Table S1. Primers used in this study.

Function	Gene	Forward primer	Reverse primer	Product length (bp)
	CsaV3_4G024970(Actin)	CTGGAGATGGTGTCAGTCAC	AGTCAAGGGCAATGTAGGC	204
	CsaV3_1G009130	CCAAGGACAATGAAGAGAAGG	AAGGTAGGCAATCCACAGG	226
	CsaV3_1G041400	GCACCAGAGAGTGAGTGGAAG	AGCAACGAGAGCCCTTTC	202
	CsaV3_3G019090	TGTTGTAGCCTTCTCTCTCACC	CGAATCGTTTCATCTTGGAG	225
q-PCR	CsaV3_4G034970	CAATCACACGCAGAGTCATC	AATGGGCTTTGAACCTCG	201
	CsaV3_6G039530	CGTAAGGTGTCTTTGGTGAGAG	CAGTGTAAACGAGAACGAAGG	202
	CsaV3_5G023870(CsGORK)	TTGTGGGAGGAGAGAGGAGG	AAGCGGGAAGAGTAGTTGCC	206
	CsaV3_1G029650(CsAKT1)	GTTCACTGTGCCGCATGTTT	CAAATCGCCGTAGCCAACAG	174
	CsaV3_7G028990(CsHAK5;3)	AAAGTCGGGTTGATACCAAG	AACGGAGATGGAAGGAGTG	210
Subcellular localization of CsAKT1		ATGGACGAGCTGTACAGATCTATGGACACCCTTAGAAACAGAGG	GCCGGGCGGCCGCTTTTGTGGTTCTTCCATCACTGACA	2622
Heterologous expression of CsAKT1 in yeast	CsaV3_1G029650(CsAKT1)	AGGGAATATTAAGCTTATGGACACCCTTAGAAACAGAGG	ACCCCCCATGGTAAGCTTTTATGTGGTTCTTCCATCACTGACA	2622
Hi-TOM sequencing of CsAKT1		ggagtgagtacggtgtgcAGGAGGAGGAATAAGGCATAC	gagttggatgctggatggTTGACTCTGCGATTGCTTC	240

Table S2. Statistical table of genome alignment results.

Treatment	Tissue	Replication	Total reads	Total mapped	Multiple mapped	Uniquely mapped
Ctrl	Leaf	1	42766312	41075578(96.05%)	3145958(7.36%)	37929620(88.69%)
Ctrl	Leaf	2	42940438	41277467(96.13%)	3801116(8.85%)	37476351(87.28%)
Ctrl	Leaf	3	41779822	40358637(96.6%)	2555988(6.12%)	37802649(90.48%)
Ctrl	Root	1	52784946	50135398(94.98%)	4105224(7.78%)	46030174(87.2%)
Ctrl	Root	2	45219426	43279159(95.71%)	3415428(7.55%)	39863731(88.16%)
Ctrl	Root	3	44432454	42345555(95.3%)	3460633(7.79%)	38884922(87.51%)
PNC/Leaf	Leaf	1	51703330	49902207(96.52%)	4429158(8.57%)	45473049(87.95%)
PNC/Leaf	Leaf	2	48665994	46866505(96.3%)	2851355(5.86%)	44015150(90.44%)
PNC/Leaf	Leaf	3	54404872	52619672(96.72%)	2980992(5.48%)	49638680(91.24%)
PNC/Leaf	Root	1	51801696	48998287(94.59%)	2746285(5.3%)	46252002(89.29%)
PNC/Leaf	Root	2	49941074	47117073(94.35%)	3244299(6.5%)	43872774(87.85%)
PNC/Leaf	Root	3	50273726	47409363(94.3%)	3523105(7.01%)	43886258(87.29%)
PNC/Root	Leaf	1	42114732	40654936(96.53%)	2491649(5.92%)	38163287(90.62%)
PNC/Root	Leaf	2	48193550	46705357(96.91%)	2840267(5.89%)	43865090(91.02%)
PNC/Root	Leaf	3	47455756	46018891(96.97%)	2955522(6.23%)	43063369(90.74%)
PNC/Root	Root	1	46948744	44202371(94.15%)	1885730(4.02%)	42316641(90.13%)
PNC/Root	Root	2	54780586	51851293(94.65%)	3262498(5.96%)	48588795(88.7%)
PNC/Root	Root	3	45735838	43122915(94.29%)	2161840(4.73%)	40961075(89.56%)

(1) Total reads: the number of filtered sequences of the sequencing sequence (Clean reads); (2) Total mapped: number of Clean reads that can be mapped into the genome; (3) Multiple mapped: number of Clean reads with Multiple mapped locations on the reference sequence; (4) Unique mapped: number of Clean reads with Unique mapped positions in the reference sequence.

a *CsGORK*
$y = 4.4956x + 6.4146$
$R^2 = 0.9900$

b *CsAKT1*
$y = 3.477x + 10.763$
$R^2 = 0.9998$

c *CsHAK5;3*
$y = 3.5395x + 9.5282$
$R^2 = 0.9994$

Cycle threshold

log(Dilution of the template DNA)
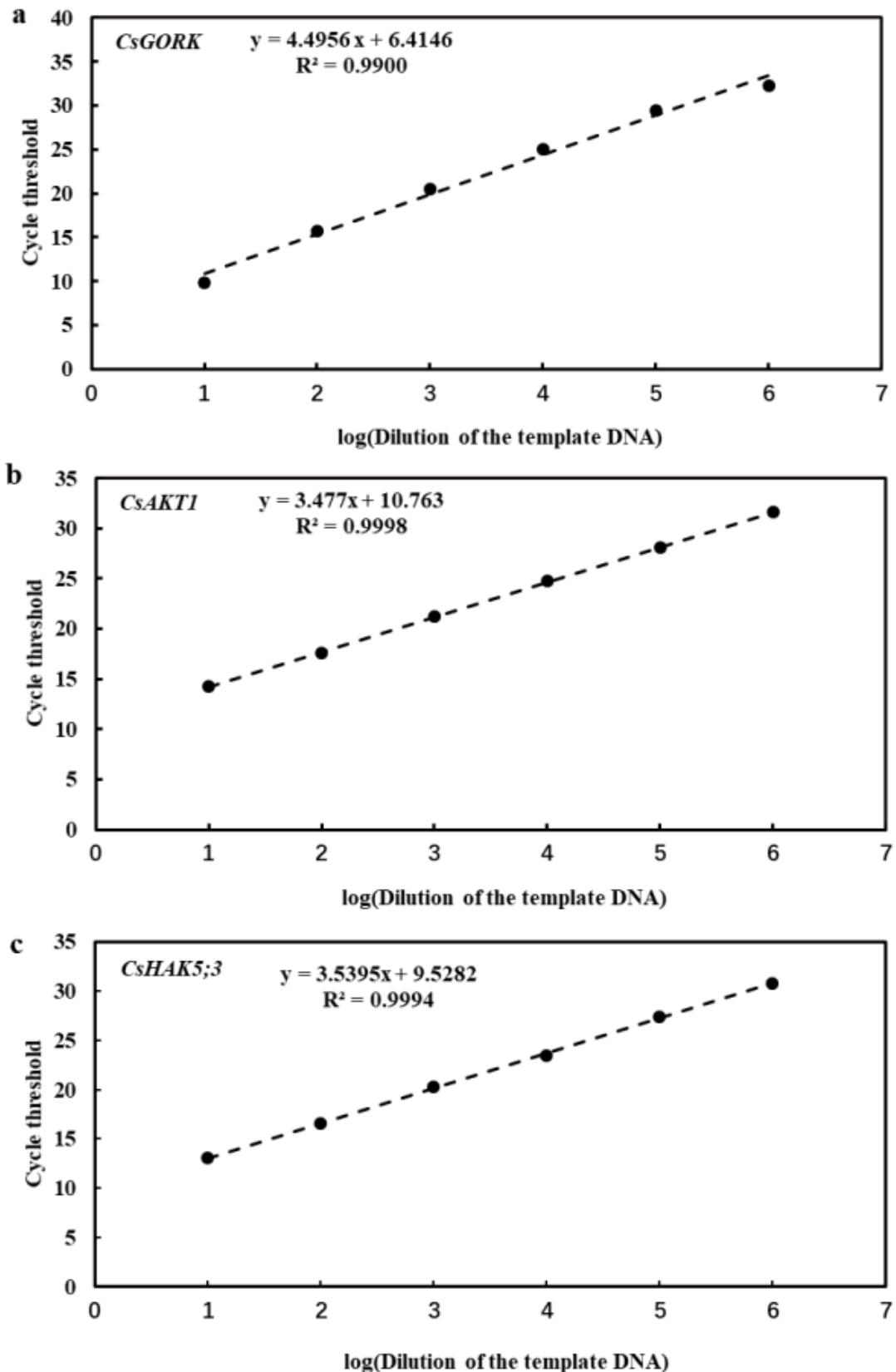
Figure S1. Standard curve for absolute quantification of *CsGORK* (a), *CsAKT1* (b) and *CsHAK5;3* (c) in cucumber.

