

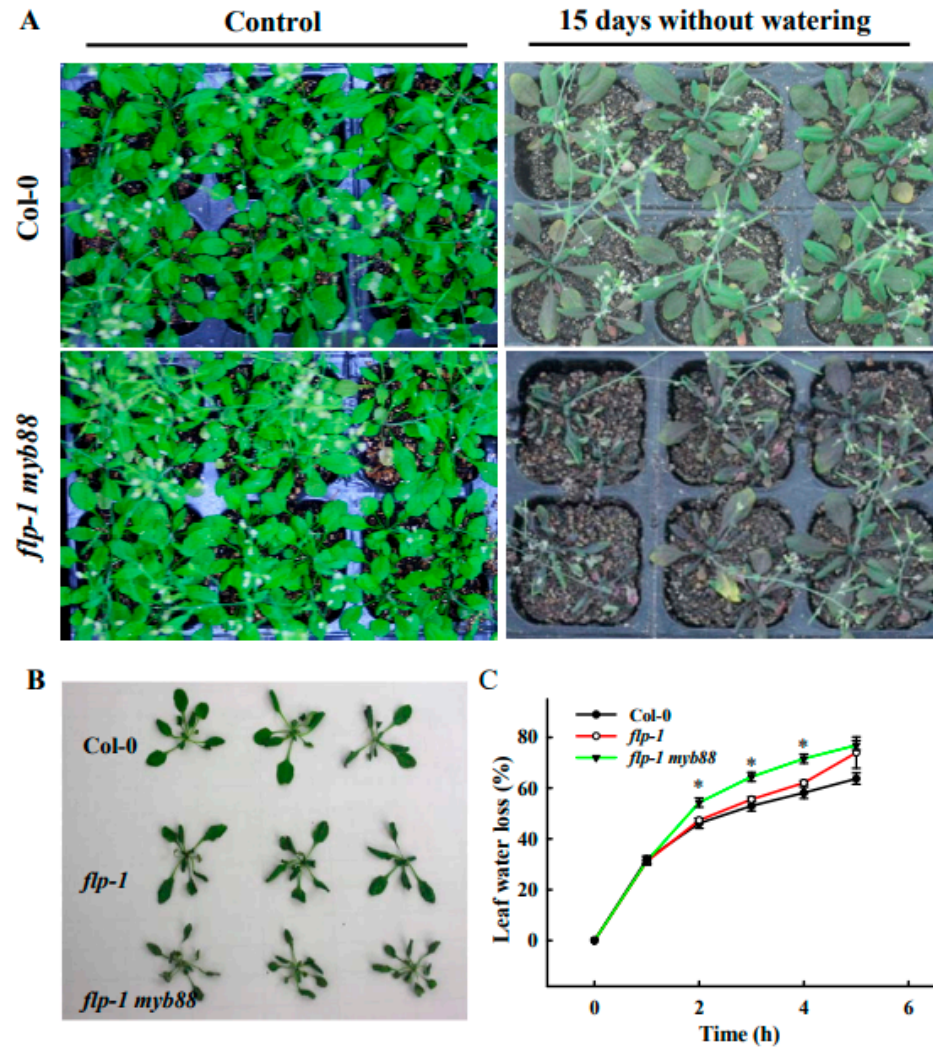
**Table S1.** Cis-acting elements in the promoter region of *OsNAC1* and *OsNAC6* binding by MYB transcription factor.

| Matrix ID             | Score     | Position       | Strand | Sequence<br>(CAPITALS: core sequences) |
|-----------------------|-----------|----------------|--------|--|
| OsNAC1<br>NC_029258.1 | 8.491339  | -551 to -542   | +      | CAACCTAAGA                             |
|                       | 6.766874  | -699 to -690   | +      | AAACCTTAAA                             |
|                       | 6.0062394 | -1208 to 1219  | -      | AAACCTCAAG                             |
|                       | 5.913508  | -623 to -614   | +      | TGTCCTAATT                             |
|                       | 5.6907196 | -1361 to -1352 | +      | AAAACCTAAAA                            |
|                       | 5.5058193 | -307 to -298   | +      | TGACCTCGGC                             |
|                       | 4.659336  | -698 to -689   | +      | AACCTTAAAA                             |
|                       | 4.070128  | -782 to -773   | -      | TAAACTATTT                             |
|                       | 3.9510279 | -1052 to -1043 | -      | TACTCTACTT                             |
|                       | 3.7640855 | -1779 to -1770 | +      | AAACCCAACC                             |
|                       | 3.6692517 | -1778 to -1769 | +      | AACCCAACCA                             |
| OsNAC6<br>NC_029256.1 | 8.695591  | -1332 to -1323 | +      | AGACCTACTT                             |
|                       | 6.7416577 | -1200 to -1191 | +      | GACCCTACAG                             |
|                       | 6.2968206 | -1054 to 1495  | -      | ACACCTAAGC                             |
|                       | 6.090226  | -86 to -77     | +      | AACACTAGTA                             |
