Supplementary Information for

**A novel stable QTL in chromosome A04 for salt tolerance at the seed germination stage of upland cotton via a resequencing-based high-density genetic map**

This PDF file includes:

Table of Contents

Fig. S1-5, Table S1-4. (Table S1-4 are provided in the separate Excel files)

**Table of Contents:**

|  |  |  |
| --- | --- | --- |
| **Supplementary item** | **Title** | **Page** |
| Fig. S1 | The salt-tolerance phenotypes parts of RIL lines obtained in the field condition | 2 |
| Fig. S2 | Phenotypic diversity of RGR for the RIL population based on 0.3% salt treatment | 2 |
| Fig. S3 | The relative expression of 21 genes in germination between two parents | 3 |
| Fig. S4 | The transcript-level of GA-related genes between both parents in germination under salt stress | 4 |
| Fig. S5 | DAB staining of H2O2 in *GhADC2*-overexpressing *Arabidopsis* after salt stress | 5 |
| Fig. S6 | The expression levels of genes related to GAs biosynthesis in TRV:*GASA1* after salt stress | 5 |
|  |  |  |
| Table S1 | Correlation coefficients for RGR among five environments | - |
| Table S2 | The detailed information of all the RGR-related QTLs in five environments and BLUP | - |
| Table S3 | A list of all the primers for gene cloning, vector construction and qRT-PCR. | - |
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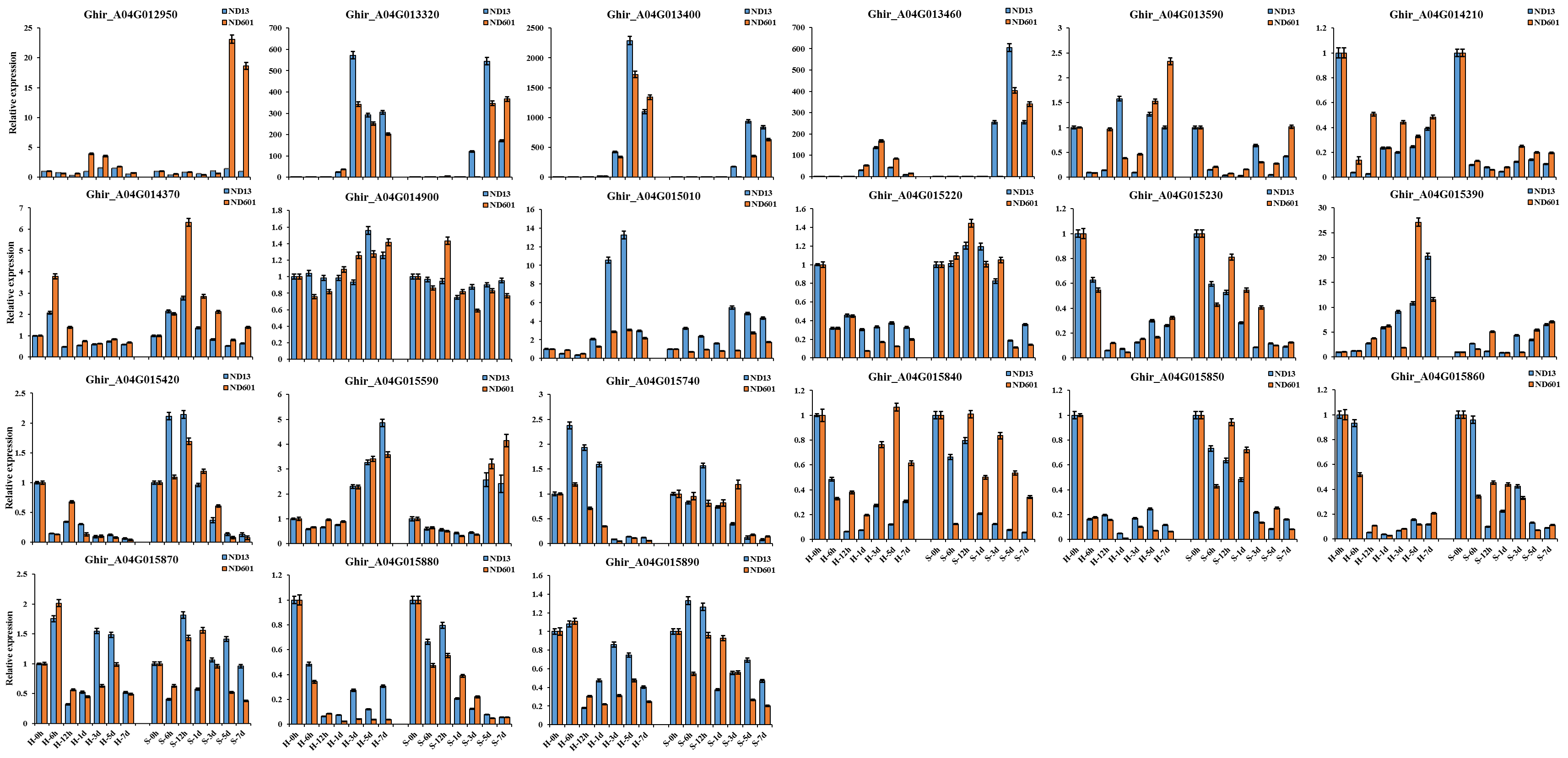
**Fig. S1 The salt-tolerance phenotypes parts of RIL lines obtained in the field condition.**

