**Table S1** The primers for qRT-PCR analysis.

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Forward primers (5′-3′)** | **Reserve primers (5′-3′)** |
| gene-LOC8085162 | CTGCTTGGAGAGAACCTTGGAT | GCTTCCTTTCCTTCCTTTGC |
| gene-LOC8082181 | CCATAAAACGAACGGTCAAGT | TTTCTGTCCTACATCCAACTCACT |
| gene-LOC8078430 | AGAGTATGCTTTGCTATGTCGG | GAGCACCATCCTTTATTACCCA |
| gene-LOC8058543 | TGGAGAAGCAAACATTGGTGA | TAGTGGCGGAATCTCGTAGC |
| gene-LOC8056614 | GAGTGAAGCCAATGCTGTTCG | CTTGTTCCTCGTCGTTGCC |
| gene-LOC8055227 | TGAAGCACCTGCCAAACG | TCCTCACTGAACCTCACCTCC |
| gene-LOC8070790 | AAGGCTGGTGGTGCTTACAC | GAACCCCAATATGCCGAAC |
| gene-LOC8084948 | TGGCTGATTGATTTGCTGG | CTGTTCGATCTTTGCTTTGACA |
| gene-LOC8059789 | TGAGACCTCGAATACAAAAGCC | GGGAGTAGTGGTGGATGGAG |
| gene-LOC8076648 | ACTCGGATCAGTCAAGAACAACT | CACAAGAAACCCCAAAAGAACA |
| gene-LOC8055234 | TGCTTAGCGACGACGAGTTA | CAAGCTGACGGTTTGTTGG |
| gene-LOC110429509 | TGGAGCAGTGGTATCCGTAGT | CCTTAGCATCTTCCTCGTCGTT |
| Sorghum\_bicolor\_newGene\_8048 | CCACGTAGCGTTCATACAATACA | GAACCTCTTGAGCGACACCTT |
| gene-LOC8079914 | ACGCAGCATTAGTTGATTAGTGTC | GGCTGCTGTTGGAGGTGTT |
| gene-LOC8054416 | CTCTTGATGCTCGGGCTTAT | TACACGTTTTACCTTCATCTCCTC |
| Sorghum\_bicolor\_newGene\_1242 | AGCAGGTGGTTCATGTTGGG | TGGCATTGGACACGGAAGA |
| gene-LOC8065743 | CGTCCCGTTGTCTGCTTTC | GCTTTCCCTTTTGGATGTTCTT |
| gene-LOC8071420 | AGGATGACTTATGCGTTCTCG | TCGGCACTTCTTGCTTGTTA |
| gene-LOC8061392 | CCAGATCGGAAGGCAAGAG | AGGTGGTGGTGTTAGGATGAAC |
| gene-LOC8077869 | CCCTCGGAGTAGAACTGGTATC | GTTGGTATGAGTGGCATGTGAA |
| *SbActin1* | ACGGCCTGGATGGCGACGTACATG | CAGAAGGACGCCTACGTTGGTGA |
| *SbHKT1;5* | CAAAATGAGGCACAATCCG | TGAAGATGGTTAGGCACGAGA |
| *SbCLCc* | TCTTAGCTCAACCGTCCCG | CCCGAATACCCCACCAATT |
| *SbNPF7.3-1* | TCTTGTTGGTGAAGCCCTCC | TAGGTGGACAGGTAGAACAGCG |