a DiI-PNC Chloroplast Overlay

H₂O

Leaf + PNC

10 μm

b DiI-PNC Bright field Overlay

H₂O

Root + PNC

20 μm
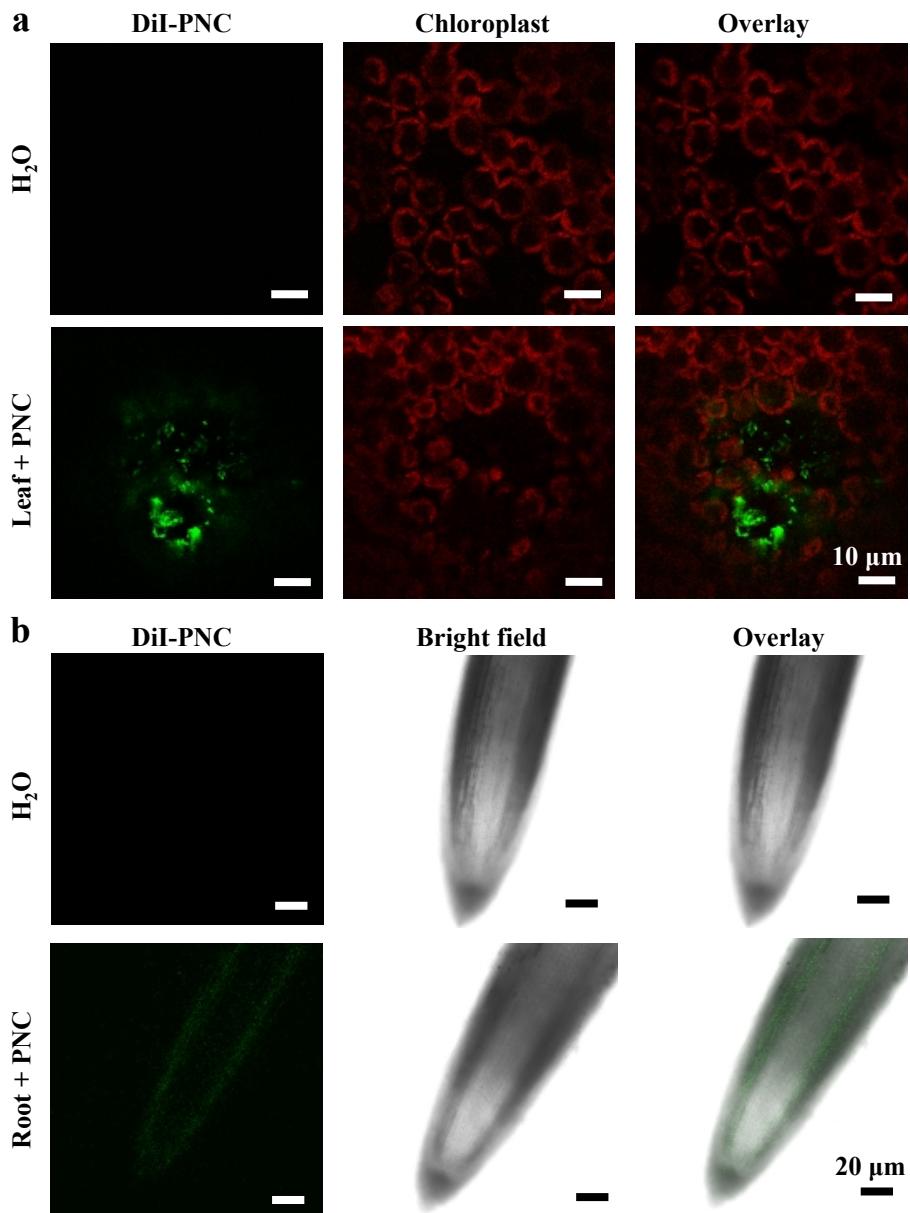
Figure S2. Confocal imaging of DiI-PNC. Confocal imaging shows the distribution of PNC in leaves of the plants with foliar PNC application (a). Confocal imaging shows the distribution of PNC in roots of the plants with root PNC application (b).
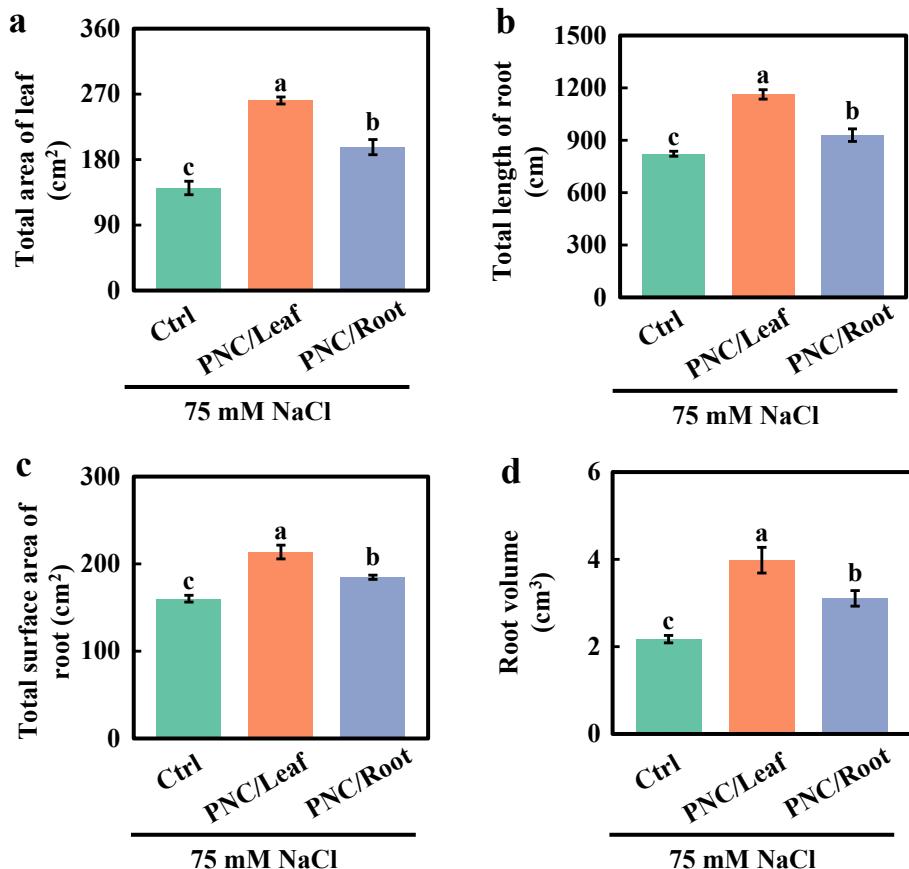
Figure S3. The phenotypic parameters in salt stressed (75 mM NaCl, Day 7) cucumber plants with foliar delivery or root application of PNC. Total area of leaf (a), total length of root (b), total surface area of root (c), root volume (d). Mean ± SE (n = 3). Different lowercase letters indicate significant differences among different treatments at the $P < 0.05$ level. Ctrl, control cucumber plants under 75 mM NaCl (7 days); PNC/Leaf, cucumber plants with leaf PNC application under 75 mM NaCl (7 days); PNC/Root, cucumber plants with leaf PNC application under 75 mM NaCl (7 days).

