Figure S1. The expression profile of CaSBP12 gene under salt stress in pepper. After 400 mM NaCl treatment, the expression of CaSBP12 was detected at $0 \mathrm{~h}, 2 \mathrm{~h}, 4 \mathrm{~h}, 8 \mathrm{~h}$, 12 h , and 24 h . h: hour. * and ** represent significant differences at $\mathrm{P} \leq 0.05$ and $\mathrm{P} \leq$ 0.01 respectively. Mean values and SDs for three replicates are shown.


Figure S2. The total chlorophyll contents of CaPDS-silenced, CaSBP12-silenced, and control plants after forty days post-infiltration. Bars with different letters indicate significant differences at $\mathrm{P} \leq 0.05$. Mean values and SDs for three replicates are shown.


Figure S3. The expression level of ion transport genes in CaSBP12-silenced and control plants without any treatment were measured using quantitative real-time PCR. CaSOS1: CA08g01100; CaHKT2-1: CA07g09810; CaHKT2-2: CA01g10660. Bars with different letters indicate significant differences at $\mathrm{P} \leq 0.05$. Mean values and SDs for three replicates are shown.


Figure S4. The expression of CaSBP12 gene in transgenic lines and wild-type lines of Nicotiana benthamiana. The expression of CaSBP12 gene in transgenic lines and wild-type lines of Nicotiana benthamiana was measured using quantitative real-time PCR. ** represent significant differences at $\mathrm{P} \leq 0.01$ respectively. Mean values and SDs for three replicates are shown.


Figure S5. The expression level of NbSOS1 (Niben101Scf02321g00027.1) gene in transgenic lines and wild-type lines of Nicotiana benthamiana was measured using quantitative real-time PCR without any treatment. Bars with different letters indicate significant differences at $\mathrm{P} \leq 0.05$. Mean values and SDs for three biologic replicates are shown.


Table S1. The detail data of damage severity index percentage of transgenic (line 4, line 7 , and line 8 ) and wild-type plants after salt stress twenty-two days.

|  | 0 level <br> plants | 1 level <br> plants | 2 level <br> plants | 3 level <br> plants | Total number <br> of treatment <br> plants | Damage <br> severity index <br> percentage |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| WT | 3 | 8 | 8 | 1 | 20 | 45.00 |
| Line 4 | 3 | 1 | 8 | 8 | 20 | 68.33 |
| Line 7 | 0 | 5 | 6 | 10 | 21 | 74.60 |
| Line 8 | 1 | 4 | 14 | 6 | 25 | 66.67 |
| WT | 1 | 15 | 5 | 0 | 21 | 39.68 |
| Line 4 | 0 | 0 | 11 | 10 | 21 | 82.54 |
| Line 7 | 0 | 3 | 15 | 3 | 21 | 66.67 |
| Line 8 | 0 | 9 | 7 | 5 | 21 | 60.31 |

Table S2. Primers names and their sequences used for vector construction in this study.

| Olig name | Primer Abbreviation | Primer Sequence (5'-3') |
| :---: | :---: | :---: |
| $\boldsymbol{C a S B P 1 2}$ | CaSBP12-VIGS-F | CGGGATCCATCCTCCGTTATGCTTTCTGGC |
|  | CaSBP12-VIGS-R | GGGGTACCTACCTTGGGAATGGGTGAAACA |
| $\boldsymbol{C a S B P 1 2}$ | CaSBP12-PBI121-F | GCTCTAGAATGTTGGACTATGACTGGGGAG |
|  | CaSBP12-PBI121-R | CGGGATCCTGGTCTTTGCCTAAAACAATCC |

Table S3. Primers names and their sequences used in this study for quantitative real-time PCR.

| Olig name | Primer Abbreviation | Primer Sequence ( $5^{\prime} 3^{\prime}$ ) | Gene amplification length(bp) | Location of each primer |
| :---: | :---: | :---: | :---: | :---: |
| CaSBP12 | RTCaSBP12-VIGS-F | GTTTCACCCATTCCCAAGGTAATT | 213 | exon |
|  | RTCaSBP12-VIGS-R | TAGTACGTCGGTAAAGTCGATTAACAA |  |  |
| CaActin2 | CaActin2-F | TCCACCTCTTCACTCTCTGCTC | 213 | exon |
|  | CaActin2-R | TGACCCATCCCTACCATAACAC |  |  |
| CaAPX | CaAPX-F | AGAGGACAAGCCAGAACCAC | 271 | exon |
|  | CaAPX-R | CCTTGTCTGATGGCAACTGT |  |  |
| CaCAT2 | CaCAT2-F | GAAGCCAAATCCTAAGTCCC | 258 | exon |
|  | CaCAT2-R | CCAACTCGGATTGCCTCTT |  |  |
| CaSOD | CaSOD-F | TATGGAGCCTTAGAACCTGC | 173 | exon |
|  | CaSOD-R | CCATTGAACTTGATAGCACCT |  |  |
| CaPOD | CaPOD-F | TCСТССТССТАСТТСТААСС | 302 | exon |
|  | CaPOD-F | ACAGACCTCTTTTGCTCACT |  |  |
| CaSOS1 | CaSOS1-F | GTTCGTGTCTCGTTTCCGC | 163 | exon |
|  | CaSOS1-R | TCAAATCGGTCTGAACAGCATC |  |  |
| CaHKT2-1 | CaHKT2-1-F | GGCATTCATATCAGTTCAGTTTGT | 231 | exon |
|  | CaHKT2-1-R | TTATCAACAGGCAAAAAAGTAGTAGAG |  |  |
| CaHKT2-2 | CaHKT2-2-F | AAACACAGTGTATTGCAGAACAACGAT | 77 | exon |
|  | CaHKT2-2-R | TCAAGATTATGAAGACCTTCACCATTA |  |  |
| Nbactin-97 | Nbactin-F | TATGGAAACATTGTGCTCAGTGG | 218 | Exon |
|  | Nbactin-R | CCAGATTCGTCATACTCTGCC |  |  |
| NbAPX | NbAPX-F | CCAAGGGTTCTGACCATCTG | 304 | exon |
|  | NbAPX-R | GCATAGTCGGCAAAGAAAGC |  |  |
| NbCAT1 | NbCAT1-RT-F | TCTATTGTGGTTCCAGGGGTTT | 375 | exon |
|  | NbCAT-RT-R | CACCCACCGACGAATAAAGC |  |  |
| NbSOD | NbSOD-RT-F | GCAGACGGACCTTAGCAACA | 230 | exon |
|  | NbSOD-RT-R | TGGCGACGGTAGGAGCAT |  |  |
| NbPOD | NbPOD-RT-F | AGGCTCAGGGGACAACAACT | 194 | exon |
|  | NbPOD-RT-R | TCACAAAATCAGTGGCGAAA |  |  |
| NbSOS1 | NbSOS1-F | TCCCTTGGGGCAGTGG | 200 | exon |
|  | NbSOS1-F | GCTACAGCTGAGTAGAACATCCC |  |  |