|                       | 5.926167  | -872 to -863   | -      | AGCCGTAGCT                             |
|                       | 5.786418  | -797 to -788   | -      | TGACATAGAA                             |
|                       | 5.460014  | -1021 to -1012 | -      | AAACCTTCTT                             |
|                       | 5.359429  | -745 to -736   | -      | AACCTCTAAAC                            |
|                       | 5.177283  | -1515 to -1506 | +      | TCCCCTACGA                             |
|                       | 5.139875  | -1361 to -1352 | +      | TACCCAAAAA                             |
|                       | 5.0971913 | -300 to -291   | +      | TGACGTAAGC                             |
|                       | 4.9563427 | -889 to -880   | -      | TGCTCTAAAT                             |
|                       | 4.770077  | -81 to -72     | -      | TATCCTACTA                             |
|                       | 4.5864944 | -106 to -97    | +      | AGCCCTCCTC                             |
|                       | 4.4865985 | -1999 to -1990 | -      | TGATCTAACT                             |
|                       | 4.3426924 | -1764 to -1755 | -      | ATCCCTTATA                             |
|                       | 4.3426924 | -1580 to -1571 | +      | ATCCCTTATA                             |
|                       | 4.1384006 | -394 to -385   | +      | CACCCTGCGG                             |
|                       | 3.942666  | -814 to -805   | +      | TTACCTTACA                             |

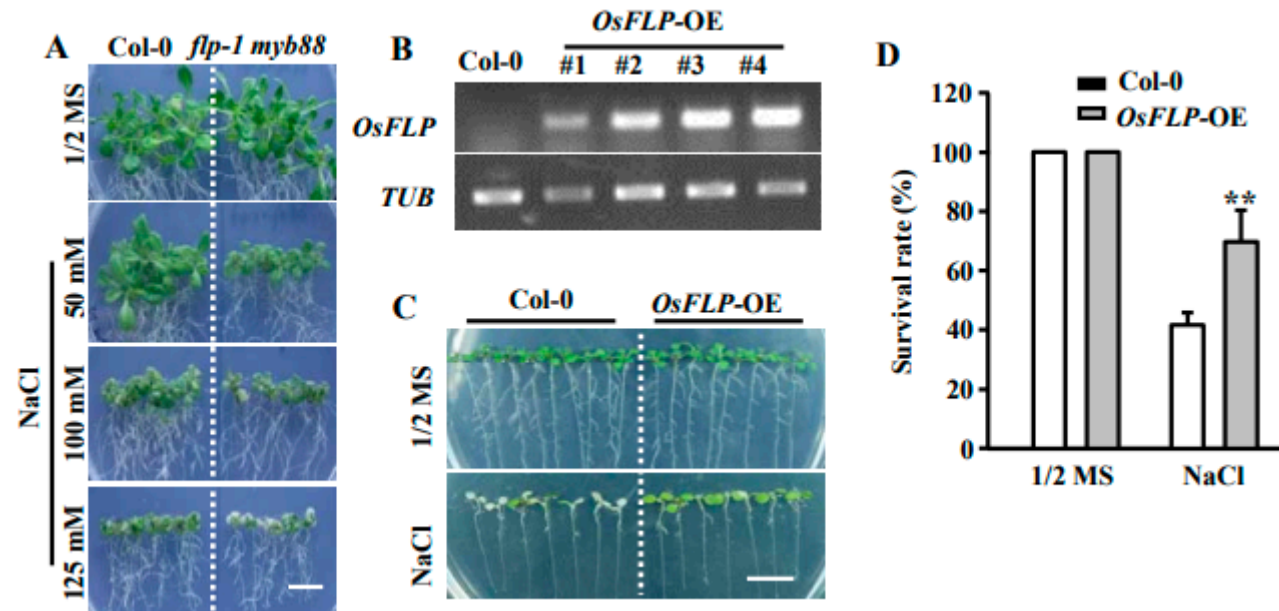
|           |                |   |            |
|-----------|----------------|---|------------|
| 3.8799586 | -473 to -464   | + | TTCCCTCGCC |
| 3.7542815 | -1220 to -1211 | - | CGACCTCACA |
| 3.6927981 | -1816 to -1807 | - | ATTCCTAATT |
| 3.487473  | -1141 to -1132 | + | AAATCTACAC |