**Table S2** RNA sequencing production statistics.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Samples | Clean reads | Clean bases | GC content | %≥Q30 |
| C6R-1 | 21,685,513 | 6,492,025,670 | 51.84% | 90.19% |
| C6R-2 | 21,233,187 | 6,353,745,880 | 52.20% | 91.58% |
| C6R-3 | 21,606,754 | 6,467,788,398 | 52.10% | 91.27% |
| S6R-1 | 21,515,441 | 6,439,315,572 | 52.62% | 90.32% |
| S6R-2 | 20,097,384 | 6,012,174,714 | 52.35% | 90.52% |
| S6R-3 | 20,990,964 | 6,284,440,252 | 52.42% | 89.99% |
| C6LS-1 | 28,104,739 | 8,414,582,254 | 54.33% | 89.85% |
| C6LS-2 | 20,845,787 | 6,237,048,094 | 54.64% | 90.81% |
| C6LS-3 | 21,969,154 | 6,574,479,452 | 53.65% | 90.58% |
| S6LS-1 | 28,741,639 | 8,600,456,600 | 54.81% | 90.54% |
| S6LS-2 | 22,028,872 | 6,592,878,370 | 54.47% | 91.47% |
| S6LS-3 | 26,194,256 | 7,841,811,600 | 54.72% | 90.10% |
| C6LB-1 | 20,158,254 | 6,032,714,478 | 53.44% | 91.86% |
| C6LB-2 | 21,992,758 | 6,581,387,904 | 54.49% | 90.62% |
| C6LB-3 | 27,775,529 | 8,313,354,526 | 55.79% | 87.87% |
| S6LB-1 | 21,024,819 | 6,292,190,276 | 53.52% | 90.58% |
| S6LB-2 | 21,528,712 | 6,442,747,000 | 53.92% | 90.38% |
| S6LB-3 | 21,783,002 | 6,519,895,574 | 55.13% | 90.43% |
| C48R-1 | 24,884,696 | 7,449,241,432 | 51.72% | 91.03% |
| C48R-2 | 23,771,732 | 7,118,292,168 | 51.50% | 91.54% |
| C48R-3 | 20,918,074 | 6,258,920,318 | 52.37% | 92.44% |
| S48R-1 | 27,922,513 | 8,359,596,758 | 52.69% | 89.56% |
| S48R-2 | 24,897,142 | 7,451,136,196 | 52.21% | 91.13% |
| S48R-3 | 28,331,032 | 8,479,638,056 | 52.01% | 91.13% |
| C48LS-1 | 25,869,891 | 7,741,653,466 | 53.17% | 90.42% |
| C48LS-2 | 25,190,278 | 7,541,864,158 | 54.06% | 89.83% |
| C48LS-3 | 25,412,707 | 7,606,135,144 | 54.14% | 90.51% |
| S48LS-1 | 23,437,249 | 7,012,940,050 | 53.70% | 90.69% |
| S48LS-2 | 28,746,121 | 8,604,160,636 | 54.23% | 90.10% |
| S48LS-3 | 23,830,152 | 7,136,317,078 | 53.39% | 89.27% |
| C48LB-1 | 26,155,517 | 7,823,294,822 | 53.15% | 94.27% |
| C48LB-2 | 21,980,635 | 6,578,056,582 | 54.15% | 94.35% |
| C48LB-3 | 25,056,506 | 7,492,470,902 | 54.58% | 94.26% |
| S48LB-1 | 29,157,844 | 8,726,376,028 | 52.54% | 94.65% |
| S48LB-2 | 21,907,906 | 6,557,487,796 | 53.25% | 94.31% |
| S48LB-3 | 29,696,308 | 8,884,796,634 | 52.62% | 95.17% |

**Note:** Sweet sorghum seedlings were treated with Hoagland solution (C) and 200 mM NaCl (S) for 6 and 48 h, then root (R), leaf sheath (LS) and leaf blades (LB) were harvested for RNA sequencing.