a Ctrl　　PNC/Leaf　　PNC/Root
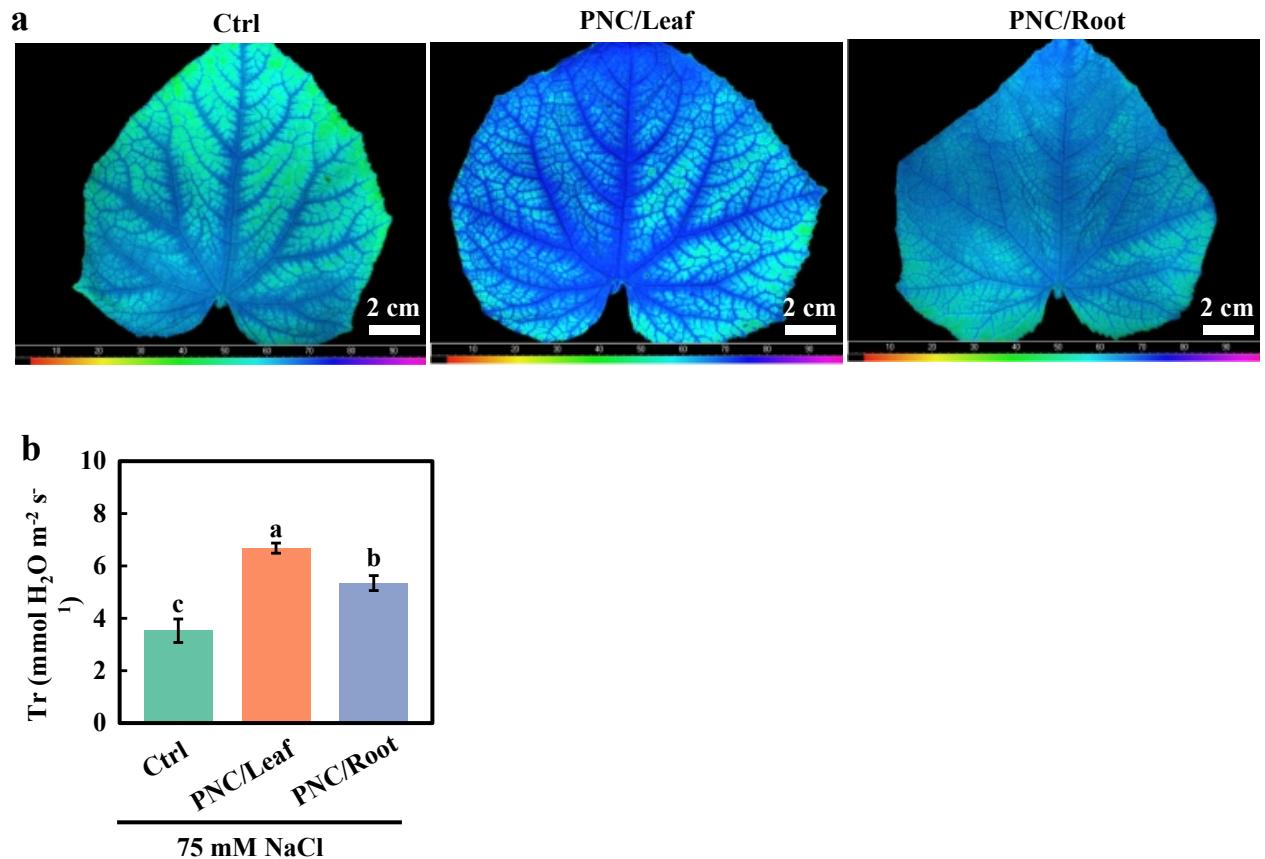
Figure S4. Fv/Fm and transpiration rate (Tr) in salt stressed (75 mM NaCl, Day 7) cucumber plants with foliar delivery or root application of PNC. a, after salt stress (75 mM NaCl, 7 days), leaf Fv/Fm in control cucumber plants, cucumber plants with foliar PNC delivery and cucumber plants with root PNC application. b, after salt stress (75 mM NaCl, 7 days), leaf Tr in control cucumber plants, cucumber plants with foliar PNC delivery and cucumber plants with root PNC application. Mean ± SE (n = 3). Different lowercase letters indicate significant differences among different treatments at the $P < 0.05$ level. Ctrl, control cucumber plants under 75 mM NaCl (7 days); PNC/Leaf, cucumber plants with leaf PNC application under 75 mM NaCl (7 days); PNC/Root, cucumber plants with leaf PNC application under 75 mM NaCl (7 days).
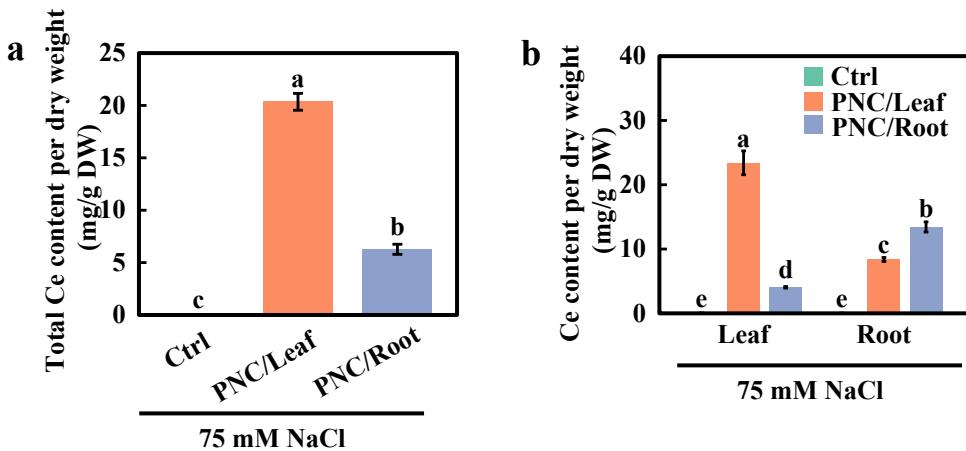
