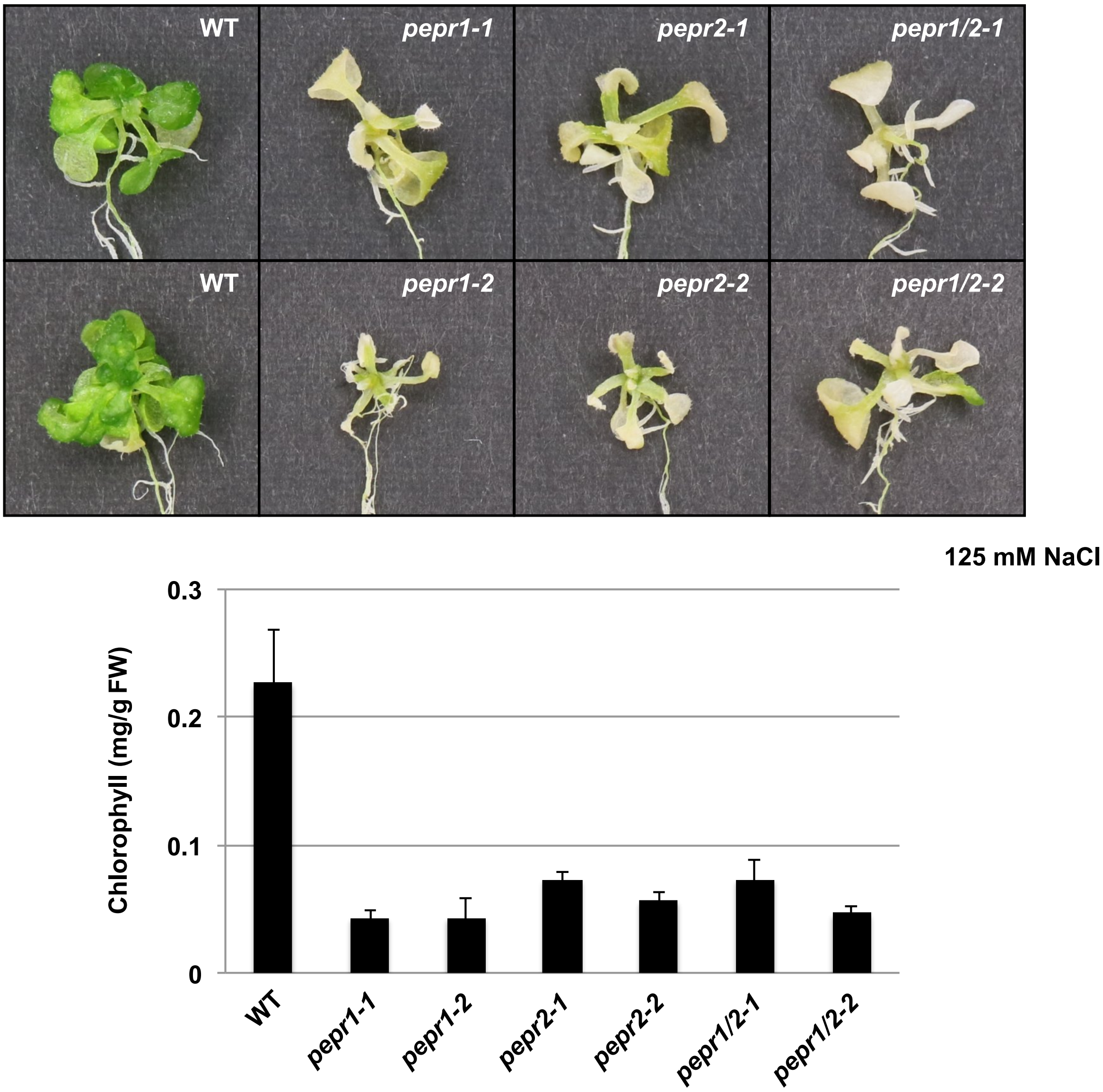
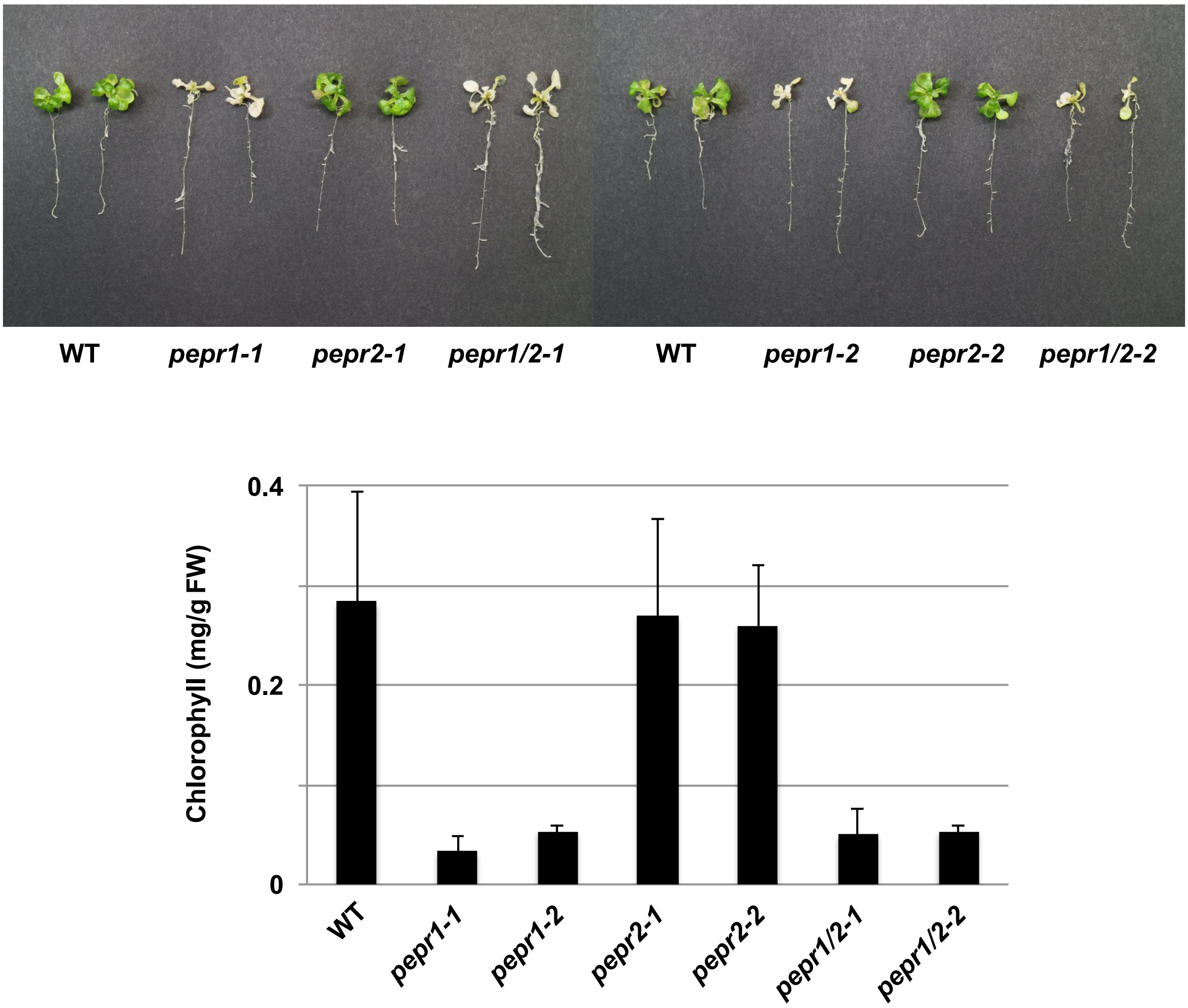

WT
*pepr1-1*
*pepr2-1*
*pepr1/2-1*
WT
*pepr1-2*
*pepr2-2*
*pepr1/2-2*
125 mM NaCl
Chlorophyll (mg/g FW)
0.3
0.2
0.1
0
WT
*pepr1-1*
*pepr1-2*
*pepr2-1*
*pepr2-2*
*pepr1/2-1*
*pepr1/2-2*

**Fig. S16**


WT
pepr1-1
pepr2-1
pepr1/2-1
WT
pepr1-2
pepr2-2
pepr1/2-2
Chlorophyll (mg/g FW)
0.4
0.2
0
WT
pepr1-1
pepr1-2
pepr2-1
pepr2-2
pepr1/2-1
pepr1/2-2