**Table S3** The statistics of results by mapping the RNA-seq data to sorghum reference genome sequence

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Samples | Total reads | Mapped reads | Reads map to “+” | Reads map to “-” |
| C6R-1 | 43,371,026 | 38,069,628 (87.78%) | 19,710,682 (45.45%) | 19,898,943 (45.88%) |
| C6R-2 | 42,466,374 | 37,845,248 (89.12%) | 19,447,547 (45.80%) | 19,615,511 (46.19%) |
| C6R-3 | 43,213,508 | 38,374,997 (88.80%) | 19,849,744 (45.93%) | 20,019,019 (46.33%) |
| S6R-1 | 43,030,882 | 37,324,778 (86.74%) | 19,576,281 (45.49%) | 19,757,452 (45.91%) |
| S6R-2 | 40,194,768 | 34,485,560 (85.80%) | 18,103,839 (45.04%) | 18,265,626 (45.44%) |
| S6R-3 | 41,981,928 | 35,791,386 (85.25%) | 19,030,194 (45.33%) | 19,197,395 (45.73%) |
| C6LS-1 | 56,209,478 | 49,344,015 (87.79%) | 25,439,033 (45.26%) | 25,611,101 (45.56%) |
| C6LS-2 | 41,691,574 | 36,359,794 (87.21%) | 19,055,329 (45.71%) | 19,153,020 (45.94%) |
| C6LS-3 | 43,938,308 | 38,477,728 (87.57%) | 19,882,229 (45.25%) | 20,036,908 (45.60%) |
| S6LS-1 | 57,483,278 | 50,439,106 (87.75%) | 26,012,219 (45.25%) | 26,146,753 (45.49%) |
| S6LS-2 | 44,057,744 | 38,981,598 (88.48%) | 20,154,201 (45.74%) | 20,248,097 (45.96%) |
| S6LS-3 | 52,388,512 | 45,572,110 (86.99%) | 23,605,340 (45.06%) | 23,765,759 (45.36%) |
| C6LB-1 | 40,316,508 | 35,352,759 (87.69%) | 18,540,209 (45.99%) | 18,626,006 (46.20%) |
| C6LB-2 | 43,985,516 | 38,845,218 (88.31%) | 20,053,183 (45.59%) | 20,173,413 (45.86%) |
| C6LB-3 | 55,551,058 | 45,757,244 (82.37%) | 24,581,265 (44.25%) | 24,890,528 (44.81%) |
| S6LB-1 | 42,049,638 | 36,797,978 (87.51%) | 18,998,626 (45.18%) | 19,181,437 (45.62%) |
| S6LB-2 | 43,057,424 | 37,731,052 (87.63%) | 19,523,975 (45.34%) | 19,683,816 (45.72%) |
| S6LB-3 | 43,566,004 | 38,128,602 (87.52%) | 19,926,958 (45.74%) | 20,069,397 (46.07%) |
| C48R-1 | 49,769,392 | 44,051,546 (88.51%) | 22,680,304 (45.57%) | 22,877,198 (45.97%) |
| C48R-2 | 47,543,464 | 42,162,668 (88.68%) | 21,741,573 (45.73%) | 21,902,460 (46.07%) |
| C48R-3 | 41,836,148 | 37,658,794 (90.01%) | 19,424,935 (46.43%) | 19,553,847 (46.74%) |
| S48R-1 | 55,845,026 | 47,337,035 (84.76%) | 24,284,167 (43.48%) | 24,555,073 (43.97%) |
| S48R-2 | 49,794,284 | 44,037,992 (88.44%) | 22,642,492 (45.47%) | 22,830,208 (45.85%) |
| S48R-3 | 56,662,064 | 50,213,260 (88.62%) | 25,824,759 (45.58%) | 26,036,372 (45.95%) |
| C48LS-1 | 51,739,782 | 45,315,969 (87.58%) | 23,387,619 (45.20%) | 23,595,282 (45.60%) |
| C48LS-2 | 50,380,556 | 44,088,539 (87.51%) | 22,753,909 (45.16%) | 22,951,860 (45.56%) |
| C48LS-3 | 50,825,414 | 44,646,440 (87.84%) | 23,045,305 (45.34%) | 23,201,756 (45.65%) |
| S48LS-1 | 46,874,498 | 41,348,439 (88.21%) | 21,304,418 (45.45%) | 21,448,462 (45.76%) |
| S48LS-2 | 57,492,242 | 50,531,900 (87.89%) | 26,084,986 (45.37%) | 26,293,729 (45.73%) |
| S48LS-3 | 47,660,304 | 41,725,172 (87.55%) | 21,344,824 (44.79%) | 21,547,989 (45.21%) |
| C48LB-1 | 52,311,034 | 47,294,936 (90.41%) | 24,827,121 (47.46%) | 24,794,296 (47.40%) |
| C48LB-2 | 43,961,270 | 40,676,282 (92.53%) | 21,118,062 (48.04%) | 21,089,411 (47.97%) |
| C48LB-3 | 50,113,012 | 45,969,091 (91.73%) | 24,047,689 (47.99%) | 23,994,421 (47.88%) |
| S48LB-1 | 58,315,688 | 53,739,643 (92.15%) | 27,852,391 (47.76%) | 27,859,498 (47.77%) |
| S48LB-2 | 43,815,812 | 40,215,598 (91.78%) | 21,143,529 (48.26%) | 21,138,233 (48.24%) |
| S48LB-3 | 59,392,616 | 52,779,798 (88.87%) | 28,606,642 (48.17%) | 28,605,605 (48.16%) |