Figure S5. Leaf and root cerium content in salt stressed (75 mM NaCl, Day 7) cucumber plants with foliar sprayed or root applied PNC. Total cerium content (a), leaf cerium content and root cerium content (b). Mean ± SE (n = 3). Different letters indicate significant differences among different treatments at the *P* < 0.05 level. Ctrl, control cucumber plants under 75 mM NaCl (7 days); PNC/Leaf, cucumber plants with leaf PNC application under 75 mM NaCl (7 days); PNC/Root, cucumber plants with leaf PNC application under 75 mM NaCl (7 days).
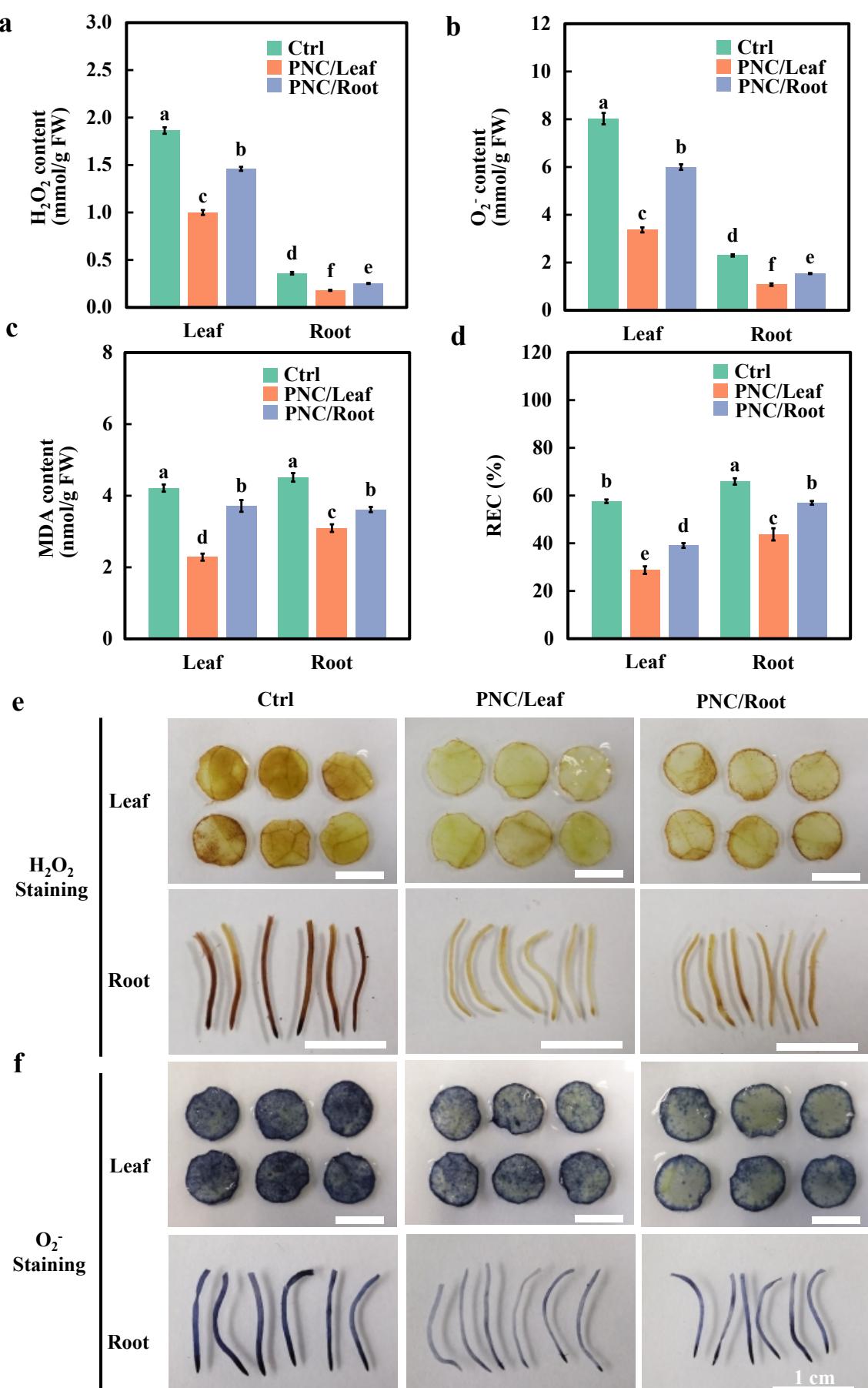
Figure S6. The ROS level, MDA content and REC (relative electric conductivity) in salt stressed (75 mM NaCl, Day 7) cucumber plants with foliar delivery or root application of PNC. Contents of H_2O_2 (a) and $O_2 \cdot {}^-$ (b), MDA content (c) and REC (d) in cucumber leaves and roots of plant with foliar sprayed or root applied PNC. DAB staining (e, indicating