## Table S1. Summary of up-regulated genes in NaCl treatment (2h or 6h)

| Gene ID [a] | Fold changes | | Gene Description | Secreted signaling [b] | The number of plant species with homolog [c] | Transgenetic plants |
|---|---|---|---|---|---|---|
| | NaCl 2h | NaCl 6h | | | | |
| AT1G65510 | 6.9 | 7.3 | similar to unknown protein | YES | 6 | NO |
| AT1G65500 | 5.5 | 17.7 | similar to unknown protein | YES | 6 | NO |
| AT1G68765 | 6.5 | 22.2 | IDA (INFLORESCENCE DEFICIENT IN ABSCISSION) | YES | 8 | NO |
| AT1G29640 | 7.3 | 16.5 | similar to unknown protein | NO | 15 | YES |
| AT1G53903 | 15.4 | 26.6 | senescence-associated protein-related | NO | 7 | NO |
| AT1G63245 | 11.3 | 6.1 | CLE14 (CLAVATA3/ESR-RELATED 14) | YES | 10 | NO |
| AT1G61255 | 8.4 | 9.6 | similar to glycine-rich protein | YES | 5 | YES |
| AT1G51920 | 9.1 | 15.6 | unknown protein | YES | 0 | NO |
| AT1G05340 | 14.0 | 14.4 | similar to unknown protein | NO | 0 | NO |
| AT1G07985 | 16.8 | 3.9 | Expressed protein | NO | 0 | NO |
| AT1G06135 | 23.0 | 12.4 | similar to unknown protein | YES | 5 | YES |
| AT1G53610 | 5.0 | 4.2 | similar to unknown protein | YES | 0 | NO |
| AT1G15010 | 7.8 | 7.6 | similar to unknown protein | NO | 7 | YES |
| AT1G64107 | 4.9 | 13.7 | Encodes a defensin-like (DEFL) family protein. | YES | 6 | YES |
| AT1G64195 | 3.5 | 10.7 | Encodes a defensin-like (DEFL) family protein. | YES | 8 | NO |
| AT1G67856 | 14.0 | 29.0 | protein binding / zinc ion binding | NO | 13 | NO |
| AT2G22860 | 12.4 | 23.8 | ATPSK2 (PHYTOSULFOKINE 2 PRECURSOR) | YES | 5 | YES |
| AT2G41730 | 15.9 | 11.5 | similar to unknown protein | NO | 6 | NO |
| AT2G36440 | 5.8 | 15.2 | unknown protein | NO | 4 | NO |
| AT2G21820 | 9.0 | 5.9 | similar to hypothetical protein | NO | 5 | NO |
| AT2G44578 | 5.3 | 6.3 | protein binding / zinc ion binding | NO | 11 | YES |
| AT2G36261 | 4.1 | 18.0 | unknown protein | NO | 0 | NO |
| AT2G44581 | 6.1 | 13.9 | protein binding / zinc ion binding | NO | 12 | YES |
| AT3G02480 | 6.5 | 7.3 | ABA-responsive protein-related | NO | 5 | YES |
| AT3G23170 | 14.1 | 15.2 | similar to unknown protein | NO | 0 | NO |
| AT3G10930 | 7.4 | 5.8 | similar to unknown protein | YES | 8 | YES |
| AT3G53232 | 8.5 | 6.7 | DVL20/RTFL1 | NO | 6 | NO |
| AT3G60966 | 6.1 | 8.4 | protein binding / zinc ion binding | NO | 2 | NO |
| AT3G03341 | 8.6 | 9.1 | similar to Os01g0644200 | NO | 8 | NO |
| AT3G15518 | 9.7 | 9.0 | similar to hypothetical protein [Nicotiana benthamiana] | NO | 6 | NO |
| AT3G15534 | 7.3 | 9.9 | similar to unknown protein | NO | 8 | NO |
| AT4G27530 | 20.1 | 10.7 | similar to unknown protein | NO | 6 | NO |
| AT4G28703 | 12.5 | 7.2 | similar to unknown protein | NO | 0 | NO |
| AT4G36500 | 23.2 | 11.1 | similar to unknown protein | NO | 5 | NO |
| AT4G27654 | 6.1 | 5.1 | unknown protein | NO | 0 | NO |
| AT4G21920 | 4.4 | 8.6 | unknown protein | NO | 0 | NO |
| AT4G18980 | 17.9 | 6.2 | similar to unknown protein | NO | 9 | NO |
| AT5G44575 | 2.1 | 13.1 | unknown protein | NO | 0 | NO |
| AT5G01225 | 1.3 | 2.1 | similar to unknown protein | NO | 6 | YES |
| AT5G46295 | 8.2 | 7.0 | unknown protein | NO | 0 | NO |
| AT5G45630 | 9.5 | 7.6 | similar to unknown protein | NO | 2 | NO |
| AT5G09980 | 11.2 | 4.8 | PROPEP4 | NO | 0 | NO |
| AT5G24640 | 10.6 | 14.8 | similar to unknown protein | NO | 4 | NO |
| AT5G05300 | 7.0 | 24.6 | similar to unknown protein | YES | 6 | YES |
| AT5G33355 | 0.9 | 4.5 | Encodes a defensin-like (DEFL) family protein. | NO | 8 | NO |
| AT5G35110 | 12.5 | 7.0 | similar to unknown protein | NO | 0 | NO |
| AT5G64905 | 19.1 | 5.6 | PROPEP3 | NO | 4 | YES |
| AT5G64890 | 8.0 | 4.3 | PROPEP2 | NO | 4 | NO |
| AT5G43570 | 4.5 | 8.4 | serine-type endopeptidase inhibitor | NO | 4 | NO |
| AT5G19875 | 8.1 | 3.8 | similar to unknown protein | YES | 3 | NO |
| AT5G36920 | 4.7 | 22.8 | similar to unknown protein | YES | 5 | NO |
| AT5G47175 | 14.9 | 21.2 | LCR3 | YES | 9 | YES |
| AT5G54165 | 11.4 | 10.2 | unknown protein | NO | 8 | YES |
| AT5G44585 | 4.4 | 5.8 | unknown protein | YES | 2 | NO |
| sORF5958 | 7.1 | 7.6 | Located on unannotated full length cDNA (RAFL04-20-O22) | NO | 3 | NO |
| sORF7775 | 3.2 | 4.0 | Located on unannotated full length cDNA (RAFL21-83-H09) | NO | 7 | YES |
| sORF4875 | 6.0 | 2.8 | chr3_+_20317641-20317931 | YES | 6 | YES |
| sORF0625 | 15.2 | 9.1 | chr1_+_11440203-11440469 | NO | 0 | NO |
| sORF0541 | 7.3 | 6.6 | chr1_+_9952787-9952909 | NO | 0 | NO |
| sORF7215 | 5.5 | 5.7 | chr5_+_14889303-14889482 | NO | 0 | NO |
| sORF6740 | 16.2 | 14.5 | chr5_-_9156935-9157072 | NO | 2 | NO |
| sORF7726 | 5.1 | 21.7 | Located on unannotated full length cDNA (EF182830) | YES | 3 | NO |
| AT1G71000 | 4.1 | 54.7 | DNAJ heat shock N-terminal domain-containing protein | | | |
| AT1G28480 | 24.5 | 11.4 | GRX480; thiol-disulfide exchange intermediate | | | |
| AT1G45145 | 13.8 | 9.7 | ATTRX5 (thioredoxin H-type 5); thiol-disulfide exchange intermediate | | | |
| AT1G55780 | 5.6 | 9.7 | heavy-metal-associated domain-containing protein | | | |
| AT1G32560 | 9.1 | 8.4 | late embryogenesis abundant group 1 domain-containing protein | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| AT2G42530 | 6.5 | 5.9 | COR15B, a protein that protects chloroplast membranes during freezing. | | | |
| AT2G41280 | 9.7 | 3.8 | LEA (Late Embryogenesis Abundant) proteins | | | |
| AT2G40170 | 6.5 | 11.9 | ATEM6/GEA6 (ARABIDOPSIS EARLY METHIONINE-LABELLED 6) | | | |
| AT2G43510 | 3.7 | 15.5 | ATTI1 (ARABIDOPSIS THALIANA TRYPSIN INHIBITOR PROTEIN 1) | | | |
| AT2G35730 | 10.4 | 11.3 | heavy-metal-associated domain-containing protein | | | |
| AT2G37870 | 15.3 | 17.7 | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein | | | |
| AT3G21890 | 19.8 | 2.6 | zinc finger (B-box type) family protein | | | |
| AT3G18250 | 4.6 | 4.2 | contains domain PROKAR LIPOPROTEIN (PS51257) | | | |
| AT4G33040 | 9.1 | 6.0 | glutaredoxin family protein | | | |
| AT5G13080 | 7.7 | 7.7 | WRKY75 (WRKY DNA-BINDING PROTEIN 75); transcription factor | | | |
| AT5G59310 | 8.3 | 14.4 | LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding | | | |
| AT5G59320 | 7.1 | 14.6 | LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding | | | |
| AT5G43580 | 10.7 | 8.3 | serine-type endopeptidase inhibitor | | | |
| AT5G05365 | 5.0 | 6.8 | metal ion binding | | | |

a) Gene ID registered in The Arabidopsis Information Resource (TAIR, https://www.arabidopsis.org/) and our previous paper (Hanada et al., PNAS 2013)

b) Secreted signal by Signal IP software (Petersen et al., Nature Methods, 8:785-786, 2011)

c) The following genomes were used to assess conservation of small coding genes: Physcomitrella patens (http://genome.jgi-psf.org/Phypa1_1/), Selaginella moellendorffii (http://genome.jgi-psf.org/Selmo1/), Zea mays (http://www.maizesequence.org/), Sorghum bicolor (http://genome.jgi-psf.org/Sorbi1/Sorbi1.home.html), Brachypodium distachyon (http://www.jgi.doe.gov/), Oryza sativa (http://rapdb.dna.affrc.go.jp/download/), Mimulus guttatus (http://genome.jgi-psf.org/mimulus/), Vitis vinifera (http://www.genoscope.cns.fr/externe/GenomeBrowser/Vitis/), Ricinus communis (http://castorbean.jcvi.org/downloads.php), Manihot esculenta (ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Mesculenta), Populus trichocarpa (ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Ptrichocarpa), Cucumis sativus (ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Csativus/), Glycine max (ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v4.0/Gmax), Medicago truncatula (http://www.medicago.org/genome/downloads/Mt3/), Carica papaya (ftp://asgpb.hawaii.edu/papaya/annotation/) and Arabidopsis lyrata (http://genome.jgi-psf.org/Araly1/). Sequence pairs were regarded as homologous sequences if they had less than 1 e-value by BLAST search (tblastn)