**Note:** A public genome data (NCBI accession number: GCF\_000003195.3) was used as the reference genome sequence.

**Table S4** Functional annotation of new genes that cannot map to reference genome sequence

|  |  |
| --- | --- |
| Annotated databases | New gene number |
| COG | 190 |
| GO | 1,147 |
| KEGG | 680 |
| KOG | 432 |
| Pfam | 763 |
| Swiss-Prot | 513 |
| TrEMBL | 2,412 |
| eggNOG | 1,020 |
| nr | 2,477 |
| All | 2,574 |

**Table S5** The expression change of DEGs related to ion transport in roots of sweet sorghum after 200 mM NaCl treatment for 6 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC8074408 | 1.642605 | NHX2 |
| gene-LOC8084417 | 3.403835 | CHX19-1 |
| gene-LOC8084418 | 2.65564 | CHX19-2 |
| gene-LOC8057212 | 3.068639 | CCX-1 |
| gene-LOC8071496 | 2.004107 | CCX-2 |
| gene-LOC110434083 | 1.117284 | NCX1 |
| gene-LOC8081919 | 1.273911 | CNGC20 |
| gene-LOC8078183 | 1.606078 | HKT1;5 |
| gene-LOC8076484 | -1.00874 | KEA2 |
| gene-LOC8071480 | -1.48248 | KEA3 |
| gene-LOC8072046 | 2.208412 | HAK1 |
| gene-LOC8067862 | 2.527079 | HAK5-1 |
| gen-LOC8078559 | 1.486856 | HAK9 |
| gene-LOC8063025 | 3.19092 | HAK16 |
| gene-LOC8062763 | 1.869305 | HAK17 |
| gene-LOC8065633 | 2.340472 | HAK21 |
| gene-LOC8079532 | -1.49882 | KUP5-1 |
| gene-LOC8083092 | -2.03063 | KUP5-2 |
| gene-LOC8061543 | -1.20175 | KUP8 |
| gene-LOC8058492 | 1.213374 | AKT2 |
| gene-LOC8057743 | -1.68167 | AKT2/3 |
| gene-LOC8075862 | -2.35421 | KOR2 |
| gene-LOC8069763 | 1.650568 | CLCa |
| gene-LOC8080343 | 2.792361 | CLCc |
| gene-LOC8079456 | -1.76868 | CLCg |
| gene-LOC8077536 | -1.4744 | SLAH1 |
| gene-LOC8079295 | 2.556683 | SLAH2 |
| gene-LOC8076556 | -1.07108 | SLAH3 |
| gene-LOC8077536 | -1.4744 | SLAH4 |
| gene-LOC8073008 | 3.450748 | ALMT1 |
| gene-LOC8065254 | 1.71191 | NPF2.11 |
| gene-LOC8085131 | 1.682452 | NPF3.1-1 |
| gene-LOC8061532 | -1.35763 | NPF3.1-2 |
| gene-LOC8075842 | 1.903989 | NPF4.5 |
| gene-LOC8067440 | -2.29952 | NPF5.2 |
| gene-LOC8075730 | -1.99354 | NPF5.9 |
| gene-LOC8062396 | -1.17969 | NPF5.10 |
| gene-LOC8067856 | 1.05965 | NPF6.3 |
| gene-LOC8070561 | 1.327672 | NPF6.4 |
| gene-LOC8071782 | 5.152358 | NPF7.3-1 |
| gene-LOC8073896 | 1.809284 | NPF7.3-2 |
| gene-LOC8062975 | 1.194403 | P-H+-ATPase |
| gene-LOC8072298 | 1.67756 | P-Ca2+-ATPase 5 |
| gene-LOC8064910 | 2.918003 | P-Ca2+-ATPase 7 |
| gene-LOC8081867 | 1.393817 | P-Ca2+-ATPase 10 |