**Table S2.** Primers were used in this study.

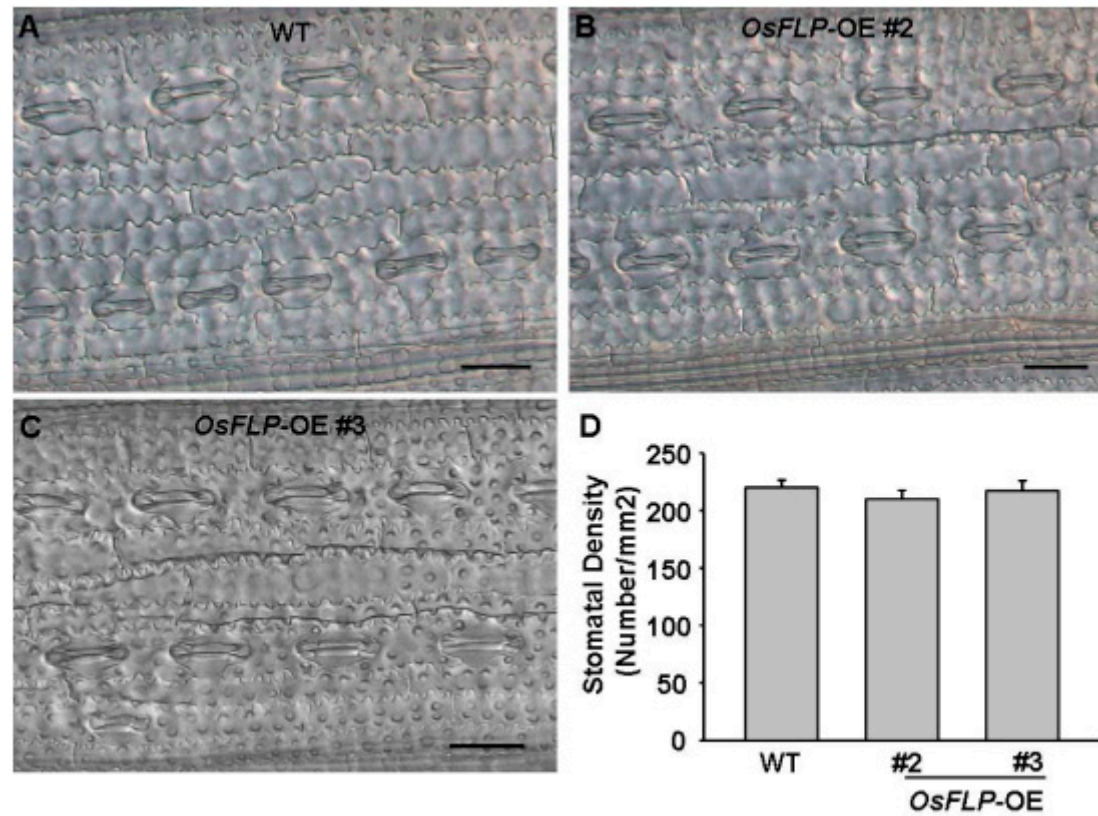
| Primer name               | Forward sequence (5'-3')             | Reverse sequence (5'-3')             | Purpose                         |
|---------------------------|--------------------------------------|--------------------------------------|---------------------------------|
| OsACTIN                   | GGATCCATCTTGGCATCTCTCA               | GGGCCAGACTCGTCGTACTC                 | qRT-PCR                         |
| OsFLP                     | AGTTCTTGGAACAAATGGAC                 | TGTACCAATGCCCTCTTTGA                 | qRT-PCR                         |
| OsNAC1                    | CATGGTCCC GTTCTGAGGTG                | CACACGTTGCAGCATCGATC                 | qRT-PCR                         |
| OsNAC4                    | GGTGAAGGAGGACAACGACT                 | TCAGAATGGTGGCAGGATTGT                | qRT-PCR                         |
| OsNAC5                    | GGTTGGATGATTGGGTGTTGT                | CGTAGAACCCATAGTCGGAGA                | qRT-PCR                         |
| OsNAC6                    | CTGTACGGAGAGAAGGAGTGG                | GTGCATGATCCAGTTGGTCT                 | qRT-PCR                         |