**Table S2. Results of the initial screening of AT-ox plants using a plate-based salinity stress test**

| Gene ID | Line number | Survival ratio ox/WT | Tolerance[a)] | Gene ID | Line number | Survival ratio ox/WT | Tolerance[a)] |
|---|---|---|---|---|---|---|---|
| AT4<br>(sORF7775) | 1 | 1.25 | | AT23<br>(AT1G06135) | 1 | 0.33 | |
| | 2 | 1.25 | | | 2 | 0.67 | |
| | 3 | 1.17 | | | 3 | 1.78 | |
| | 4 | 0.83 | | | 4 | 1.50 | |
| | 5 | 1.33 | | | 5 | 0.80 | |
| | 6 | 2.00 | + | | 6 | 0.60 | |
| | 7 | 2.50 | + | | 7 | 1.00 | |
| | 8 | 1.00 | | | 8 | 2.00 | + |
| | 9 | 1.20 | | | 9 | 0.63 | |
| | 10 | 1.80 | | | 10 | 0.50 | |
| | 11 | 1.40 | | | 11 | 1.00 | |
| | 12 | 1.20 | | | 12 | 1.50 | |
| | 13 | 1.00 | | | 13 | 1.33 | |
| | 14 | 0.67 | | | 14 | 8.00 | + |
| | 15 | 1.50 | | | 15 | 0.63 | |
| | 16 | 1.50 | | | 16 | 0.75 | |
| | 17 | 1.50 | | | 17 | 6.00 | + |
| AT5<br>(AT5G05300) | 1 | 3.50 | + | AT32<br>(AT1G64107) | 1 | - | |
| | 2 | 0.00 | | | 2 | - | |
| | 3 | N.A. | | | 3 | - | |
| | 4 | 1.33 | | | 4 | - | |
| | 5 | 2.33 | + | | 5 | - | |
| | 6 | 4.33 | + | | 6 | - | |
| | 7 | 2.00 | + | | 7 | 0.50 | |
| | 8 | 0.60 | | | 8 | 0.25 | |
| | 9 | 0.36 | | | 9 | 0.00 | |
| | 10 | 0.55 | | | 10 | 0.83 | |
| | 11 | 0.56 | | | 11 | 0.00 | |
| | 12 | 1.40 | | | 12 | 0.40 | |
| | 13 | 0.00 | | | 13 | 0.00 | |
| | 14 | 1.63 | | | 14 | 0.00 | |
| | 15 | 2.67 | + | | 15 | 2.50 | + |
| | 16 | 1.67 | | | 16 | 1.50 | |
| | 17 | 1.22 | | | 17 | 0.67 | |
| AT10<br>(AT2G22860) | 1 | 1.25 | | AT33<br>(AT5G01225) | 1 | 0.70 | |
| | 2 | 2.00 | + | | 2 | 1.10 | |
| | 3 | 1.67 | | | 3 | 0.50 | |
| | 4 | 2.00 | + | | 4 | 0.30 | |
| | 5 | 1.25 | | | 5 | 0.44 | |
| | 6 | 0.88 | | | 6 | 0.63 | |
| | 7 | 1.00 | | | 7 | 0.50 | |
| | 8 | 1.17 | | | 8 | 0.75 | |
| | 9 | 1.00 | | | 9 | 0.00 | |
| | 10 | 0.00 | | | 10 | 0.31 | |
| | 11 | 0.44 | | | 11 | 0.69 | |
| | 12 | 0.56 | | | 12 | 0.50 | |
| | 13 | 1.11 | | | 13 | 0.50 | |
| | 14 | 1.00 | | | 14 | 0.25 | |
| | 15 | 0.20 | | | 15 | 1.00 | |
| | 16 | 0.20 | | | 16 | 0.50 | |
| | 17 | 0.88 | | | 17 | 3.00 | + |
| AT11<br>(AT2G44581) | 1 | 1.18 | | AT35<br>(AT5G54165) | 1 | 5.00 | + |
| | 2 | 1.18 | | | 2 | 5.00 | + |
| | 3 | 2.20 | + | | 3 | 1.45 | |
| | 4 | 0.40 | | | 4 | 1.00 | |
| | 5 | 1.00 | | | 5 | 1.44 | |
| | 6 | 1.00 | | | 6 | 1.17 | |
| | 7 | 0.75 | | | 7 | 3.00 | + |
| | 8 | 0.50 | | | 8 | 2.50 | + |
| | 9 | 0.57 | | | 9 | 2.33 | + |
| | 10 | 1.14 | | | 10 | 4.33 | + |
| | 11 | 9.00 | + | | 11 | 1.00 | |
| | 12 | 1.00 | | | 12 | 0.00 | |
| | 13 | 1.67 | | | 13 | 0.67 | |
| | 14 | 1.00 | | | 14 | 0.00 | |
| | 15 | 0.83 | | | 15 | 0.75 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 16 | 0.83 | | | 16 | 0.56 | |
| | 17 | 0.17 | | | 17 | 1.11 | |
| AT12<br>(AT2G44578) | 1 | 4.00 | + | AT47<br>(AT3G02480) | 1 | 0.75 | |
| | 2 | 6.00 | + | | 2 | 1.13 | |
| | 3 | N.A. | | | 3 | 1.00 | |
| | 4 | N.A. | | | 4 | 1.00 | |
| | 5 | 1.50 | | | 5 | 1.44 | |
| | 6 | 1.33 | | | 6 | 0.78 | |
| | 7 | 0.50 | | | 7 | - | |
| | 8 | 0.75 | | | 8 | - | |
| | 9 | 1.67 | | | 9 | 1.13 | |
| | 10 | 1.50 | | | 10 | 1.13 | |
| | 11 | 3.00 | + | | 11 | 2.00 | + |
| | 12 | 7.00 | + | | 12 | 0.00 | |
| | 13 | 0.67 | | | 13 | 1.00 | |
| | 14 | 0.33 | | | 14 | 0.40 | |
| | 15 | 1.75 | | | 15 | 0.80 | |
| | 16 | 0.71 | | | 16 | 0.30 | |
| | 17 | 2.50 | + | | 17 | 0.83 | |
| AT13<br>(AT5G64905) | 1 | 1.17 | | AT56<br>(AT1G15010) | 1 | 4.50 | + |
| | 2 | 1.00 | | | 2 | 1.50 | |
| | 3 | 1.00 | | | 3 | 9.00 | + |
| | 4 | 0.00 | | | 4 | 5.00 | + |
| | 5 | 0.00 | | | 5 | N.A. | |
| | 6 | 2.00 | + | | 6 | N.A. | |
| | 7 | 1.50 | | | 7 | 0.63 | |
| | 8 | 0.50 | | | 8 | 0.75 | |
| | 9 | 1.00 | | | 9 | 6.50 | + |
| | 10 | 0.43 | | | 10 | 3.50 | + |
| | 11 | 1.33 | | | 11 | 7.00 | + |
| | 12 | 0.83 | | | 12 | 4.50 | + |
| | 13 | 1.22 | | | 13 | 1.50 | |
| | 14 | 0.78 | | | 14 | 4.50 | + |
| | 15 | 1.67 | | | 15 | 1.75 | |
| | 16 | 1.67 | | | 16 | 1.25 | |
| | 17 | 2.50 | + | | 17 | 1.13 | |
| AT18<br>(AT1G29640) | 1 | 1.25 | | AT68<br>(AT3G10930) | 1 | 0.40 | |
| | 2 | 1.50 | | | 2 | 0.93 | |
| | 3 | 1.00 | | | 3 | 2.80 | + |
| | 4 | 0.25 | | | 4 | 2.00 | + |
| | 5 | 3.50 | + | | 5 | 0.78 | |
| | 6 | 0.50 | | | 6 | 1.11 | |
| | 7 | 0.67 | | | 7 | 0.58 | |
| | 8 | 1.33 | | | 8 | 0.33 | |
| | 9 | 0.00 | | | 9 | 1.00 | |
| | 10 | 0.00 | | | 10 | 1.75 | |
| | 11 | 0.67 | | | 11 | 1.67 | |
| | 12 | 0.67 | | | 12 | 1.50 | |
| | 13 | - | | | 13 | 1.50 | |
| | 14 | - | | | 14 | 2.00 | + |
| | 15 | - | | | 15 | 0.75 | |
| | 16 | - | | | 16 | 0.91 | |
| | 17 | - | | | 17 | 2.00 | + |
| AT19<br>(AT1G61255) | 1 | - | | sORF4875 | 1 | 0.70 | |
| | 2 | 1.75 | | | 2 | 0.70 | |
| | 3 | 0.67 | | | 3 | 2.00 | + |
| | 4 | - | | | 4 | 1.33 | |
| | 5 | 3.50 | + | | 5 | 0.73 | |
| | 6 | 3.50 | + | | 6 | 0.55 | |
| | 7 | 5.00 | + | | 7 | 0.94 | |
| | 8 | 2.00 | + | | 8 | 0.59 | |
| | 9 | 7.00 | + | | 9 | 1.30 | |
| | 10 | 5.00 | + | | 10 | 1.60 | |
| | 11 | 1.13 | | | 11 | 0.64 | |
| | 12 | 1.25 | | | 12 | 1.00 | |
| | 13 | 2.00 | + | | 13 | 1.70 | |
| | 14 | 2.25 | + | | 14 | 1.90 | |
| | 15 | 1.73 | | | 15 | 1.00 | |
| | 16 | 0.75 | | | 16 | 1.50 | |

| | | | |
|---|---|---|---|
| | 17 | 0.50 | |
| AT20<br>(AT5G47175) | 1 | 1.13 | |
| | 2 | 2.13 | + |
| | 3 | 0.38 | |
| | 4 | 0.38 | |
| | 5 | 1.00 | |
| | 6 | 0.67 | |
| | 7 | 1.13 | |
| | 8 | 1.63 | |
| | 9 | 0.73 | |
| | 10 | 0.40 | |
| | 11 | 0.58 | |
| | 12 | 1.08 | |
| | 13 | 0.63 | |
| | 14 | 1.38 | |
| | 15 | - | |
| | 16 | - | |
| | 17 | 2.60 | + |

| | | | |
|---|---|---|---|
| | 17 | 2.00 | + |

a) "tolerance", "+" indicates salinity stress tolerant line by this test, which showed "survival ratio ox/WT" > 2
"-" indicates not tested and "N.A." indicates survival proportion of WT was "0".

