

Title: *Arabidopsis* YL1/BPG2 Is Involved in Seedling Shoot Response to Salt Stress through ABI4

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Supplementary information

Supplementary Figure 1. Root phenotype of *yli-1*.

Supplementary Figure 2. Mature plant phenotypes of wild type, *yli-1*, *yli-2*, *yli-1com*, and *yli-1 yli-2* (cross F1 line).

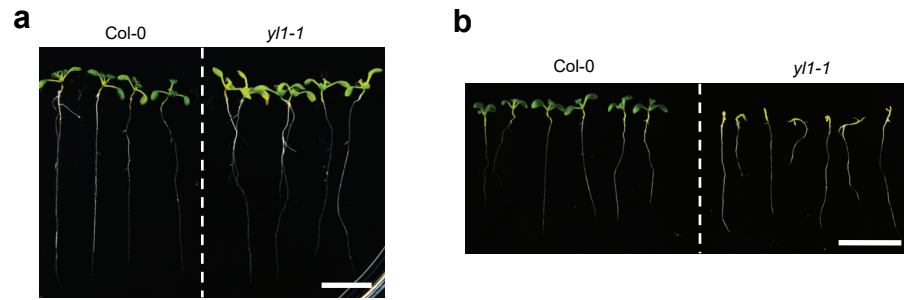
Supplementary Figure 3. GUS activity analysis of the *pYLI-GUS* transgenic plants under salinity treatment.

Supplementary Figure 4. Transcriptional analysis of *YLI* in roots under salt-treatment.

Supplementary Figure 5. Transcriptional analysis of SOS pathway genes, *NHX1*, and ABA biosynthesis pathway genes in seedling shoots.

Supplementary Figure 6. Transcriptional analysis of SOS pathway genes, *NHX1*, and ABA biosynthesis pathway genes in seedling roots.

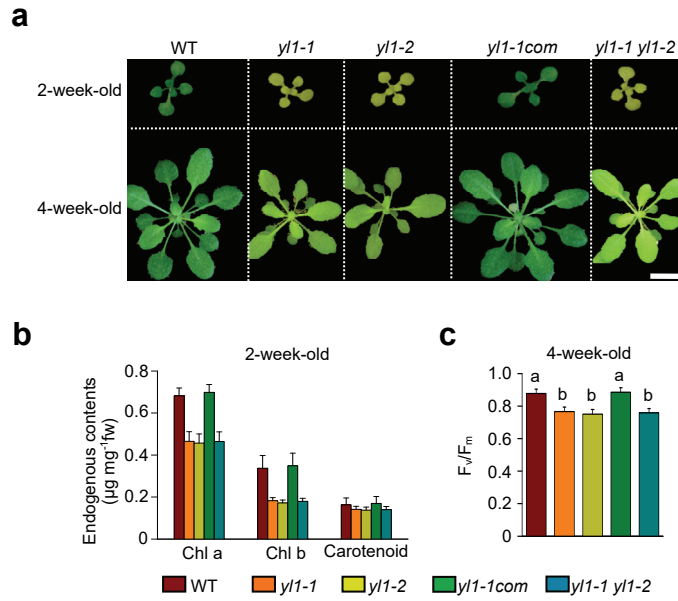
Supplementary Table 1. Key primers used in this study.



Supplementary Figure 1. Root phenotype of *y11-1*.

(a) Phenotype of 10-d-old seedling roots under control conditions. Scale bars = 5 mm.

(b) Phenotype of 10-d-old seedling roots under 150 mM NaCl conditions. Scale bars = 5 mm.



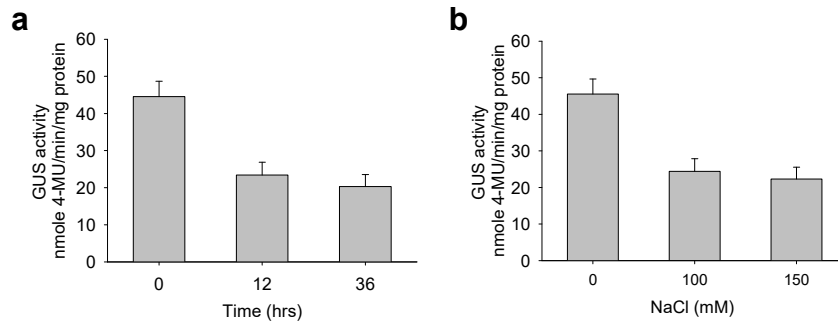
Supplementary Figure 2. Mature plant phenotypes of wild type, *yll-1*, *yll-2*, *yll-1com*, and *yll-1 yll-2* (cross F1 line).