**Table S6** The expression change of DEGs related to ion transport in roots of sweet sorghum after 200 mM NaCl treatment for 48 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC8084417 | 2.252446 | CHX19-1 |
| gene-LOC8084418 | 1.737723 | CHX19-2 |
| gene-LOC8057212 | 1.482209 | CCX-1 |
| gene-LOC8071496 | 1.275421 | CCX-2 |
| gene-LOC8067475 | -1.70542 | CNGC4 |
| gene-LOC8081919 | 1.054428 | CNGC20 |
| gene-LOC8076484 | -1.08529 | KEA2 |
| gene-LOC8072092 | 3.079258 | KT3 |
| gene-LOC8063025 | 2.169547 | HAK16 |
| gene-LOC8065633 | 3.380665 | HAK21 |
| gene-LOC8081576 | 1.273335 | HAK22 |
| gene-LOC8065785 | 1.009076 | HAK24 |
| gene-LOC8057743 | -1.74723 | AKT2/3 |
| gene-LOC8075862 | -3.87659 | KOR2 |
| gene-LOC8080343 | 1.264192 | CLCc |
| gene-LOC8079456 | -1.9079 | CLCg |
| gene-LOC8079295 | 2.208967 | SLAH2 |
| gene-LOC8066616 | 1.792982 | SLAH3 |
| gene-LOC8073008 | 2.230816 | ALMT1 |
| gene-LOC8065254 | 1.485028 | NPF2.11 |
| gene-LOC8061309 | 2.283274 | NPF2.7 |
| gene-LOC8085131 | 3.015571 | NPF3.1-1 |
| gene-LOC8061532 | -2.19179 | NPF3.1-2 |
| gene-LOC8060182 | 1.335163 | NPF4.3-1 |
| gene-LOC8060184 | 1.069603 | NPF4.3-2 |
| gene-LOC8085518 | -2.17604 | NPF5.2 |
| gene-LOC8055690 | -1.16613 | NPF5.6 |
| gene-LOC8075730 | -2.11996 | NPF5.9 |
| gene-LOC8063327 | 1.397916 | NPF6.1 |
| gene-LOC8058104 | -1.97736 | NPF6.3 |
| gene-LOC8070561 | 1.190999 | NPF6.4 |
| gene-LOC8071782 | 3.871156 | NPF7.3-1 |
| gene-LOC8073896 | 2.932143 | NPF7.3-2 |
| gene-LOC110433327 | 1.897474 | NPF8.1 |
| gene-LOC8083625 | 2.170176 | NPF8.3 |
| gene-LOC8062975 | 1.096462 | P-H+-ATPase |

**Table S7** The expression change of DEGs related to ion transport in leaf sheaths of sweet sorghum after 200 mM NaCl treatment for 6 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC8070185 | 1.441058 | NCX |
| gene-LOC8065479 | -1.21121 | NCX |
| gene-LOC8076497 | -1.29114 | NCX |
| gene-LOC8072309 | 2.33587 | HKT1;4 |
| gene-LOC8085586 | -1.78833 | KT1 |
| gene-LOC8083518 | 1.906225 | HAK4 |
| gene-LOC8078559 | 1.06849 | HAK9 |
| gene-LOC8058236 | 1.270356 | AKT1 |
| gene-LOC8080343 | 1.379157 | CLCc |
| gene-LOC8079230 | 1.610902 | NPF1.2 |
| gene-LOC8076953 | 2.827796 | NPF3.1 |
| gene-LOC8076954 | -1.58151 | NPF3.1 |
| gene-LOC8076956 | -1.34564 | NPF3.1 |
| gene-LOC8084233 | -3.31167 | NPF4.3 |
| gene-LOC8055194 | 1.519585 | NPF5.10 |
| gene-LOC8071782 | 1.625425 | NPF7.3-1 |
| gene-LOC8083627 | -1.23059 | NPF8.3 |
| gene-LOC8055893 | -1.41426 | P-Ca2+-ATPase 5 |
| gene-LOC8081867 | 1.210822 | P-Ca2+-ATPase 10 |