(A, D) lines under water treatment; (B-C, E-F) lines under salt treatment

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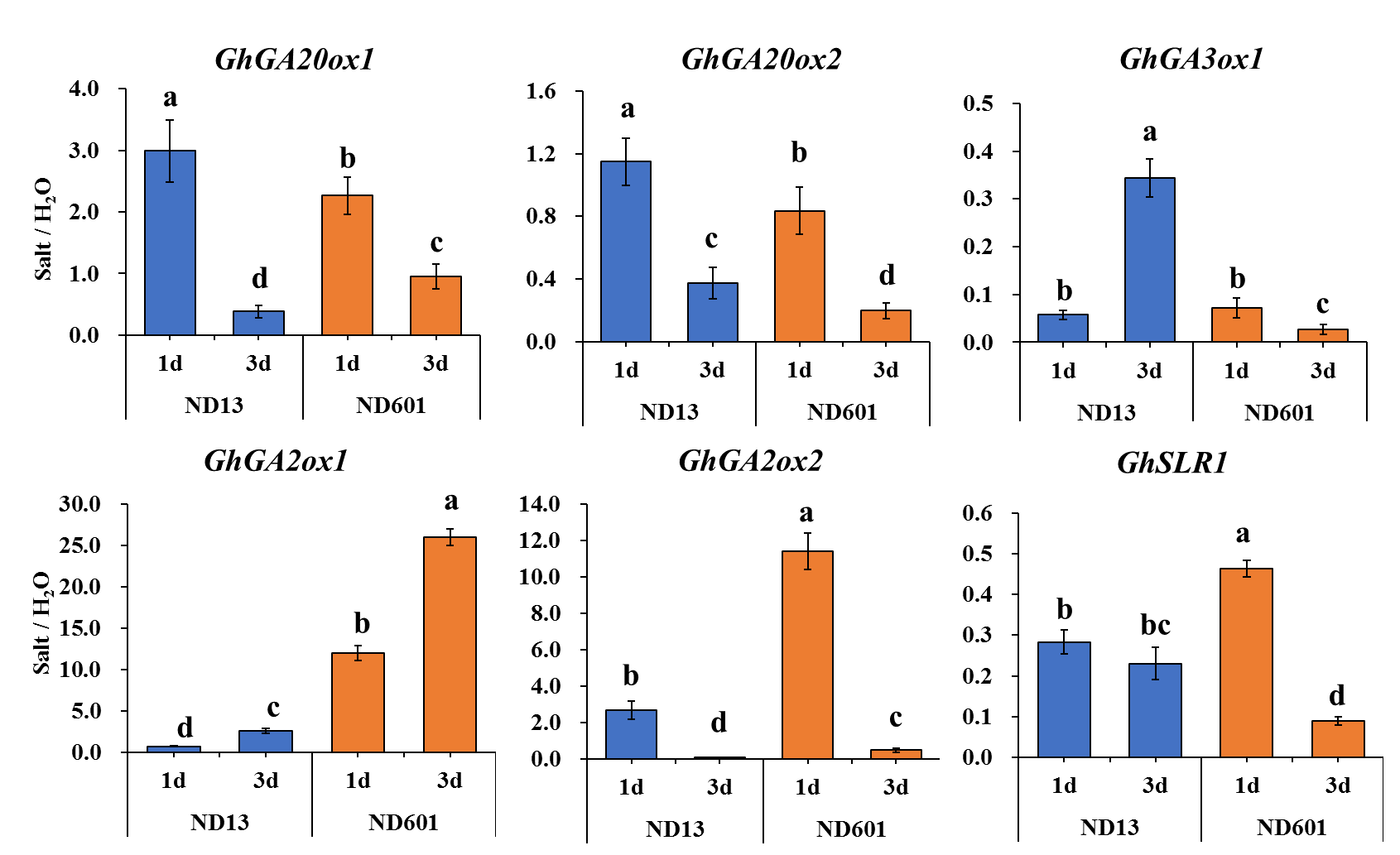
**Fig. S2 Phenotypic diversity of RGR for the RIL population based on 0.3% salt treatment.**