(a) Phenotypes of 2/4-week-old wild type, *yll-1*, *yll-2*, *yll-1com*, and *yll-1 yll-2* (F1) grown under normal growth conditions. Scale bars = 10 mm.

(b) Endogenous contents of chlorophyll a, chlorophyll b, and carotenoid in 2-week-old wild type, *yll-1*, *yll-2*, *yll-1com*, and *yll-1 yll-2* (F1).

(c) F_v/F_m of 4-week-old wild type, *yll-1*, *yll-2*, *yll-1com*, and *yll-1 yll-2* (F1).

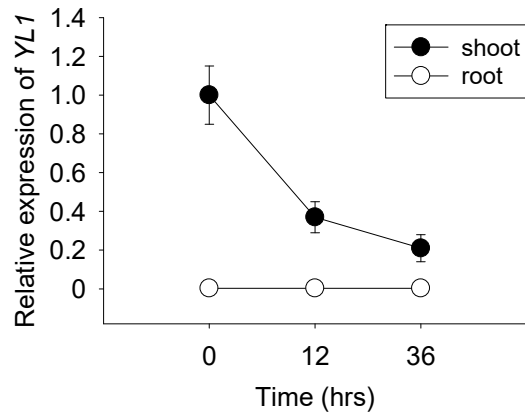
Data are mean values of three replicates \pm SE. Statistical significant differences are indicated by different lowercase letters ($P < 0.01$).



Supplementary Figure 3. GUS activity analysis of the *pYL1-GUS* transgenic plants under salinity treatment.

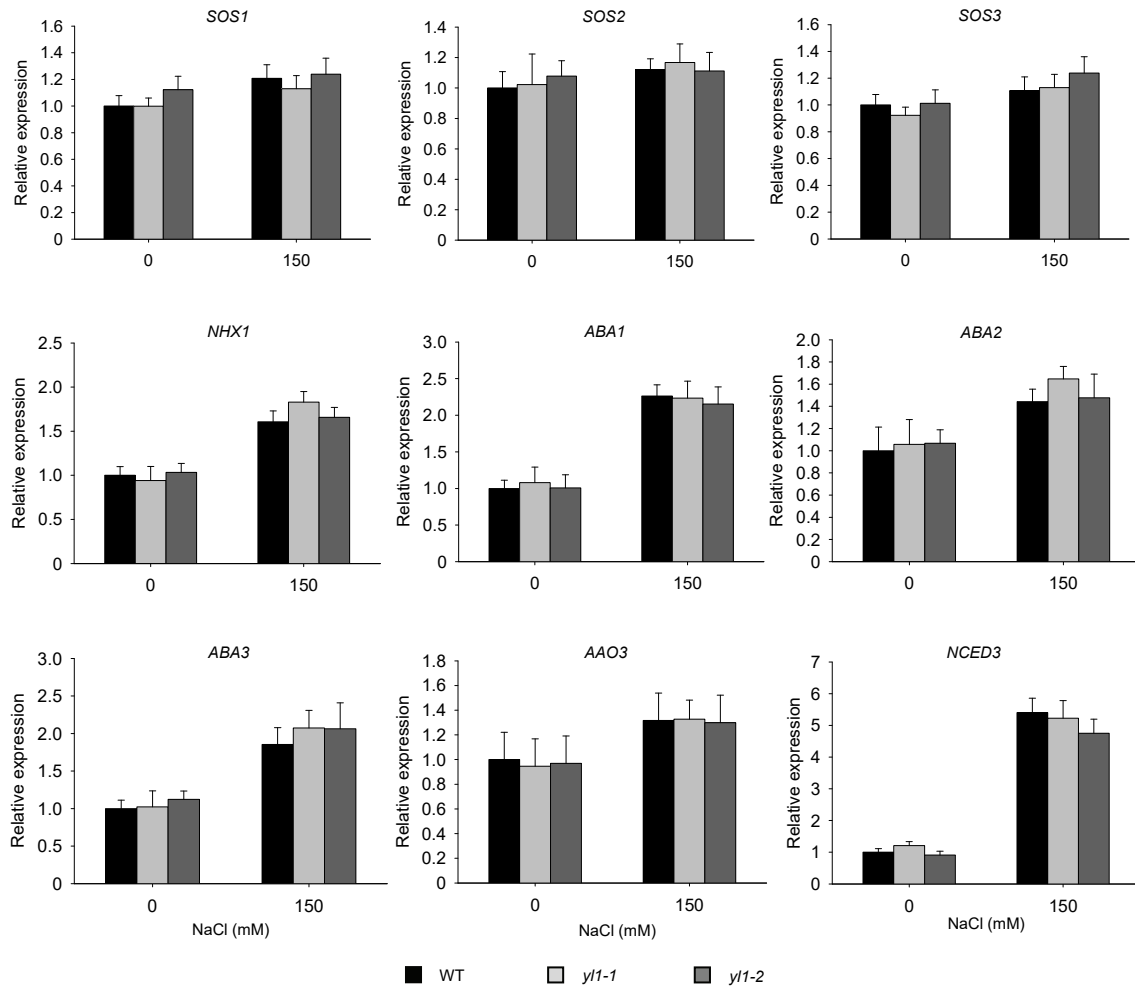
(a) GUS activity analysis of 5-d-old seedlings treated with 150 mM NaCl for 0, 12, or 36 h.