| OsDST                     | ATCCAAGAAGGCAAGGTCAATC               | CACACGAGGAGGAATTGGAAG                | qRT-PCR                         |
| Osperoxidase 24 precursor | GTCTCCAGGACCTCGTCGTC                 | AAAAGGTTGCAGTGCCCG                   | qRT-PCR                         |
| OsLEA3                    | CGGCAGCGTCCTCCAAC                    | CGGTCATCCCCAGCGTG                    | qRT-PCR                         |
| OsDREB2A                  | GCTGCACATCAGCACCTTCA                 | TCCTGCACCTCAGGGACTAC                 | qRT-PCR                         |
| proOsNAC1                 | GGAATTCCACACATCTCGCATGG-TAAC         | GCGTCGACCGCTTCTTGCTT-GCTTCTC         | Y1H                             |
| proOsNAC4                 | GGGTACCGGTGTCACATCGGA-TATTTG         | CAGCCTCTGACAAAGCAGTC                 | Y1H                             |
| proOsNAC5                 | GGAATTCCTATTGTAC-GAGCCAAGG           | GGGTAC-CTCAATCTCCGATCTGAGGCC         | Y1H                             |
| proOsNAC6                 | GGAATTCCAATGTTGAC-GGGTCAATGAG        | CCTCGAGCTCTCTCCCCCTTCTCCGGT          | Y1H                             |