H_2O_2 level) and NBT staining (f, indicating $O_2 \cdot {}^-$ level) of leaves and roots of cucumber plants with foliar sprayed or root applied PNC. Different lowercase letters indicate significant differences among different treatments at the $P < 0.05$ level.
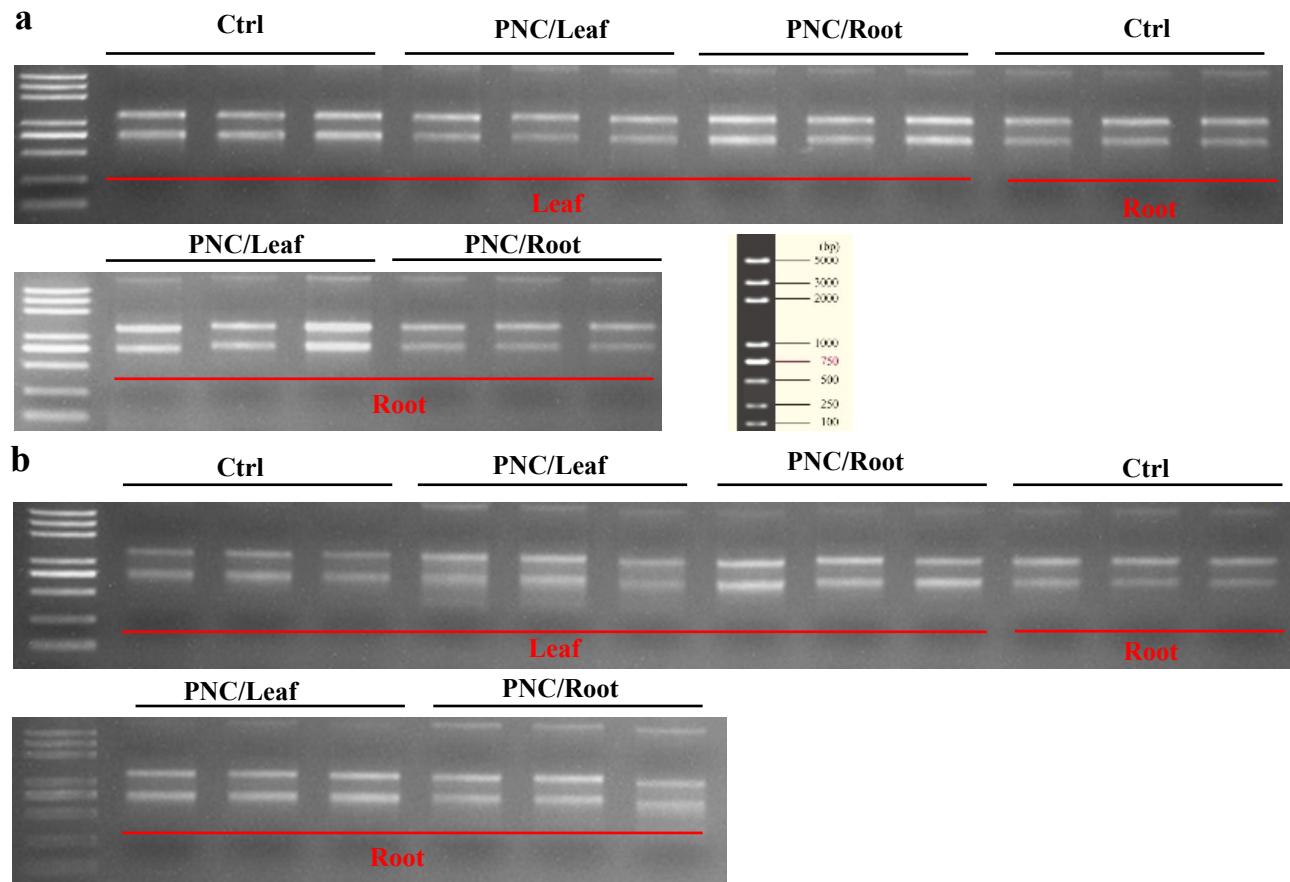
Figure S7. RNA electrophoresis detection of cucumber plants with foliar delivery or root application of PNC. Electrophoretic detection of RNA for RNA seq (a), Electrophoretic detection of RNA for qPCR (b).
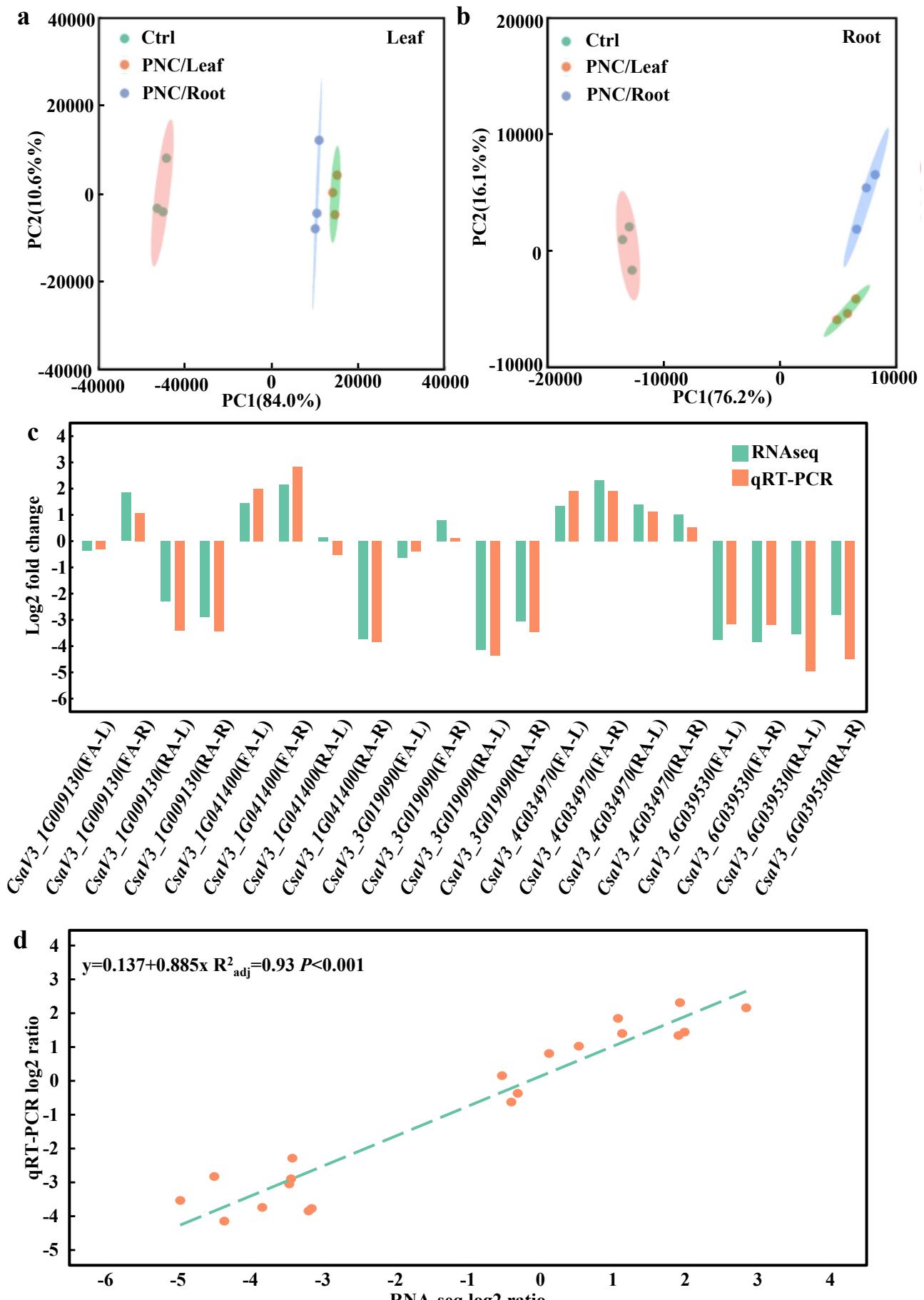
Figure S8. Transcriptome quality analysis of cucumber leaves and roots with leaf and root PNC application. PCA analysis of transcriptomic data from cucumber leaves (a) and roots (b). qPCR analysis (c) and correlation analysis (d) of cucumber leaves and roots. FA-L(R): leaves (root) of cucumber with leaf PNC application, RA-L(R): leaves (root) of cucumber with root PNC application.