(b) GUS activity analysis of 5-d-old seedlings treated with 0, 100, or 150 mM NaCl for 36 h.



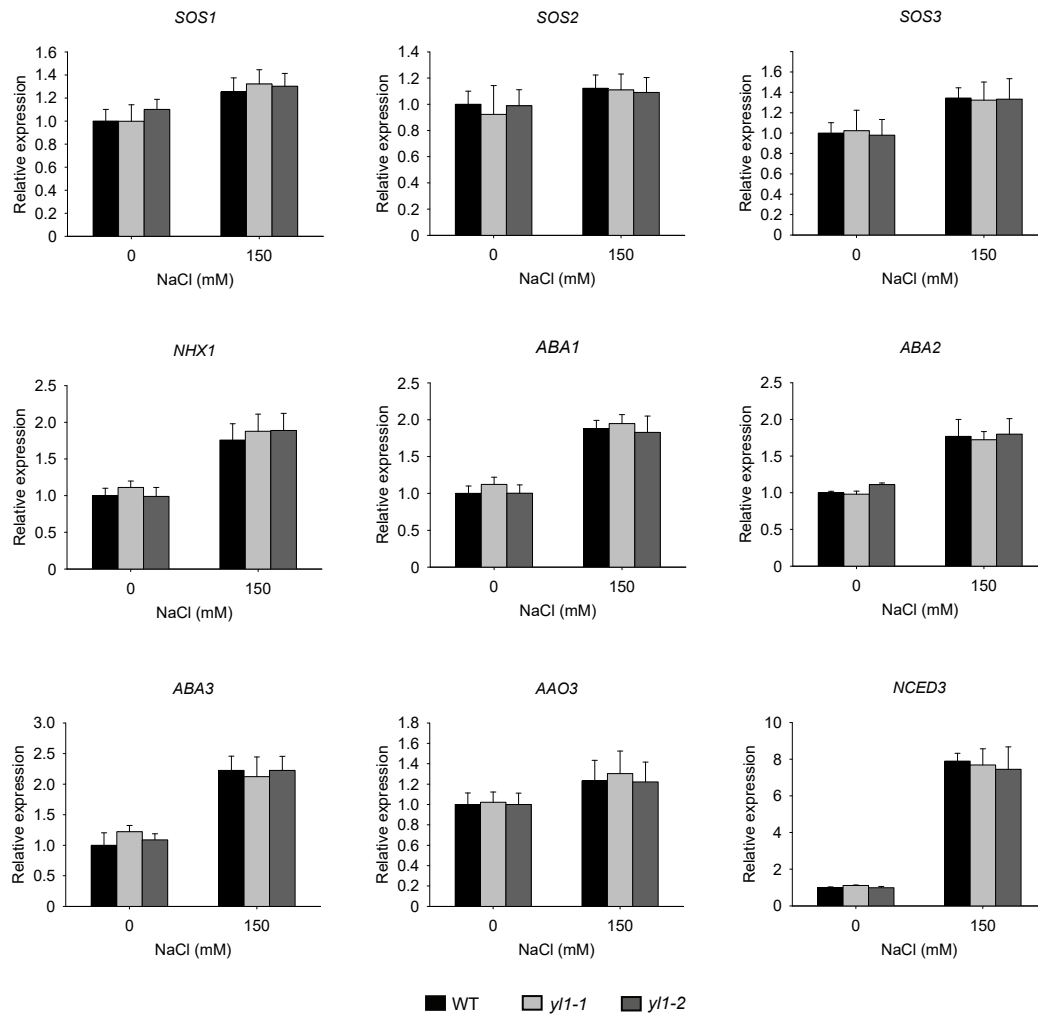
Supplementary Figure 4. Transcriptional analysis of *YL1* in roots under salt-treatment.