| OsFLP-RNAi                | GCGTCGACCCCGGGTGTGCTTCG-TACTCAAATTGC | GGGGATCCGAGCTCAG-TTCTGCCTGAGACAACCTT | Knockdown line generation       |
| OsFLP-OE                  | ATGGCGACCGGACCCGATCTG                | TCATAGGCTATTAAGGAGAGC                | Over-expression line generation |



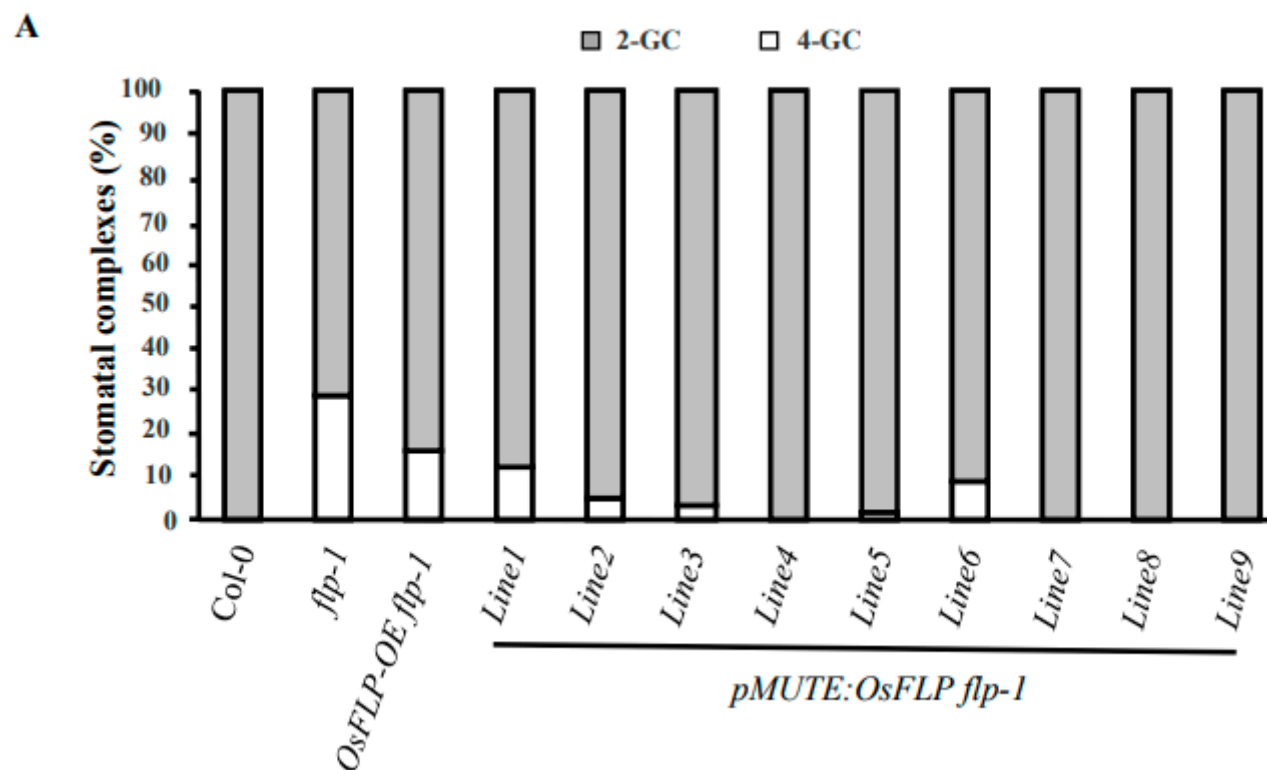
**Figure S1.** Arabidopsis *flp-1 myb88* double mutants were sensitive to drought stress. (A) Drought sensitivity was rescued in *flp-1 myb88* mutants compared with Col-0 after 15 days without water. (B,C) Water loss were detected from detached leaves. Asterisks indicate a significant difference *flp-1 myb88* mutants to Col-0. (Student's *t*-test, \**P* < 0.05).



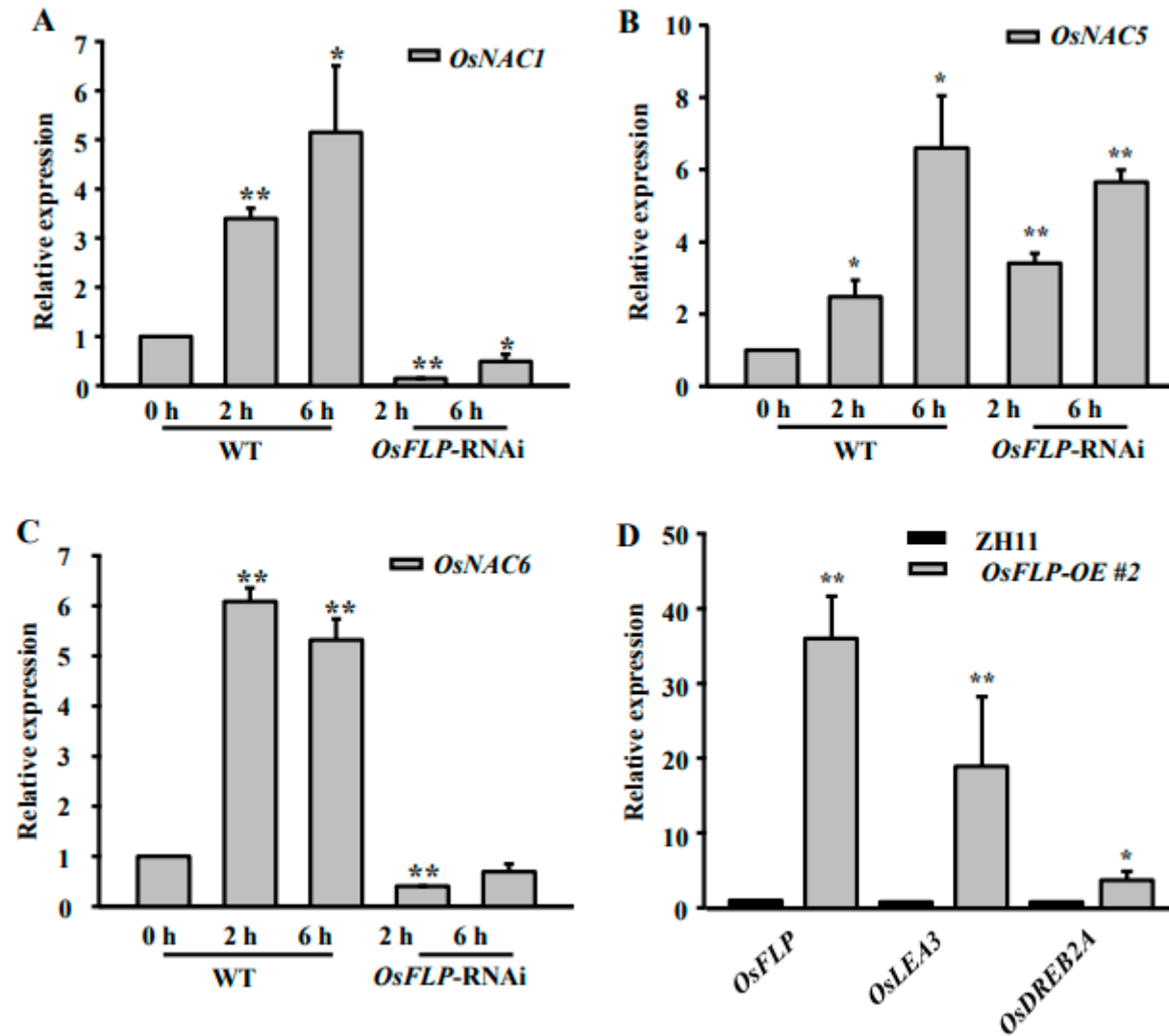
**Figure S2.** Overexpression of OsFLP enhanced salt tolerance both in rice and Arabidopsis. (A) Five days Col-0 and *flp-1 myb88* seedlings were treated by 50 mM 100 mM and 125 mM NaCl for one week. Bars = 1.0 cm. (B) Expression levels of OsFLP overexpression lines were detected by semi-quantitative reverse transcription PCR (SqRT-PCR). (C) Five days Col-0 and OsFLP seedlings were treated by 150 mM NaCl for one week. Bars = 1.0 cm. (D) Analysis