## Table S3. Chemically synthesized peptide fragments of AtPep3/AT13 peptide

| Peptide Name | Sequence: NH2-Sequence-COOH | Purity analysed by HPLC (%) | M.W. (theoretical) | M.W. detected by MALDI-TOF MS | Isoelectric point | Average hydrophobicity (Kyte /Doolittle) | Charge Density |
|---|---|---|---|---|---|---|---|
| AT13-1 | MENLRNGEDNGSLIPFTFFDQSSVTIPLLK | 91.52 | 3383.78 | 3384.48 | 4.1 | -0.18 | 0.27 |
| AT13-2 | FTFFDQSSVTIPLLKCSGLESSSSSSSSCD | 61.82 | 3147.40 | 3148.81 | 3.9 | 0.11 | 0.20 |
| AT13-3 | CSGLESSSSSSSSCDLSSSHSEEDESIDIK | 53.95 | 3080.09 | 3082.01 | 3.7 | -0.72 | 0.33 |
| AT13-4 | LSSSHSEEDESIDIKEEEEEEEEDGMTIEI | 60.66 | 3468.48 | 3467.11 | 3.4 | -1.37 | 0.60 |
| AT13-5 | EEDGMTIElKARGKNKTKPTPSSGKGGKHN | 68.97 | 3196.55 | 3196.09 | 10.5 | -1.61 | 0.43 |
| Pep3 | ElKARGKNKTKPTPSSGKGGKHN | 55.56 | 2420.73 | 2421.07 | 11.5 | -1.87 | 0.43 |
| AT13(9-23) | KTKPTPSSGKGGKHN | 58.63 | 1523.69 | 1523.85 | 11.3 | -1.98 | 0.40 |
| AT13(10-23) | TKPTPSSGKGGKHN | 81.19 | 1395.52 | 1395.80 | 11.1 | -1.84 | 0.36 |
| AT13(11-23) | KPTPSSGKGGKHN | 62.17 | 1294.42 | 1294.60 | 11.1 | -1.93 | 0.38 |
| AT13(12-23) | PTPSSGKGGKHN | 84.58 | 1166.24 | 1166.20 | 10.8 | -1.77 | 0.33 |
| AT13(13-23) | TPSSGKGGKHN | 69.28 | 1069.13 | 1069.40 | 10.8 | -1.78 | 0.36 |
| AT13(14-23) | TPSSGKGGKHN | 50.36 | 968.03 | 968.00 | 10.8 | -1.89 | 0.40 |
| AT13(9-22) | KTKPTPSSGKGGKH | 58.67 | 1409.59 | 1409.70 | 11.3 | -1.87 | 0.43 |
| AT13(9-21) | KTKPTPSSGKGGK | 52.23 | 1272.45 | 1272.50 | 11.3 | -1.77 | 0.46 |
| AT13(9-20) | KTKPTPSSGKGG | 59.91 | 1144.28 | 1144.20 | 11.1 | -1.59 | 0.42 |
| AT13(9-19) | KTKPTPSSGKG | 70.16 | 1087.23 | 1087.20 | 11.1 | -1.70 | 0.45 |
| AT13(9-18) | KTKPTPSSGK | 78.88 | 1030.18 | 1030.20 | 11.1 | -1.83 | 0.50 |
| Pep3-90% | ElKARGKNKTKPTPSSGKGGKHN | 95.96 | 2420.73 | 2421.37 | 11.5 | -1.87 | 0.43 |
| AT13(11-23)-90% | KPTPSSGKGGKHN | 99.04 | 1294.42 | 1294.89 | 11.1 | -1.93 | 0.38 |