Total RNA was isolated from roots of 5-d-seedlings treated with control or 150 mM NaCl for 0, 12, or 36 h. Values are means \pm SE of three independent replicates.



Supplementary Figure 5. Transcriptional analysis of SOS pathway genes, *NHX1*, and ABA biosynthesis pathway genes in seedling shoots.

SOS1, *SOS2*, and *SOS3* are SOS pathway genes; *ABA1*, *ABA2*, *ABA3*, *AAO3*, and *NCED3* are ABA biosynthesis associated genes. Total RNA was isolated from shoots of 5-d-seedlings treated with control or 150 mM NaCl for 12 h. Values are means \pm SE of three independent replicates.



Supplementary Figure 6. Transcriptional analysis of SOS pathway genes, *NHX1*, and ABA biosynthesis pathway genes in seedling roots.

SOS1, *SOS2*, and *SOS3* are SOS pathway genes; *ABA1*, *ABA2*, *ABA3*, *AAO3*, and *NCED3* are ABA biosynthesis associated genes. Total RNA was isolated from roots of 5-d-seedlings treated with control or 150 mM NaCl for 12 h. Values are means \pm SE of three independent replicates.

Supplementary Table 1. Primers used in this study.

| Purpose | Primer name | Sequence (5'-3') |
|---|-----------------------|---|
| Complementation and overexpression constructs | YL1-forward (P1) | GGATCCATGGTGGTTTTGATTCAAGTACAG |
| | YL1-reverse (P2) | TGCGACCTAAGCAACACTATCAGAGAGAAAATC |
| GFP expression constructs | YL1-forward | TCTAGAATGGTGGTTTTGATTCAAGTACAGTG |
| | YL1-reverse | GGATCCAGCAACACTATCAGAGAGAAAATCTGT |
| | GFP-forward | GGATCCGGTGGTGGTAGTAGTGGTGGTGG- -TATGAAGACTAATCTTTTTCTCTTTCTC |
| | GFP-reverse | GTCGACTTAAAGCTCATCATGTTTGTATAGTTC |
| GUS expression constructs | YL1-promoter-forward | GTCGACATGGTGGTTGATTCAAGTACAG |
| | YL1-promoter-reverse | GGATCCAGCAACACTATCAGAGAGAAAATC |
| qRT-PCR | ABA1-forward | TGCTACTCTATCAATCCATCTCC |
| | ABA1-reverse | TCTTCTCCTCCTTCTCAACTAAC |
| | ABA2-forward | AGGAGCCACAGGGATAGG |
| | ABA2-reverse | ACTCACCACGAAGCAGAC |
| | ABA3-forward | CCGAGGAGAGTGTGCTGAC |
| | ABA3-reverse | AACCGCCCAATGATGTGAAATG |
| | AAO3-forward | TGCTTATGGTCTCGGTATGG |
| | AAO3-reverse | CCTAACGGCTTCACAACCTG |
| | NCED3-forward | GGTCGTGTGAGTTCTTATGTG |
| | NCED3-reverse | ACTGGTAAATCTCGCTCTCTC |
| | ABI5-forward | AACCTAATCCAACCCGAACC |
| | ABI5-reverse | ACCCTCCTCCTCCTGTCC |
| | ABI4-forward | CTTCTCCTCCTCGTCTC |
| | ABI4-reverse | GTTGGCTCCTCCTCCTAC |
| | HKT1-forward | TCTGGTCTCATCTGGCTCCTAATC |
| | HKT1-reverse | CACCGTCACTCCAAGAAGAACAC |
| | SOS1-forward | TGGAGGAAGCGACCGATTTC |
| | SOS1-reverse | CGATAACGAGAAGAGCGACAG |
| | SOS2-forward | CTGTTGCTCATTGCTACTG |
| | SOS2-reverse | CGTAACCCTGTCCACTAAG |
| | SOS3-forward | GTCACGCCATTACGGTAG |
| | SOS3-reverse | CACTCCATTCGCTTCACATC |
| | NHX1-forward | AGGTGCTGTATCTATGGCTCTTG |
| | NHX1-reverse | GCTCGTGGTGGCGTTCTG |
| YL1-forward (qP1) | GGATTGATGTAACCTTGAGAG | |
| YL1-reverse (qP2) | GCTGTCTTGTGCTTCTTC | |
| Actin2-forward | CTTCGCTTCCACTTCAG | |
| Actin2-reverse | ATCATACCAGTCTCAACAC | |