**Table S8** The expression change of DEGs related to ion transport in leaf sheaths of sweet sorghum after 200 mM NaCl treatment for 48 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC110433848 | 1.820332 | NCX1a |
| gene-LOC8083092 | -1.01034 | KUP5 |
| gene-LOC8062763 | 1.921104 | HAK17 |
| gene-LOC8080343 | 1.0635 | CLCc |
| gene-LOC8076043 | 3.286561 | ALMT10 |
| gene-LOC8085131 | 3.551471 | NPF3.1 |
| gene-LOC8076953 | 2.222769 | NPF3.1 |
| Sorghum\_bicolor\_newGene\_2569 | -2.41239 | NPF4.5 |
| gene-LOC8071782 | 5.487174 | NPF7.3-1 |
| gene-LOC8073896 | 1.713527 | NPF7.3-2 |
| gene-LOC8067856 | 1.021939 | NPF8.1 |
| gene-LOC8079011 | -1.17202 | NPF8.3 |
| gene-LOC8078037 | -1.08319 | P-H+-ATPase |
| gene-LOC8067356 | 1.158969 | P-Ca2+-ATPase 4 |
| gene-LOC8085626 | 1.258629 | P-Ca2+-ATPase 9 |
| gene-LOC8081867 | 1.033328 | P-Ca2+-ATPase 10 |

**Table S9** The expression change of DEGs related to ion transport in leaf blades of sweet sorghum after 200 mM NaCl treatment for 6 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC8063860 | -1.27592 | NHX1 |
| gene-LOC8074408 | -1.08542 | NHX2 |
| gene-LOC8067369 | 1.323903 | CCX1 |
| gene-LOC8062242 | -1.70832 | NCX |
| gene-LOC8056537 | 1.767412 | NCX |
| gene-LOC110433848 | 1.150777 | NCX1a |
| gene-LOC8072046 | 1.996546 | HAK1 |
| gene-LOC8067862 | 2.603512 | HAK5-1 |
| gene-LOC8067863 | 1.637198 | HAK5-2 |
| gene-LOC8085154 | 1.222118 | HAK12 |
| gene-LOC8080343 | 1.641406 | CLCc |
| gene-LOC8071767 | 1.079116 | CLCf |
| gene-LOC8069523 | -1.28811 | ALMT12 |
| gene-LOC8079230 | 2.105721 | NPF1.2 |
| gene-LOC8076956 | -1.66676 | NPF3.1 |
| gene-LOC8084233 | -2.51835 | NPF4.3 |
| gene-LOC8067439 | 1.568329 | NPF5.2 |
| gene-LOC8062396 | -2.9792 | NPF5.10 |
| gene-LOC8067856 | 1.364558 | NPF6.3 |
| gene-LOC110433833 | 2.216318 | NPF8.1 |
| gene-LOC8073241 | -1.32138 | P-H+-ATPase |
| gene-LOC8076135 | 1.389746 | P-Ca2+-ATPase 5 |
| gene-LOC8063993 | 1.364938 | P-Ca2+-ATPase 5 |
| gene-LOC8064910 | 2.451387 | P-Ca2+-ATPase 7 |
| gene-LOC8081867 | 2.365042 | P-Ca2+-ATPase 10 |