**Table S4. Up/Down-regulated genes in both AtPROPEP3/AT13-ox plants and AtPep3/AT13 peptide treated plants**

| AGI[a)], Full length cDNA ID[b)] and sORF ID[c)] | Description | DMSO | | | AT13pep | | | AT13pep / DMSO | WT | | | AT13ox | | | AT13ox /WT |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | rep1 | rep2 | rep3 | rep1 | rep2 | rep3 | | rep1 | rep2 | rep3 | rep1 | rep2 | rep3 | |
| AT1G03010 | Phototropic-responsive NPH3 family protein | 133.03 | 126.62 | 113.62 | 197.62 | 190.34 | 184.54 | 1.5 | 147.65 | 143.12 | 125.61 | 201.69 | 186.89 | 173.86 | 1.4 |
| AT1G03020 | Thioredoxin superfamily protein | 50.457 | 28.88 | 37.25 | 217.58 | 253.59 | 266.56 | 6.3 | 53.978 | 52.455 | 53.571 | 296.85 | 304.54 | 325.6 | 5.8 |
| AT1G03400 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | 93.856 | 106.42 | 114.94 | 164.36 | 160.51 | 169.1 | 1.6 | 137.23 | 130.22 | 136.71 | 184.74 | 187.65 | 191.52 | 1.4 |
| AT1G03820 | unknown protein | 634.81 | 604.05 | 692.32 | 1399.4 | 1485.8 | 1316.1 | 2.2 | 765.33 | 845.63 | 810.32 | 588.62 | 549.98 | 617.99 | 0.7 |
| AT1G05560 | UDP-glucosyltransferase 75B1 | 177.93 | 172.88 | 180.67 | 67.786 | 87.244 | 66.658 | 0.4 | 346.95 | 433.28 | 386.83 | 220.77 | 210.56 | 230.75 | 0.6 |
| AT1G08310 | alpha/beta-Hydrolases superfamily protein | 101.2 | 93.428 | 90.656 | 229.08 | 253.87 | 204.55 | 2.4 | 147.57 | 125.86 | 124.61 | 372.31 | 405.93 | 363.7 | 2.9 |
| AT1G10585 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | 364.24 | 452.48 | 388.34 | 170.92 | 162.05 | 168.57 | 0.4 | 342.52 | 333.05 | 327.06 | 245.24 | 216.59 | 252.61 | 0.7 |
| AT1G10640 | Pectin lyase-like superfamily protein | 422.09 | 440.85 | 402.9 | 256.92 | 285.76 | 252.6 | 0.6 | 602.43 | 631.13 | 575.68 | 480.96 | 491.62 | 503.95 | 0.8 |
| AT1G11740 | ankyrin repeat family protein | 1587.1 | 1538.5 | 1656.9 | 1237.6 | 1277.5 | 1169.4 | 0.8 | 1283.6 | 1358.9 | 1343.9 | 2214.8 | 1812.4 | 2284.6 | 1.6 |
| AT1G13420 | sulfotransferase 4B | 704.41 | 647.82 | 723.01 | 354.33 | 419.48 | 361.74 | 0.5 | 465.6 | 390.27 | 509.14 | 708.58 | 745.14 | 787.49 | 1.6 |
| AT1G14220 | Ribonuclease T2 family protein | 469.77 | 542.51 | 506.67 | 286.37 | 294.63 | 236.1 | 0.5 | 384.82 | 348.23 | 404.18 | 526.9 | 517.86 | 548.73 | 1.4 |
| AT1G14250 | GDA1/CD39 nucleoside phosphatase family protein | 12.242 | 12.683 | 13.653 | 115.87 | 104.13 | 116.07 | 8.7 | 23.973 | 22.946 | 31.146 | 57.9 | 70.795 | 79.694 | 2.7 |
| AT1G17710 | Pyridoxal phosphate phosphatase-related protein | 50.707 | 40.057 | 43.953 | 546.77 | 481.78 | 482.78 | 11.2 | 236.28 | 151.66 | 224.08 | 848.48 | 725.96 | 784.61 | 3.9 |
| AT1G18200 | RAB GTPase homolog A6B | 428.82 | 429.5 | 432.44 | 610.59 | 562.96 | 584.1 | 1.4 | 654.56 | 631.37 | 610.18 | 802.27 | 733.59 | 767.02 | 1.2 |
| AT1G20300 | Pentatricopeptide repeat (PPR) superfamily protein | 294.43 | 303.34 | 296.91 | 265.26 | 264.99 | 271 | 0.9 | 485.31 | 503.74 | 503.83 | 312.56 | 364.15 | 374.88 | 0.7 |
| AT1G21460 | Nodulin MtN3 family protein | 1474.5 | 1324.5 | 1396.6 | 2222.1 | 2239.7 | 2010.3 | 1.5 | 882.28 | 865.06 | 850.34 | 1277.1 | 1294.5 | 1317.9 | 1.5 |
| AT1G23060 | unknown protein | 317.1 | 334.02 | 303.18 | 240.78 | 243.09 | 229.35 | 0.7 | 284.59 | 280.74 | 259.7 | 344.47 | 326.37 | 344.47 | 1.2 |
| AT1G25560 | AP2/B3 transcription factor family protein | 20980 | 19819 | 19179 | 29889 | 28203 | 30052 | 1.5 | 22348 | 20161 | 20658 | 26832 | 25805 | 24616 | 1.2 |
| AT1G26730 | EXS (ERD1/XPR1/SYG1) family protein | 178.43 | 174.08 | 178.6 | 293.97 | 299.96 | 316.94 | 1.7 | 292.31 | 276.26 | 293.19 | 348.35 | 332.09 | 360.48 | 1.2 |
| AT1G26930 | Galactose oxidase/kelch repeat superfamily protein | 3483.5 | 3632.8 | 3573.9 | 2831.3 | 2759.7 | 2856 | 0.8 | 3560.3 | 3932.1 | 3730.7 | 2688 | 2810.1 | 2861.4 | 0.7 |
| AT1G31550 | GDSL-like Lipase/Acylhydrolase superfamily protein | 242.2 | 254.85 | 275.89 | 361.62 | 361.31 | 342.73 | 1.4 | 218.64 | 186.03 | 238.72 | 313.73 | 362.38 | 354.62 | 1.6 |
| AT1G35183 | unknown protein | 32.488 | 35.553 | 32.825 | 50.629 | 46.449 | 48.104 | 1.4 | 21.599 | 20.855 | 21.033 | 36.64 | 32.538 | 29.823 | 1.6 |
| AT1G48260 | CBL-interacting protein kinase 17 | 144.72 | 152.41 | 152.43 | 277.01 | 310.18 | 266.19 | 1.9 | 184.74 | 192.22 | 178.44 | 243.65 | 229.45 | 234.82 | 1.3 |
| AT1G52690 | Late embryogenesis abundant protein (LEA) family protein | 619.79 | 660.61 | 527.9 | 91.9 | 128.97 | 54.369 | 0.2 | 306.55 | 335.65 | 251.03 | 135.79 | 122.71 | 124.7 | 0.4 |
| AT1G54210 | Ubiquitin-like superfamily protein | 406.64 | 410.38 | 428.01 | 533.18 | 534.98 | 559.1 | 1.3 | 570.74 | 499.22 | 516.54 | 792.91 | 754.06 | 753.49 | 1.5 |
| AT1G55740 | seed imbibition 1 | 291.28 | 303.89 | 264.19 | 161.22 | 153.78 | 143.25 | 0.5 | 219.6 | 232.07 | 211.27 | 258.21 | 265.11 | 264.71 | 1.2 |
| AT1G58420 | Uncharacterised conserved protein UCP031279 | 117.23 | 145.83 | 138.62 | 288.63 | 253.7 | 275.52 | 2.0 | 135.26 | 127.61 | 125.63 | 160.81 | 187.1 | 162.46 | 1.3 |
| AT1G59730 | thioredoxin H-type 7 | 135.68 | 113.69 | 128.19 | 52.282 | 53.925 | 53.617 | 0.4 | 133.46 | 108.46 | 115.69 | 167.62 | 168.76 | 151.19 | 1.4 |
| AT1G62500 | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | 1431.4 | 1616.3 | 1574.3 | 2000.8 | 2101.1 | 2088.6 | 1.3 | 2007.3 | 2022.8 | 2167.2 | 1508.9 | 1532 | 1765 | 0.8 |
| AT1G63057 | unknown protein | 133.51 | 124.22 | 128.26 | 80.567 | 78.51 | 60.905 | 0.6 | 116.68 | 113.07 | 91.474 | 199.45 | 209.13 | 186.86 | 1.9 |
| AT1G64170 | cation/H+ exchanger 16 | 480.42 | 510.2 | 438.73 | 788.15 | 701.94 | 795.67 | 1.6 | 567.03 | 537.47 | 570.38 | 607.93 | 636.38 | 624 | 1.1 |
| AT1G64750 | deletion of SUV3 suppressor 1(I) | 25400 | 24907 | 24833 | 23306 | 23089 | 22935 | 0.9 | 21783 | 20658 | 20817 | 24361 | 25819 | 25196 | 1.2 |
| AT1G67600 | Acid phosphatase/vanadium-dependent haloperoxidase-related protein | 102.48 | 89.093 | 115.46 | 183.13 | 184.64 | 187.74 | 1.8 | 94.296 | 81.288 | 88.886 | 202.46 | 199.82 | 216.02 | 2.3 |
| AT1G68740 | EXS (ERD1/XPR1/SYG1) family protein | 182.79 | 152.67 | 133.75 | 512.85 | 414.79 | 461.34 | 3.0 | 323.34 | 238 | 323.15 | 629.68 | 467.36 | 587.44 | 1.9 |
| AT1G68825 | ROTUNDIFOLIA like 15 | 216.05 | 219.13 | 230.05 | 94.434 | 89.874 | 90.285 | 0.4 | 202.57 | 207.72 | 212.12 | 239.44 | 236.57 | 235.05 | 1.1 |
| AT1G72990 | beta-galactosidase 17 | 462.21 | 463.01 | 452.32 | 508.22 | 527.59 | 510.81 | 1.1 | 492.35 | 479.58 | 463.25 | 544.14 | 531.14 | 545.6 | 1.1 |
| AT1G80450 | VQ motif-containing protein | 51.667 | 57.989 | 55.918 | 82.166 | 80.472 | 81.056 | 1.5 | 95.69 | 100.72 | 104.95 | 67.752 | 82.378 | 65.773 | 0.7 |
| AT2G14900 | Gibberellin-regulated family protein | 860.96 | 842.63 | 924.8 | 1487.8 | 1394.9 | 1362.6 | 1.6 | 750.25 | 733 | 787.86 | 1062.3 | 1025.4 | 1060.8 | 1.4 |
| AT2G16700 | actin depolymerizing factor 5 | 4937 | 4998.9 | 4968.9 | 5638.5 | 5596 | 5579.1 | 1.1 | 7198.7 | 6940.9 | 6795.2 | 5372.3 | 4702.5 | 5379.9 | 0.7 |
| AT2G18730 | diacylglycerol kinase 3 | 1093.8 | 1081.1 | 1134.2 | 1364.9 | 1392.2 | 1395.5 | 1.3 | 1282.4 | 1138.9 | 1263.6 | 1584.9 | 1633.1 | 1651.5 | 1.3 |
| AT2G20750 | expansin B1 | 152.77 | 151.01 | 153.74 | 80.838 | 86.809 | 67.473 | 0.5 | 149.58 | 124.24 | 150.18 | 83.692 | 99.8 | 94.381 | 0.7 |
| AT2G20780 | Major facilitator superfamily protein | 3533.1 | 3584.8 | 3630.6 | 3851.3 | 3810.8 | 3821.1 | 1.1 | 3081 | 2951.3 | 3162.7 | 3464.8 | 3615.2 | 3557.1 | 1.2 |
| AT2G21560 | unknown protein | 1083.5 | 1168.7 | 1141.6 | 580.86 | 607.53 | 580.86 | 0.5 | 1524.4 | 1408.4 | 1592.3 | 740.53 | 760.38 | 749.15 | 0.5 |
| AT2G23840 | HNH endonuclease | 524.15 | 496.45 | 496.96 | 596.81 | 609.16 | 605.57 | 1.2 | 1047.7 | 1124 | 1100.6 | 1286.6 | 1376.6 | 1498 | 1.3 |
| AT2G28430 | unknown protein | 4553.2 | 4667.3 | 4731.7 | 5106.8 | 5123.4 | 5101.3 | 1.1 | 3899.6 | 3933.6 | 3612.7 | 4876.7 | 5253.5 | 4552.1 | 1.3 |
| AT2G28660 | Chloroplast-targeted copper chaperone protein | 411.93 | 394.42 | 422.25 | 589.48 | 548.27 | 608.14 | 1.4 | 478.66 | 415.43 | 464.45 | 549.98 | 564.36 | 591.32 | 1.3 |
| AT2G29180 | unknown protein | 3941 | 4132.5 | 3957.8 | 3179.4 | 3342 | 3211 | 0.8 | 3334.1 | 3344.1 | 3434.7 | 4283.9 | 4566.1 | 4678.9 | 1.3 |
| AT2G29310 | NAD(P)-binding Rossmann-fold superfamily protein | 3759.5 | 3721.8 | 4097 | 5062.8 | 5304.6 | 5543.7 | 1.4 | 4189 | 4073.2 | 4880.6 | 5938.3 | 5898.3 | 6204.9 | 1.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AT2G29490 | glutathione S-transferase TAU 1 | 532.88 | 588.57 | 564.63 | 265.6 | 252.07 | 275.4 | 0.5 | 616.5 | 670.86 | 597.18 | 442.7 | 412.09 | 485.89 | 0.7 |
| AT2G31750 | UDP-glucosyl transferase 74D1 | 638.93 | 665.77 | 670 | 485.08 | 490.99 | 538.45 | 0.8 | 1002.7 | 1098.9 | 1050.3 | 806.35 | 824.71 | 880.65 | 0.8 |
| AT2G34210 | Transcription elongation factor Spt5 | 2.8952 | 4.7498 | 2.038 | 28.393 | 23.958 | 27.515 | 8.2 | 8.8881 | 7.0153 | 7.5104 | 43.282 | 37.599 | 49.476 | 5.6 |
| AT2G37460 | nodulin MtN21 /EamA-like transporter family protein | 479.27 | 608.39 | 470.08 | 960.71 | 1006.6 | 976.62 | 1.9 | 809.47 | 810.25 | 871.67 | 482.94 | 480.02 | 486.44 | 0.6 |
| AT2G39140 | pseudouridine synthase family protein | 83.967 | 88.312 | 83.564 | 70.49 | 71.244 | 71.273 | 0.8 | 151.77 | 179.54 | 152.86 | 95.984 | 111.08 | 113.67 | 0.7 |