Leaf			
Ctrl	PNC/Leaf	PNC/Root	
8.4	6.8	17.6	*CsaV3_1G009130*
1.2	4.7	8.6	*CsaV3_1G041400*
2.5	1.9	2.2	*CsaV3_3G019090*
24.4	91.3	92.6	*CsaV3_4G034970*
93.5	10.5	10.2	*CsaV3_6G039530*

Root			
Ctrl	PNC/Leaf	PNC/Root	
66.3	6.2	6.1	*CsaV3_1G009130*
1497.5	1036.5	104.7	*CsaV3_1G041400*
13.3	0.6	1.2	*CsaV3_3G019090*
107.2	234.3	154.7	*CsaV3_4G034970*
295.4	9.4	13.0	*CsaV3_6G039530*
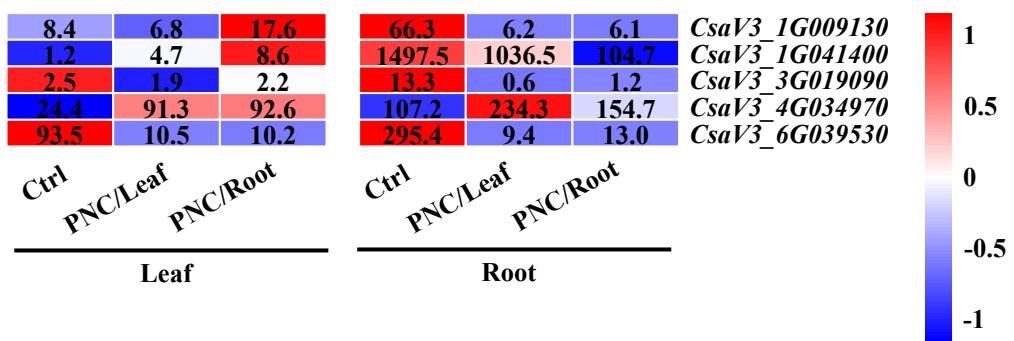
Figure S9. Heat map of gene expression for transcriptome quality verification.
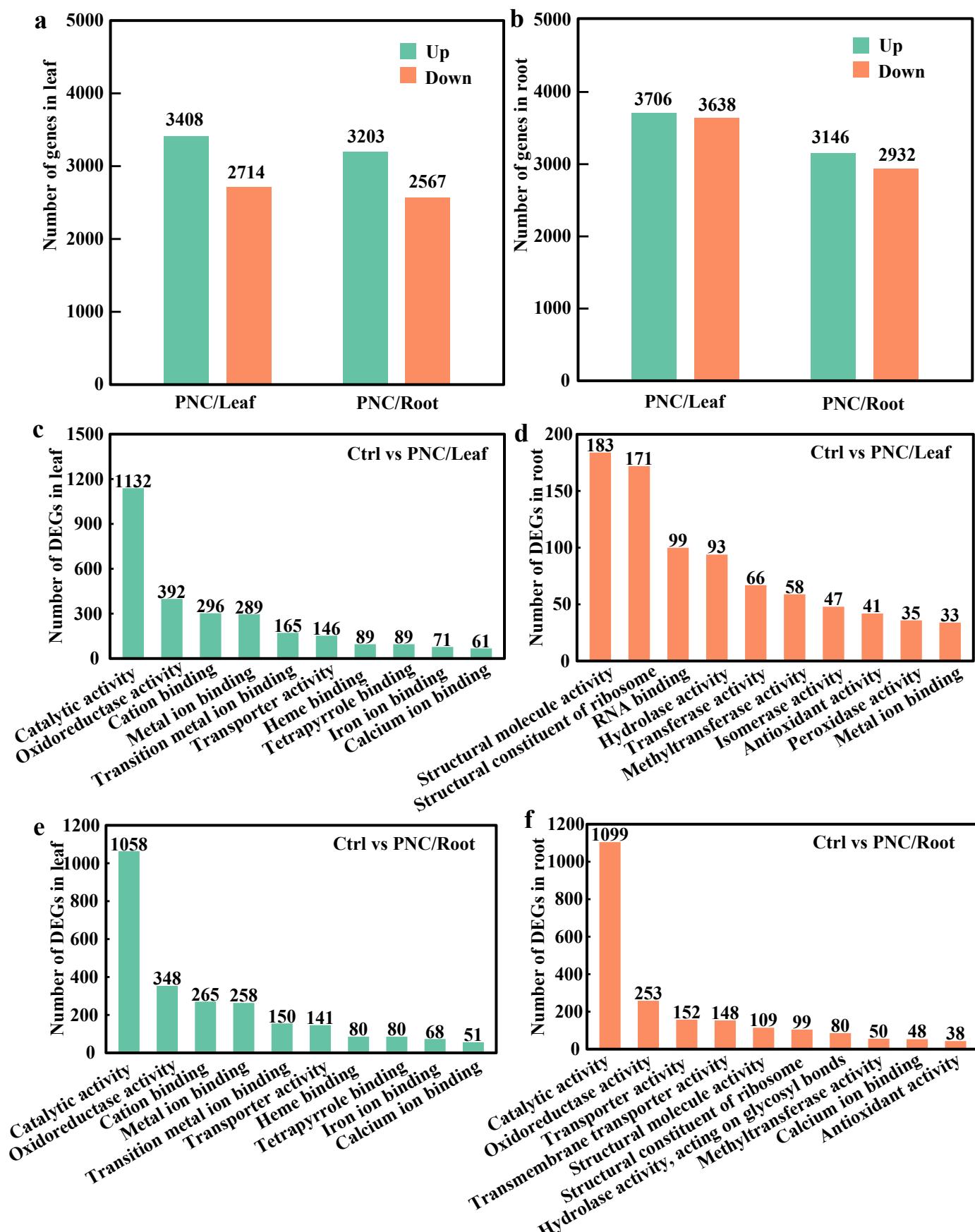
Figure S10. GO enrichment analysis of cucumber leaves and roots with leaf and root PNC application (75 mM NaCl, Day 7). GO enrichment analysis of differential expressed genes in leaves of cucumber plants with foliar sprayed (c) or root applied (d) PNC. GO enrichment analysis ($P < 0.05$) of differential expressed genes in roots of cucumber plants with foliar sprayed (e) or root applied (f) PNC.
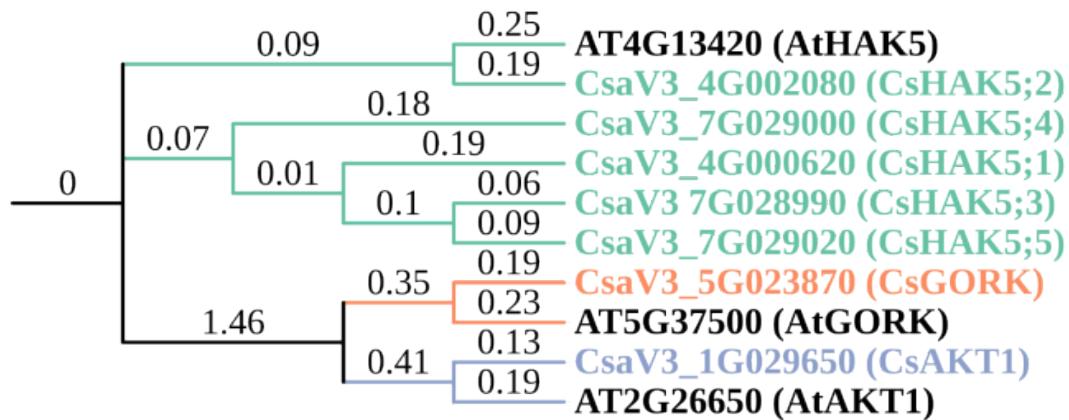
Figure S11. Phylogenetic analysis of GORK, AKT1 and HAK5 in Arabidopsis Thaliana and cucumber . The number represents the branch length of the evolutionary tree.
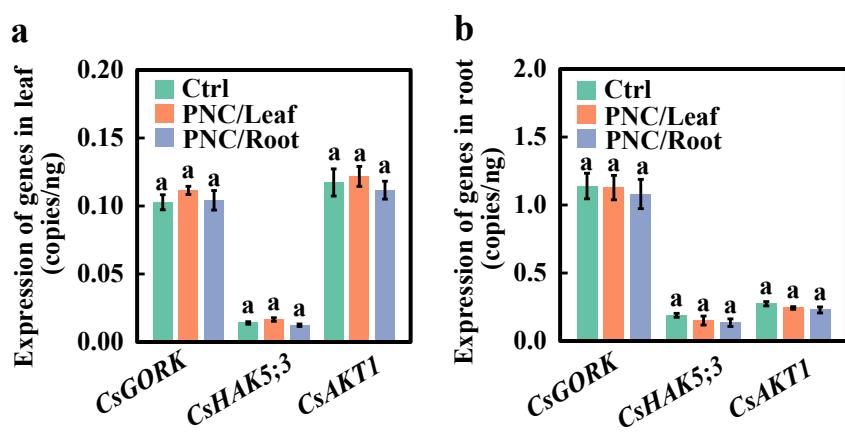
Figure S12. The gene expression level of *CsGORK*, *CsAKT1* and *CsHAK5;3* in cucumber under normal condition with leaf and root PNC application.