of survival rate after salt treatment. Error bar means  $\pm$  SD. Asterisks indicate a significant difference to wild type (Student's t-test, \*\* $P < 0.01$ , \* $P < 0.05$ ).



**Figure S3.** Overexpression of *OsFLP* gene has no obvious impact on stomatal density. (A-C) DIC images of rice leaf epidermis from 10-day-old WT and *OsFLP*-OE plants. Bars = 20  $\mu\text{m}$ . (D) No significant difference of stomatal density was found between *OsFLP*-OE and WT mature leaves ( $n = 10$ ).



**Figure S4.** Ectopic expression of OsFLP rescue the stomatal cluster of *flp-1* mutant. (A) Quantification of effects of 35S:OsFLP and pMUTE:OsFLP on *flp-1* stomatal phenotypes. Stomata from 10-20 cotyledons were scored for normal and cluster stomatal phenotypes. Grey, normal 2-GC; White, cluster stomata with 4 GCs.



**Figure S5.** Expression levels of NAC genes were reduced in *OsFLP*-RNAi transgenic rice plants. The relative expression levels of *OsNAC1* (A), *OsNAC5* (B), *OsNAC6* (C), and stress response genes *OsLEA3* and *OsDREB2A* (D) were assessed using qRT-PCR. Error bars represent SD of three biological replicates (Student's t-test, \*\*P < 0.01, \*P < 0.05).