| AT2G39700 | expansin A4 | 1328.7 | 1346.7 | 1471.9 | 2254.2 | 2556.8 | 2396.4 | 1.7 | 1581.2 | 1619.4 | 1565.2 | 1225 | 1347.9 | 1359.1 | 0.8 |
| AT2G40390 | unknown protein | 30.377 | 32.268 | 33.434 | 20.228 | 21.883 | 19.226 | 0.6 | 49.348 | 42.437 | 50.801 | 21.599 | 24.947 | 26.949 | 0.5 |
| AT2G40940 | ethylene response sensor 1 | 4147 | 4413 | 4337.6 | 5569.7 | 5238.4 | 5618.8 | 1.3 | 5823.7 | 5805.2 | 5914.3 | 5076.4 | 4965.5 | 5131.2 | 0.9 |
| AT2G41730 | unknown protein | 1028 | 1200.4 | 1120 | 2171.6 | 2179.9 | 2412.7 | 2.0 | 3446.8 | 3338.8 | 3895.4 | 4936.7 | 4843.9 | 5299 | 1.4 |
| AT2G42840 | protodermal factor 1 | 11389 | 11123 | 11855 | 7700.8 | 8328.1 | 7822.6 | 0.7 | 12519 | 14145 | 13334 | 8050.3 | 9060.6 | 8124.5 | 0.6 |
| AT2G45130 | SPX domain gene 3 | 3.582 | 3.5687 | 7.5938 | 27.736 | 23.437 | 28.115 | 5.4 | 5.7452 | 10.649 | 7.6001 | 37.741 | 36.42 | 29.788 | 4.3 |
| AT3G01450 | ARM repeat superfamily protein | 353.71 | 347.99 | 359.26 | 405.11 | 404.05 | 413.12 | 1.2 | 398.72 | 375.95 | 375.69 | 465.71 | 464 | 463.47 | 1.2 |
| AT3G05400 | Major facilitator superfamily protein | 258.01 | 242.38 | 259.21 | 470.43 | 482.01 | 461.2 | 1.9 | 263.8 | 243.91 | 259.17 | 375.85 | 373.42 | 343.93 | 1.4 |
| AT3G05980 | unknown protein | 244.78 | 220.87 | 212.84 | 146.84 | 136.62 | 136.04 | 0.6 | 185.68 | 180.14 | 174.5 | 258.11 | 243.83 | 233.73 | 1.4 |
| AT3G09162 | unknown protein | 162.48 | 176.57 | 169.63 | 251.89 | 234.91 | 238.66 | 1.4 | 153.03 | 126.2 | 130.62 | 229.92 | 198.85 | 190.45 | 1.5 |
| AT3G09405 | Pectinacetylesterase family protein | 143.62 | 136.5 | 141.1 | 232.13 | 252.62 | 232.89 | 1.7 | 137.75 | 118.4 | 122.25 | 182.57 | 199.35 | 192.66 | 1.5 |
| AT3G12970 | unknown protein | 365.78 | 407.21 | 410.92 | 247.19 | 262.72 | 231.67 | 0.6 | 547.02 | 521.98 | 499.74 | 396.47 | 427.75 | 412.32 | 0.8 |
| AT3G17790 | purple acid phosphatase 17 | 1042.9 | 926.25 | 923.43 | 3370.2 | 3551.2 | 3150.2 | 3.5 | 1537.6 | 1097.4 | 1453.4 | 3125.7 | 2681.6 | 2866.5 | 2.1 |
| AT3G18200 | nodulin MtN21 /EamA-like transporter family protein | 275.34 | 286.37 | 249.27 | 154.26 | 160.78 | 144.54 | 0.6 | 240.71 | 249.38 | 269.96 | 346.85 | 348.42 | 325.26 | 1.3 |
| AT3G19010 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | 3413.7 | 3454.2 | 3647.9 | 4856.4 | 4734.5 | 4825.2 | 1.4 | 3998 | 3810.1 | 4069.7 | 4401.9 | 4482.8 | 4732.2 | 1.1 |
| AT3G19550 | unknown protein | 51.83 | 57.779 | 47.316 | 215.17 | 213.95 | 170.08 | 3.8 | 247.83 | 152.48 | 212.02 | 350.91 | 345.06 | 326.94 | 1.7 |
| AT3G22460 | O-acetylserine (thiol) lyase (OAS-TL) isoform A2 | 1223 | 1148.3 | 1263.1 | 1650.4 | 1555 | 1629 | 1.3 | 1521.8 | 1504.5 | 1520 | 1819.7 | 1886.4 | 1843 | 1.2 |
| AT3G22640 | cupin family protein | 95.084 | 84.011 | 100.54 | 31.776 | 46.579 | 30.305 | 0.4 | 428.78 | 618.82 | 459.94 | 205.86 | 252.34 | 217.23 | 0.4 |
| AT3G22930 | calmodulin-like 11 | 635.06 | 590.82 | 590.07 | 867.21 | 928.2 | 902.35 | 1.5 | 580.97 | 575.28 | 541.9 | 751.95 | 742.02 | 680.81 | 1.3 |
| AT3G23550 | MATE efflux family protein | 789.59 | 813.99 | 716.39 | 1978.5 | 1605 | 1997.3 | 2.4 | 1083 | 1031.4 | 970.28 | 1840 | 2362.6 | 1862.1 | 2.0 |
| AT3G24520 | heat shock transcription factor C1 | 2002.9 | 2057.2 | 2099.4 | 1336.4 | 1306.6 | 1319.7 | 0.6 | 1457 | 1517.7 | 1605.8 | 971.05 | 981.04 | 1050.5 | 0.7 |
| AT3G25240 | Protein of unknown function (DUF506) | 32.252 | 18.748 | 30.962 | 114.78 | 110.58 | 92.54 | 3.9 | 30.714 | 32.304 | 25.813 | 259.7 | 156.11 | 203.52 | 7.0 |
| AT3G26200 | cytochrome P450, family 71, subfamily B, polypeptide 22 | 235.64 | 180.67 | 230.12 | 443.21 | 449.42 | 468.12 | 2.1 | 344.16 | 323.83 | 361.99 | 636.84 | 664.51 | 686 | 1.9 |
| AT3G27690 | photosystem II light harvesting complex gene 2.3 | 3535.1 | 3178.8 | 3516.2 | 2229.9 | 2398.5 | 2262.5 | 0.7 | 5759.2 | 6780.7 | 6323.8 | 8720.9 | 8034 | 9547.3 | 1.4 |
| AT3G28345 | ABC transporter family protein | 140.42 | 130.51 | 119.75 | 52.214 | 62.682 | 51.73 | 0.4 | 91.983 | 92.931 | 74.864 | 51.413 | 54.12 | 40.009 | 0.6 |
| AT3G28740 | Cytochrome P450 superfamily protein | 1675.8 | 1536.3 | 1916 | 699.82 | 751.04 | 724.18 | 0.4 | 4749.9 | 5302 | 4580 | 3332.3 | 3293 | 3593.2 | 0.7 |
| AT3G29780 | ralf-like 27 | 375.1 | 351.55 | 359.4 | 214.44 | 250.23 | 196.12 | 0.6 | 212.41 | 211.46 | 215.35 | 333.99 | 334.57 | 321.15 | 1.5 |
| AT3G44970 | Cytochrome P450 superfamily protein | 154.16 | 93.534 | 125.69 | 324.61 | 329.24 | 323.04 | 2.6 | 173.97 | 167.8 | 175.13 | 284.36 | 270.13 | 297.24 | 1.6 |
| AT3G46280 | protein kinase-related | 1339.4 | 1653.6 | 1177.5 | 3955.6 | 3501.4 | 3547.2 | 2.6 | 1681.8 | 1796.8 | 1558 | 1010.2 | 967.82 | 947.71 | 0.6 |
| AT3G46660 | UDP-glucosyl transferase 76E12 | 76.415 | 99.866 | 94.665 | 26.774 | 28.172 | 25.556 | 0.3 | 159.38 | 209.19 | 168.76 | 91.474 | 71.568 | 104.71 | 0.5 |
| AT3G46670 | UDP-glucosyl transferase 76E11 | 584.8 | 532.27 | 550.73 | 336.21 | 331.96 | 363.17 | 0.6 | 814.61 | 977.31 | 1011.5 | 585.03 | 453.36 | 629.27 | 0.6 |
| AT3G47420 | phosphate starvation-induced gene 3 | 964.07 | 836.09 | 959.24 | 3704.5 | 3566.4 | 3516.2 | 3.9 | 1578.6 | 1298.2 | 1610.4 | 4427.3 | 3650.9 | 4413.7 | 2.8 |
| AT3G48930 | Nucleic acid-binding, OB-fold-like protein | 36084 | 35581 | 34978 | 27287 | 26303 | 29045 | 0.8 | 28344 | 28851 | 27637 | 31782 | 31692 | 30827 | 1.1 |
| AT3G50480 | homolog of RPW8 4 | 23262 | 25297 | 21656 | 37183 | 34407 | 35439 | 1.5 | 24945 | 22937 | 23114 | 17293 | 16226 | 16733 | 0.7 |
| AT3G53210 | nodulin MtN21 /EamA-like transporter family protein | 511.16 | 529.07 | 532.99 | 416.69 | 441.49 | 439.46 | 0.8 | 444.37 | 441.86 | 461.25 | 494.11 | 490.18 | 499.6 | 1.1 |
| AT3G59140 | multidrug resistance-associated protein 14 | 274.91 | 305.81 | 252.13 | 145.68 | 154.16 | 154.45 | 0.5 | 486.66 | 542.3 | 475.1 | 325.21 | 285.37 | 317.91 | 0.6 |
| AT3G62270 | HCO3- transporter family | 873.76 | 888.46 | 901.33 | 699.52 | 691.06 | 636.58 | 0.8 | 897.68 | 800.6 | 859.5 | 620.46 | 690.28 | 597.71 | 0.7 |
| AT3G62410 | CP12 domain-containing protein 2 | 64932 | 70623 | 66092 | 86782 | 87714 | 86344 | 1.3 | 60273 | 51572 | 58104 | 76754 | 73344 | 77283 | 1.3 |
| AT3G62760 | Glutathione S-transferase family protein | 85.254 | 89.845 | 81.009 | 39.11 | 39.183 | 30.719 | 0.4 | 138.13 | 99.576 | 113.96 | 188.97 | 168.12 | 172.68 | 1.5 |
| AT3G63200 | PATATIN-like protein 9 | 2634.9 | 2611.7 | 2555.4 | 1785.3 | 1650 | 1472.7 | 0.6 | 2270.2 | 2455.2 | 2248 | 1868.3 | 2013.4 | 1763.1 | 0.8 |
| AT4G02330 | Plant invertase/pectin methylesterase inhibitor superfamily | 460.39 | 440.06 | 430.15 | 1097.9 | 1017.4 | 1012.6 | 2.4 | 567.36 | 567.59 | 557.06 | 344.08 | 341.37 | 315.04 | 0.6 |
| AT4G03510 | RING membrane-anchor 1 | 253.7 | 253.87 | 229.6 | 464.88 | 432.53 | 428.7 | 1.8 | 332.91 | 416.75 | 311.88 | 618.84 | 591.57 | 557.63 | 1.7 |
| AT4G03960 | Phosphotyrosine protein phosphatases superfamily protein | 308.77 | 317.57 | 356.19 | 680.82 | 695.28 | 610.89 | 2.0 | 299.36 | 288.24 | 333.39 | 917.23 | 727.11 | 896.85 | 2.8 |
| AT4G12470 | azelaic acid induced 1 | 44929 | 58649 | 48649 | 89776 | 83515 | 87714 | 1.7 | 48852 | 47648 | 47326 | 30306 | 28144 | 32251 | 0.6 |
| AT4G14030 | selenium-binding protein 1 | 4373.4 | 4367.3 | 3938.8 | 5909.1 | 5784.1 | 5906.5 | 1.4 | 4438.7 | 4929.6 | 4348.7 | 5962.7 | 6221.5 | 5653.7 | 1.3 |
| AT4G15540 | EamA-like transporter family | 1009.6 | 981.44 | 1099.7 | 1708.6 | 1720.7 | 1808.9 | 1.7 | 1291.3 | 1186.9 | 1357.1 | 2116.9 | 2188 | 2275.1 | 1.7 |
| AT4G21870 | HSP20-like chaperones superfamily protein | 4441 | 4757.1 | 5036.5 | 7284.4 | 7011 | 7862.9 | 1.6 | 5475.4 | 5605.2 | 5261.4 | 8649.1 | 7627.8 | 8261.4 | 1.5 |
| AT4G23130 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | 246.53 | 273.99 | 236.16 | 452.05 | 418.73 | 401.14 | 1.7 | 165.39 | 172.11 | 162.64 | 206.75 | 204.08 | 189.2 | 1.2 |
| AT4G25630 | fibrillarin 2 | 13522 | 14662 | 14799 | 9823.1 | 9729.7 | 10778 | 0.7 | 13238 | 13190 | 13622 | 8712.6 | 7768.2 | 9326.3 | 0.6 |
| AT4G26260 | myo-inositol oxygenase 4 | 683.84 | 609.45 | 622.33 | 1611.1 | 1736.7 | 1578.1 | 2.6 | 581.61 | 602.71 | 528.64 | 1375.1 | 1512.2 | 1303.1 | 2.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AT4G31350 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | 1506.9 | 1425 | 1506.5 | 1742.9 | 1778.7 | 1807.9 | 1.2 | 1350.9 | 1305.2 | 1379.3 | 1574.7 | 1556.3 | 1640.2 | 1.2 |
| AT4G32785 | unknown protein | 82.265 | 84.992 | 84.679 | 54.416 | 62.124 | 54.093 | 0.7 | 141.68 | 125.56 | 125.67 | 95.719 | 86.031 | 103.41 | 0.7 |
| AT4G33420 | Peroxidase superfamily protein | 772.83 | 708.4 | 666.08 | 1118.2 | 1027.6 | 1055.8 | 1.5 | 743.92 | 682.26 | 767.02 | 612.7 | 562.27 | 596.56 | 0.8 |
| AT4G33985 | Protein of unknown function (DUF1685) | 1176.7 | 1182.3 | 1129.6 | 1626.7 | 1550.9 | 1508.1 | 1.3 | 1403.9 | 1295.8 | 1348.2 | 1675 | 1667 | 1652.9 | 1.2 |
| AT4G34135 | UDP-glucosyltransferase 73B2 | 763.73 | 694.24 | 710.92 | 496.32 | 480.42 | 540.25 | 0.7 | 1330.2 | 1633.1 | 1569.2 | 846.45 | 697.47 | 868.15 | 0.5 |
| AT4G34419 | unknown protein | 282.54 | 262.06 | 278.08 | 189.61 | 172.66 | 191.26 | 0.7 | 247.14 | 223.04 | 226.34 | 370.12 | 334.4 | 333.12 | 1.5 |