a

b

c
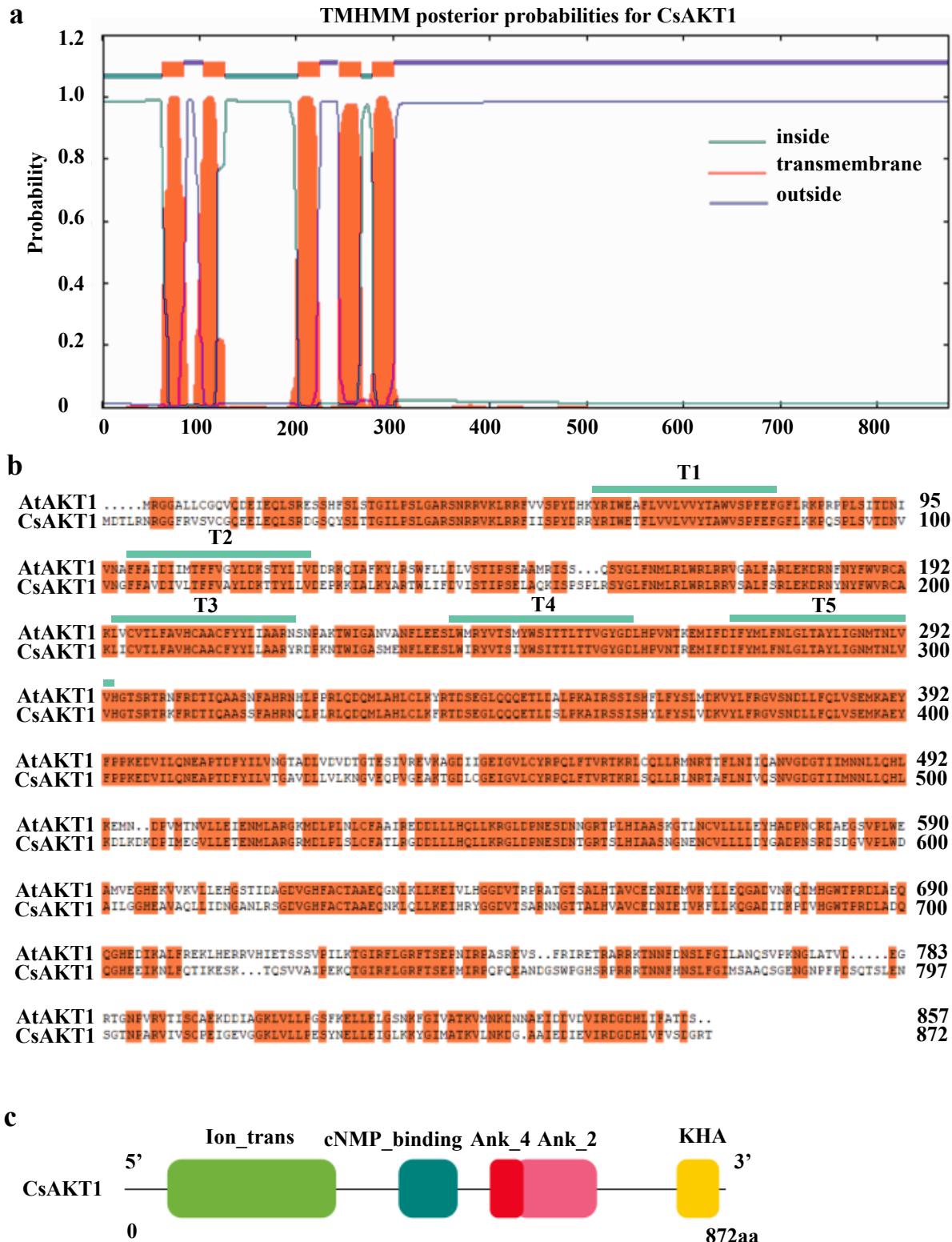
Figure S13. Structural analysis of CsAKT1. Prediction of transmembrane structure of CsAKT1 (a).Multiple alignment of AKT1 amino acid sequences from Arabidopsis and cucumber (b). Prediction of conserved domain of CsAKT1 (c).

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CsAKT1_WT    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILPSLGARSNRRVKLRRFIISFYDRRYRIWETFLVVLVVYTAWVSPFEFGFLKKPQSPLSVTDNV   100
CsAKT1_1D    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILP.............................LLALEAIAESSSGVLLFRLMT.......VDTG    63
CsAKT1_2D    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILP..................................S....WR..............         41
CsAKT1_4D    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGIL..............................LLALEAIAESSSGVLLFRLMT.......VDTG    62
CsAKT1_1I    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILP.................................SS....WR..............         42
CsAKT1_5I    MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILPLV...........................LLALEAIAESSSGVLLFRLMT.......VDTG    65
CsAKT1_SNP   MDTLRNRGGFRVSVCGQEELEQLSRDGSQYSLTTGILHSLGARSNRRVKLRRFIISFYDRRYRIWETFLVVLVVYTAWVSPFEFGFLKKPQSPLSVTDNV   100

CsAKT1_WT    VNGFFAVDIVLTFFVAYLDKTTYLLVDEPKKIALKYARTWLIFDVISTIPSELAQKISPSPLRSYGLFNMLRLWRLRRVSALFSRLEKDRNYNYFWVRCA   200
CsAKT1_1D    FGRLFSL.....FWW.......YILLGSHR...................SSLDS.LRNPNRHSPLQTMWLMDFL.LWTLFSHSLLLTLIKLP...IYLLMNPR 130
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    FGRLFSL.....FWW.......YILLGSHR...................SSLDS.LRNPNRHSPLQTMWLMDFL.LWTLFSHSLLLTLIKLP...IYLLMNPR 129
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    FGRLFSL.....FWW.......YILLGSHR...................SSLDS.LRNPNRHSPLQTMWLMDFL.LWTLFSHSLLLTLIKLP...IYLLMNPR 132
CsAKT1_SNP   VNGFFAVDIVLTFFVAYLDKTTYLLVDEPKKIALKYARTWLIFDVISTIPSELAQKISPSPLRSYGLFNMLRLWRLRRVSALFSRLEKDRNYNYFWVRCA   200

CsAKT1_WT    KLICVTLFAVHCAACFYYLLAARYRDPKNTWIGASMENFLEESLWIRYVTSIYWSITTLTTVGYGDLHPVNTREMIFDIFYMLFNLGLTAYLIGNMTNLV   300
CsAKT1_1D    KLL...........................................................................................       133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    KLL...........................................................................................       132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    KLL...........................................................................................       135
CsAKT1_SNP   KLICVTLFAVHCAACFYYLLAARYRDPKNTWIGASMENFLEESLWIRYVTSIYWSITTLTTVGYGDLHPVNTREMIFDIFYMLFNLGLTAYLIGNMTNLV   300