**Table S10** The expression change of DEGs related to ion transport in leaf blades of sweet sorghum after 200 mM NaCl treatment for 48 h

|  |  |  |
| --- | --- | --- |
| Gene ID | Log2 value | Annotation |
| gene-LOC8063860 | -1.34885 | NHX1 |
| gene-LOC8055510 | 1.804957 | CHX15 |
| gene-LOC8056257 | 1.357069 | NCX |
| gene-LOC110432929 | 1.000864 | NCX |
| gene-LOC8062242 | -1.05495 | NCX |
| gene-LOC8056537 | 1.413177 | NCX |
| gene-LOC8059087 | -1.2577 | NCX1c |
| gene-LOC8076484 | -1.22532 | KEA2 |
| gene-LOC8071480 | -1.12452 | KEA3 |
| gene-LOC8085586 | -1.13764 | KT1 |
| gene-LOC8083092 | -1.5998 | KUP5 |
| gene-LOC8077695 | 1.501153 | KUP8-1 |
| gene-LOC8061543 | 1.206681 | KUP8-2 |
| gene-LOC8065636 | -1.43424 | KUP16 |
| gene-LOC8085154 | 1.876346 | HAK12 |
| gene-LOC8064024 | -1.55661 | HAK26 |
| gene-LOC8057743 | 2.329447 | AKT2/3 |
| gene-LOC8058450 | -2.1612 | CLCa |
| gene-LOC8069763 | -1.27955 | CLCe |
| gene-LOC8071767 | 1.408988 | CLCf |
| gene-LOC8068475 | 1.465604 | CLCg-1 |
| gene-LOC8079456 | -1.11092 | CLCg-2 |
| gene-LOC8054905 | 1.232952 | SLAH3 |
| gene-LOC8073008 | 1.602577 | ALMT1 |
| gene-LOC8069523 | -1.24231 | ALMT12 |
| gene-LOC8076953 | 3.940685 | NPF3.1 |
| gene-LOC8076956 | -1.48041 | NPF3.1 |
| gene-LOC8085131 | 3.168706 | NPF3.1 |
| gene-LOC8084233 | -2.31023 | NPF4.3 |
| gene-LOC8075842 | -1.3223 | NPF4.4 |
| gene-LOC8082863 | -2.22075 | NPF4.6 |
| gene-LOC8067440 | -1.69068 | NPF5.2 |
| gene-LOC8062396 | -2.55687 | NPF5.10 |
| gene-LOC8055194 | 3.922302 | NPF5.10 |
| gene-LOC8063327 | 1.047337 | NPF6.1 |
| gene-LOC8069535 | -1.04464 | NPF6.1 |
| gene-LOC8059535 | -2.80299 | NPF6.3 |
| gene-LOC8071782 | 8.105068 | NPF7.3-1 |
| gene-LOC8073896 | 1.585449 | NPF7.3-2 |
| gene-LOC110433327 | -1.44379 | NPF8.1 |
| gene-LOC8081572 | -1.43396 | NPF8.2 |
| gene-LOC8079011 | -1.62145 | NPF8.3 |
| gene-LOC8083625 | 2.037393 | NPF8.3 |
| gene-LOC8083636 | -1.19868 | NPF8.5 |
| gene-LOC8072876 | -1.58097 | P-H+-ATPase 1 |
| gene-LOC8064910 | 2.601286 | P-Ca2+-ATPase 7 |
| gene-LOC8085626 | -1.36278 | P-Ca2+-ATPase 9 |



**Fig. S1** The number of DEGs in roots (R), leaf sheath (LS) and leaf blades (LB) after 200 mM NaCl treatment for 6 and 48 h.



**Fig. S2** Correlation analysis for expression pattern validation of 20 randomly selected DEGs under 200 mM NaCl treatment for 6 h and 48 h in roots ((**A**, **D**), respectively), leaf sheaths ((**B**, **E**), respectively), and leaf blades ((**C**, **F**), respectively) by qRT-PCR method. The X-axes and Y-axes show the gene transcript level changes obtained by RNA-seq and qRT-PCR, respectively. R2 indicates the correlation.