| AT4G34980 | subtilisin-like serine protease 2 | 3422.7 | 3489.7 | 3243.8 | 2717.8 | 2789.3 | 2732.1 | 0.8 | 4133.8 | 4286.8 | 4129.1 | 3545.3 | 3710.7 | 3654.3 | 0.9 |
| AT4G36820 | Protein of unknown function (DUF607) | 179.91 | 142.58 | 176.38 | 292.21 | 285.6 | 321.1 | 1.8 | 170.59 | 178.4 | 170.06 | 295.86 | 325.36 | 302.61 | 1.8 |
| AT4G37880 | LisH/CRA/RING-U-box domains-containing protein | 2496.6 | 2552.7 | 2535.4 | 2783.2 | 2728.1 | 2759.7 | 1.1 | 2506.8 | 2508.7 | 2549.4 | 3096.9 | 3042.6 | 2864 | 1.2 |
| AT4G39770 | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | 138.08 | 153.44 | 139.91 | 83.35 | 78.027 | 93.534 | 0.6 | 125.98 | 128.15 | 138.15 | 100.58 | 107.24 | 106.84 | 0.8 |
| AT4G39795 | Protein of unknown function (DUF581) | 534.63 | 532.14 | 563.07 | 281.63 | 293.73 | 242.01 | 0.5 | 253.5 | 239.77 | 216.75 | 422.43 | 475.18 | 427.75 | 1.9 |
| AT5G02270 | non-intrinsic ABC protein 9 | 972.4 | 909.11 | 962.88 | 720.54 | 745.09 | 679.73 | 0.8 | 757.57 | 757.27 | 726.82 | 890.72 | 856.03 | 866.55 | 1.2 |
| AT5G02580 | Plant protein 1589 of unknown function | 296.11 | 290.19 | 314.59 | 213.19 | 199.44 | 189.39 | 0.7 | 225.25 | 237.43 | 260.74 | 397.32 | 389.29 | 394.2 | 1.6 |
| AT5G03310 | SAUR-like auxin-responsive protein family | 217.06 | 207.81 | 232.45 | 340.94 | 335.87 | 332.05 | 1.5 | 197.92 | 187.07 | 191.38 | 337.59 | 382.57 | 312.96 | 1.8 |
| AT5G05300 | unknown protein | 24.418 | 16.107 | 28.467 | 74.973 | 74.139 | 67.846 | 3.1 | 38.421 | 39.26 | 39.377 | 55.024 | 58.292 | 58.482 | 1.5 |
| AT5G05440 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | 2878 | 2755.7 | 3162.4 | 4272.9 | 4135.2 | 4454 | 1.5 | 2953.5 | 2671.9 | 2529.1 | 3943.9 | 3882.5 | 4089.5 | 1.5 |
| AT5G10695 | unknown protein | 599.32 | 579.46 | 611.91 | 834.7 | 800.17 | 810.29 | 1.4 | 660.76 | 623.24 | 630.89 | 761.67 | 871.67 | 807.99 | 1.3 |
| AT5G14020 | Endosomal targeting BRO1-like domain-containing protein | 253.72 | 263.01 | 237.42 | 126.76 | 153.44 | 122.11 | 0.5 | 194.74 | 182.24 | 181.29 | 233.34 | 233.08 | 224.77 | 1.2 |
| AT5G14570 | high affinity nitrate transporter 2.7 | 407.21 | 434.47 | 424.4 | 317.66 | 341.64 | 315.65 | 0.8 | 625.05 | 639.76 | 601.88 | 499.74 | 521.62 | 486.77 | 0.8 |
| AT5G14640 | shaggy-like kinase 13 | 434.36 | 423.19 | 440.52 | 345.89 | 371.55 | 351.55 | 0.8 | 591.32 | 543.67 | 585.41 | 380.83 | 369.5 | 387.74 | 0.7 |
| AT5G20150 | SPX domain gene 1 | 3783.7 | 3785.9 | 3790.9 | 8852.9 | 10274 | 8692.2 | 2.4 | 5113 | 4756.2 | 4811.9 | 16930 | 15154 | 17503 | 3.4 |
| AT5G20790 | unknown protein | 146.7 | 127.18 | 142.22 | 640.43 | 581.99 | 543.99 | 4.2 | 153.96 | 161.15 | 144.88 | 1176.6 | 630.03 | 1072.8 | 6.3 |
| AT5G23070 | Thymidine kinase | 242.06 | 235.17 | 223.44 | 182.97 | 181.45 | 179.82 | 0.8 | 267.27 | 309.9 | 282.93 | 219.48 | 213.21 | 206.79 | 0.7 |
| AT5G24160 | squalene monoxygenase 6 | 171.79 | 180.95 | 149.33 | 368.24 | 361.02 | 352.4 | 2.2 | 447.4 | 449.7 | 469.14 | 335.53 | 375.51 | 327.16 | 0.8 |
| AT5G24640 | unknown protein | 55.896 | 87.188 | 64.279 | 291.78 | 336.6 | 278.41 | 4.4 | 874.1 | 899.72 | 817.26 | 1115.4 | 1101.9 | 1131.3 | 1.3 |
| AT5G36130 | Cytochrome P450 superfamily protein | 149.06 | 118.52 | 135.87 | 17.456 | 17.563 | 28.263 | 0.2 | 30.64 | 34.398 | 31.449 | 22.12 | 20.491 | 25.175 | 0.7 |
| AT5G36925 | unknown protein | 128.14 | 135.61 | 128.89 | 519.03 | 501.18 | 461.69 | 3.8 | 138.05 | 120.7 | 120.15 | 177.11 | 201.59 | 178.44 | 1.5 |
| AT5G41761 | unknown protein | 2016.7 | 1386.5 | 2021.3 | 3759.5 | 3697.5 | 3635 | 2.0 | 1463.7 | 1253.7 | 1223.6 | 2568.2 | 2401.6 | 2291.7 | 1.8 |
| AT5G43300 | PLC-like phosphodiesterases superfamily protein | 76.242 | 81.966 | 71.719 | 114.17 | 110.87 | 114.11 | 1.5 | 59.216 | 73.494 | 60.102 | 106.47 | 108.67 | 123.61 | 1.8 |
| AT5G44578 | unknown protein | 62.901 | 58.994 | 58.788 | 205.41 | 158.49 | 170.5 | 3.0 | 46.725 | 65.925 | 51.588 | 94.535 | 86.441 | 91.474 | 1.7 |
| AT5G46871 | Putative membrane lipoprotein | 61.876 | 81.636 | 84.11 | 258.67 | 257.79 | 257.79 | 3.4 | 238.16 | 218.24 | 273.82 | 510.3 | 567.98 | 567.82 | 2.3 |
| AT5G48940 | Leucine-rich repeat transmembrane protein kinase family protein | 122.36 | 142.14 | 118.25 | 59.887 | 59.464 | 58.72 | 0.5 | 182.61 | 188.14 | 186.58 | 133.62 | 123.83 | 128.63 | 0.7 |
| AT5G52520 | Class II aaRS and biotin synthetases superfamily protein | 1589.9 | 1668.7 | 1703.6 | 1320 | 1307.1 | 1366.2 | 0.8 | 2181 | 2399.4 | 2428.5 | 1641.6 | 1587.8 | 1919.9 | 0.7 |
| AT5G52790 | CBS domain-containing protein with a domain of unknown function (DUF21) | 62.44 | 68.448 | 60.959 | 38.647 | 37.503 | 34.542 | 0.6 | 78.935 | 72.411 | 71.878 | 56.304 | 46.925 | 52.927 | 0.7 |
| AT5G52960 | unknown protein | 10533 | 10559 | 10737 | 9882.3 | 9715.5 | 9708.6 | 0.9 | 9855.2 | 10017 | 9182.9 | 12435 | 12626 | 12833 | 1.3 |
| AT5G56120 | unknown protein | 1153 | 1173.9 | 1141 | 920.6 | 869.36 | 922.22 | 0.8 | 1025.4 | 1088 | 1023.1 | 1330.2 | 1322.8 | 1324.1 | 1.3 |
| AT5G57870 | MIF4G domain-containing protein / MA3 domain-containing protein | 16634 | 16569 | 16850 | 15218 | 15019 | 15238 | 0.9 | 16129 | 15700 | 15247 | 13509 | 14342 | 13946 | 0.9 |
| AT5G60890 | myb domain protein 34 | 1297 | 1350.7 | 1251.3 | 851.77 | 864.11 | 821.68 | 0.7 | 1048.4 | 1041.1 | 1094.4 | 853.34 | 875.72 | 791.72 | 0.8 |
| AT5G61020 | evolutionarily conserved C-terminal region 3 | 2188.4 | 2153.4 | 2143.6 | 1819.4 | 1911.1 | 1887.7 | 0.9 | 2659.7 | 2686.6 | 2485.9 | 1783.1 | 1900 | 1779.7 | 0.7 |
| AT5G62440 | Protein of unknown function (DUF3223) | 1085.1 | 1079.8 | 1135.7 | 889.76 | 814.24 | 848.93 | 0.8 | 1198.1 | 1290.1 | 1328.5 | 760.73 | 710.36 | 721.71 | 0.6 |
| AT5G63580 | flavonol synthase 2 | 87.244 | 68.144 | 77.841 | 152.81 | 139.27 | 141.39 | 1.9 | 85.899 | 90.411 | 87.971 | 36.78 | 47.231 | 57.592 | 0.5 |
| AT5G63850 | amino acid permease 4 | 741.71 | 924.08 | 691.31 | 2232.7 | 2102.4 | 1893.8 | 2.6 | 2595.8 | 2340.2 | 2203.5 | 1692.6 | 1793.9 | 1549.8 | 0.7 |
| AT5G67230 | Nucleotide-diphospho-sugar transferases superfamily protein | 311.8 | 269.24 | 294.68 | 403.89 | 398.49 | 390.39 | 1.4 | 316.76 | 333.51 | 309.08 | 435.84 | 456.5 | 434.41 | 1.4 |
| AT5G67500 | voltage dependent anion channel 2 | 1638.3 | 1589.9 | 1590.4 | 1417.3 | 1407.3 | 1364.9 | 0.9 | 1997.7 | 1898.8 | 2012.3 | 1234 | 1325.3 | 1373.6 | 0.7 |
| AY536062 | Full-length cDNA | 8192.1 | 7099.8 | 8046.3 | 17308 | 17000 | 16358 | 2.2 | 8565.7 | 7504 | 7842.5 | 21783 | 17302 | 21443 | 2.5 |
| BX817525 | Full-length cDNA | 1647.9 | 1449.5 | 1629.5 | 1026.5 | 1074.3 | 992.78 | 0.7 | 968.31 | 1001.8 | 898.32 | 1227.7 | 1194.4 | 1128.7 | 1.2 |
| BX828992 | Full-length cDNA | 642.97 | 682.13 | 642.21 | 950.21 | 910.13 | 881.76 | 1.4 | 605.27 | 490.68 | 487.19 | 773.69 | 724.85 | 769.48 | 1.4 |
| DQ108818 | Full-length cDNA | 53.474 | 38.661 | 48.566 | 124.71 | 125.42 | 110.54 | 2.6 | 54.844 | 59.481 | 48.837 | 82.892 | 87.676 | 87.927 | 1.6 |
| EF183020 | Full-length cDNA | 55.918 | 53.127 | 67.949 | 133.83 | 131.5 | 155.86 | 2.4 | 113.99 | 92.386 | 118.63 | 220.32 | 225.53 | 294.51 | 2.3 |
| EF183376 | Full-length cDNA | 731.28 | 772.15 | 760.76 | 638.59 | 648.33 | 657.35 | 0.9 | 665.92 | 760.04 | 662.87 | 898.32 | 888.94 | 869.85 | 1.3 |
| RAFL06-10-F1 | Full-length cDNA | 1486.7 | 1486.4 | 1575.2 | 2091.4 | 2175.1 | 2007.4 | 1.4 | 1406.5 | 1342.2 | 1277 | 1830.7 | 1849 | 1692.4 | 1.3 |
| RAFL07-16-D1 | Full-length cDNA | 2422 | 2335.1 | 2448.2 | 2912.8 | 2874.5 | 2868.7 | 1.2 | 1927 | 2137.8 | 1961.3 | 1421.5 | 1393.5 | 1494.8 | 0.7 |
| RAFL09-47-E1 | Full-length cDNA | 156.61 | 159.12 | 150.75 | 81.131 | 92.644 | 85.328 | 0.6 | 155.17 | 158.81 | 154.36 | 131.32 | 130.74 | 135.46 | 0.8 |
| RAFL17-06-E1 | Full-length cDNA | 286.06 | 271.85 | 290.42 | 416.95 | 393.11 | 440.64 | 1.5 | 312.56 | 330.55 | 328.83 | 456.5 | 446.86 | 490.4 | 1.4 |
| RAFL19-20-E0 | Full-length cDNA | 933.27 | 1011.5 | 988.91 | 1382.3 | 1383.7 | 1263.1 | 1.4 | 1091.9 | 1071.2 | 1000.7 | 1558.2 | 1426.1 | 1394.9 | 1.4 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RAFL19-64-O1 | Full-length cDNA | 175.21 | 178.76 | 184.64 | 237.42 | 237.29 | 223.53 | 1.3 | 185.23 | 185.31 | 156.53 | 266.93 | 283.66 | 259.28 | 1.5 |
| RAFL19-65-G2 | Full-length cDNA | 900.84 | 836.26 | 840.24 | 1300.4 | 1369 | 1210.9 | 1.5 | 930.52 | 951.07 | 838.83 | 1376.2 | 1361.6 | 1197.2 | 1.4 |
| RAFL24-01-H | Full-length cDNA | 153.12 | 152.99 | 156.38 | 125.78 | 121.85 | 118.25 | 0.8 | 139.05 | 154.19 | 163.07 | 181.27 | 194.93 | 193.68 | 1.2 |
| RAFL25-22-I1 | Full-length cDNA | 551.24 | 429.57 | 585.6 | 2413.6 | 2571.1 | 2374.7 | 4.7 | 707.14 | 561.23 | 679.12 | 2069.5 | 1864.2 | 2297.9 | 3.2 |
| sORF2655 | chr2_+_6564522-6564674 | 1694.6 | 1738.5 | 1710.1 | 1325.8 | 1342.7 | 1371.1 | 0.8 | 1021.6 | 1069.4 | 1070.3 | 1547.3 | 1337 | 1343.5 | 1.3 |
| sORF4533 | chr3_-_15205819-15205971 | 1183.4 | 1279.1 | 1224.2 | 911.49 | 932.11 | 921.73 | 0.8 | 685.08 | 706.15 | 711.08 | 1021.3 | 912.93 | 995.19 | 1.4 |
| sORF0154 | chr1_-_2407651-2407785 | 167.55 | 142.44 | 122.66 | 385.49 | 380.72 | 372.66 | 2.6 | 187.7 | 163.41 | 132.36 | 576.19 | 460.21 | 405.14 | 3.0 |