CsAKT1_WT    VHGTSRTRKFRDTIQAASSFAHRNQLPLRLQDQMLAHLCLKFRTDSEGLQQQETLDSLPKAIRSSISHYLFYSLVDKVYLFRGVSNDLLFQLVSEMKAEY   400
CsAKT1_1D    ...........................................................................................           133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    ...........................................................................................           132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    ...........................................................................................           135
CsAKT1_SNP   VHGTSRTRKFRDTIQAASSFAHRNQLPLRLQDQMLAHLCLKFRTDSEGLQQQETLDSLPKAIRSSISHYLFYSLVDKVYLFRGVSNDLLFQLVSEMKAEY   400

CsAKT1_WT    FPPKEDVILQNEAPTDFYILVTGAVDLLVLKNGVEQFVGEAKTGDLCGEIGVLCYRPQLFTVRTKRLSQLLRLNRTAFLNIVQSNVGDGTIIMNNLLQHL   500
CsAKT1_1D    ...........................................................................................           133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    ...........................................................................................           132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    ...........................................................................................           135
CsAKT1_SNP   FPPKEDVILQNEAPTDFYILVTGAVDLLVLKNGVEQFVGEAKTGDLCGEIGVLCYRPQLFTVRTKRLSQLLRLNRTAFLNIVQSNVGDGTIIMNNLLQHL   500

CsAKT1_WT    KDLKDKDPIMEGVLLETENMLARGRMDLPLSLCFATLRGDDLLLHQLLKRGLDPNESDNTGRTSLHIAASNGNENCVLLLLDYGADPNSRDSDGVVPLWD   600
CsAKT1_1D    ...........................................................................................           133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    ...........................................................................................           132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    ...........................................................................................           135
CsAKT1_SNP   KDLKDKDPIMEGVLLETENMLARGRMDLPLSLCFATLRGDDLLLHQLLKRGLDPNESDNTGRTSLHIAASNGNENCVLLLLDYGADPNSRDSDGVVPLWD   600

CsAKT1_WT    AILGGHEAVAQLLIDNGANLRSGDVGHFACTAAEQNKLQLLKEIHRYGGDVTSARNNGTTALHVAVCEDNIEIVKFLLKQGADIDKPDVHGWTPRDLADQ   700
CsAKT1_1D    ...........................................................................................           133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    ...........................................................................................           132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    ...........................................................................................           135
CsAKT1_SNP   AILGGHEAVAQLLIDNGANLRSGDVGHFACTAAEQNKLQLLKEIHRYGGDVTSARNNGTTALHVAVCEDNIEIVKFLLKQGADIDKPDVHGWTPRDLADQ   700

CsAKT1_WT    QGHEEIKNLFQTIKESKTQSVVAIPEKQTGIRFLGRFTSEPMIRFQPQEANDGSWPGHSRPRRRTNNFHNSLFGIMSAAQSGENGNPFFDSQTSLENSGT   800
CsAKT1_1D    ...........................................................................................           133
CsAKT1_2D    ...........................................................................................           41
CsAKT1_4D    ...........................................................................................           132
CsAKT1_1I    ...........................................................................................           42
CsAKT1_5I    ...........................................................................................           135
CsAKT1_SNP   QGHEEIKNLFQTIKESKTQSVVAIPEKQTGIRFLGRFTSEPMIRFQPQEANDGSWPGHSRPRRRTNNFHNSLFGIMSAAQSGENGNPFFDSQTSLENSGT   800

CsAKT1_WT    NPARVIVSCPEIGEVGGKLVLLPESYNELLEIGLKKYGIMATKVLNKDGAAIEDIEVIRDGDHLVFVSDGRT                              872
CsAKT1_1D    ...........................................................................                          133
CsAKT1_2D    ...........................................................................                          41
CsAKT1_4D    ...........................................................................                          132
CsAKT1_1I    ...........................................................................                          42
CsAKT1_5I    ...........................................................................                          135
CsAKT1_SNP   NPARVIVSCPEIGEVGGKLVLLPESYNELLEIGLKKYGIMATKVLNKDGAAIEDIEVIRDGDHLVFVSDGRT                              872
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**Figure S14. Analysis of the effect of knock out of *CsAKT1* on its protein translation.**
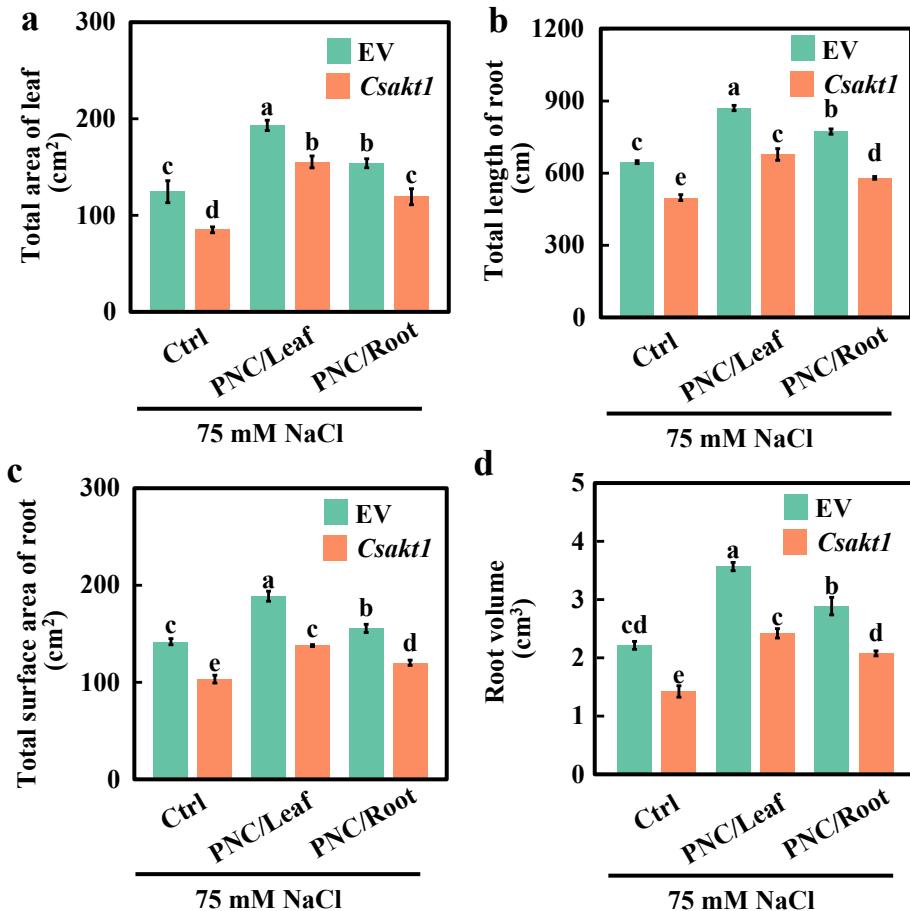
Figure S15. The phenotypic parameters of salt stressed (75 mM NaCl, Day 7) *CsAKT1* knockout cucumber plants with foliar delivery or root application of PNC. Total area of leaf (a), total length of root (b), total surface area of root (c) and root volume (d) of root knockout of *CsAKT1* cucumber seedlings with leaf application and root application of PNC under salt stress. Mean ± SE (n = 3). Different lowercase letters indicate significant differences among different treatments at the *P* < 0.05 level. Ctrl, control cucumber plants under 75 mM NaCl (7 days); PNC/Leaf, cucumber plants with leaf PNC application under 75 mM NaCl (7 days); PNC/Root, cucumber plants with leaf PNC application under 75 mM NaCl (7 days).