a) AGI: Arabidopsis gene ID and gene description from TAIR ver. 10

b). Full length cDNA IDs (http://www.brc.riken.jp/lab/epd/catalog/cdnaclone.html or http://www.ncbi.nlm.nih.gov/genbank/)

b) Small open reading frames (sORFs) identified in our previous paper (Hanada et al., PNAS 2013)

**Tabls S5. Gene ontology analysis of up- and down-regulated genes in *AtPROPEP3/AT13-ox* plants and *AtPep3/AT13* peptide treated plants**

| GO category[a)] | Gene names | Gene count | Annotation count | FDR |
|---|---|---|---|---|
| positive_regulation_of_cellular_response_to_phosphate_starvation:GO:0080040 | AT2G45130,AT5G20150 | 2 | 3 | 3.76E-27 |
| phosphate_ion_transport:GO:0006817 | AT1G68740,AT1G26730,AT2G45130,AT5G20150 | 4 | 29 | 1.04E-12 |
| galactolipid_biosynthetic_process:GO:0019375 | AT1G68740,AT1G67600,AT1G08310,AT1G17710,AT2G45130,AT3G17790,AT5G20150 | 7 | 99 | 1.34E-07 |
| anaerobic_respiration:GO:0009061 | AT2G41730,AT5G23070 | 2 | 20 | 3.09E-05 |
| syncytium_formation:GO:0006949 | AT2G39700,AT4G26260 | 2 | 21 | 4.75E-05 |
| cellular_response_to_phosphate_starvation:GO:0016036 | AT1G68740,AT1G67600,AT1G26730,AT1G08310,AT1G17710,AT2G45130,AT3G17790,AT5G20150 | 8 | 168 | 1.80E-04 |
| negative_regulation_of_transcription,_DNA-templated:GO:0045892 | AT1G68740,AT1G67600,AT1G08310,AT1G17710,AT2G45130,AT3G17790,AT5G20150 | 7 | 165 | 1.44E-03 |
| defense_response_to_insect:GO:0002213 | AT3G28740,AT5G60890 | 2 | 34 | 4.65E-03 |
| fatty_acid_catabolic_process:GO:0009062 | AT3G46660,AT3G53210,AT5G02580 | 3 | 62 | 4.65E-03 |
| plant-type_cell_wall_loosening:GO:0009828 | AT2G20750,AT2G39700 | 2 | 35 | 5.10E-03 |
| flavonoid_biosynthetic_process:GO:0009813 | AT3G19010,AT5G63580,AT5G02270 | 3 | 65 | 5.40E-03 |
| para-aminobenzoic_acid_metabolic_process:GO:0046482 | AT1G05560,AT2G29490 | 2 | 36 | 5.40E-03 |
| positive_regulation_of_flavonoid_biosynthetic_process:GO:0009963 | AT2G18730,AT2G21560,AT2G28660,AT3G19010 | 4 | 103 | 9.85E-03 |
| amino_acid_transport:GO:0006865 | AT1G80450,AT1G10585,AT3G46280,AT4G12470,AT5G63850 | 5 | 144 | 1.48E-02 |
| anion_transport:GO:0006820 | AT3G62270,AT5G67500 | 2 | 46 | 2.41E-02 |

a) Genes were functionally categorized using GO slim in TAIR.

**Tabls S6. No significant change of gene expression related to other hormones**

| Gene | Related Hormone | Function category | Symbol | AT13ox/ WT | AT13pep/ DMSO |
|---|---|---|---|---|---|
| AT2G40940 | ethylene | Hormone receptor | ERS1 | 0.86 | 1.27 |
| AT3G24520 | abscisic acid | Hormone signal transduction | HSFC1 | 0.66 | 0.64 |
| AT4G12470 | salicylic acid | Hormone signal transduction | AZI1 | 0.63 | 1.71 |
| AT5G03310 | auxin | Hormone signal transduction | SAUR44 | 1.79 | 1.53 |
| AT5G05440 | abscisic acid | Hormone receptor | PYL5 | 1.46 | 1.46 |
| AT5G67500 | abscisic acid | Hormone signal transduction | VDAC2 | 0.67 | 0.87 |