(A-F) indicated the RGR obtained in E1-E5 and the BLUP value, respectively.



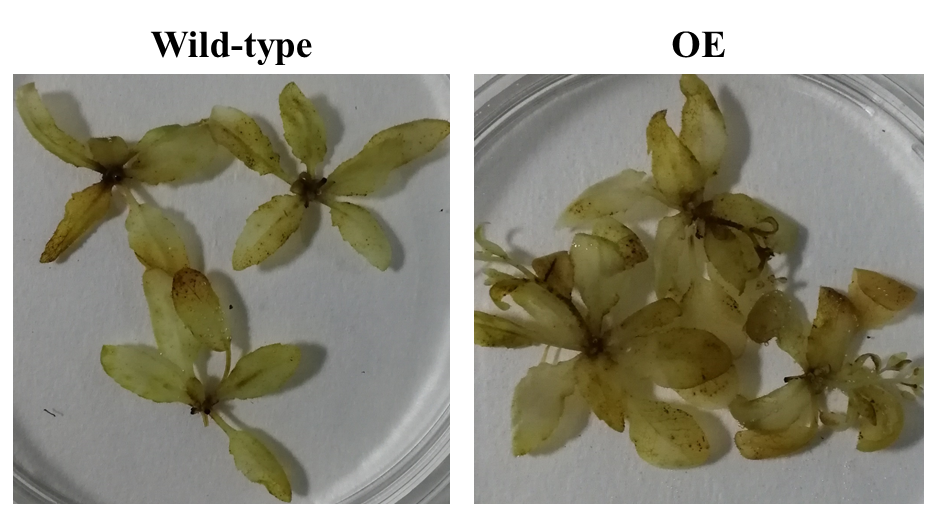
**Fig. S3 The relative expression of 21 genes in germination between two parents.**

Note: Quantification of genes in QTL qRGR-A04-1 by qRT-PCR at 0 h, 6 h, 12 h, 1 d, 3 d, 5 d and 7 d in germination between two parents. H and S indicating the seeds under the water and salt treatment, respectively. Values are means with SD (*n* = 3 biological replicates).

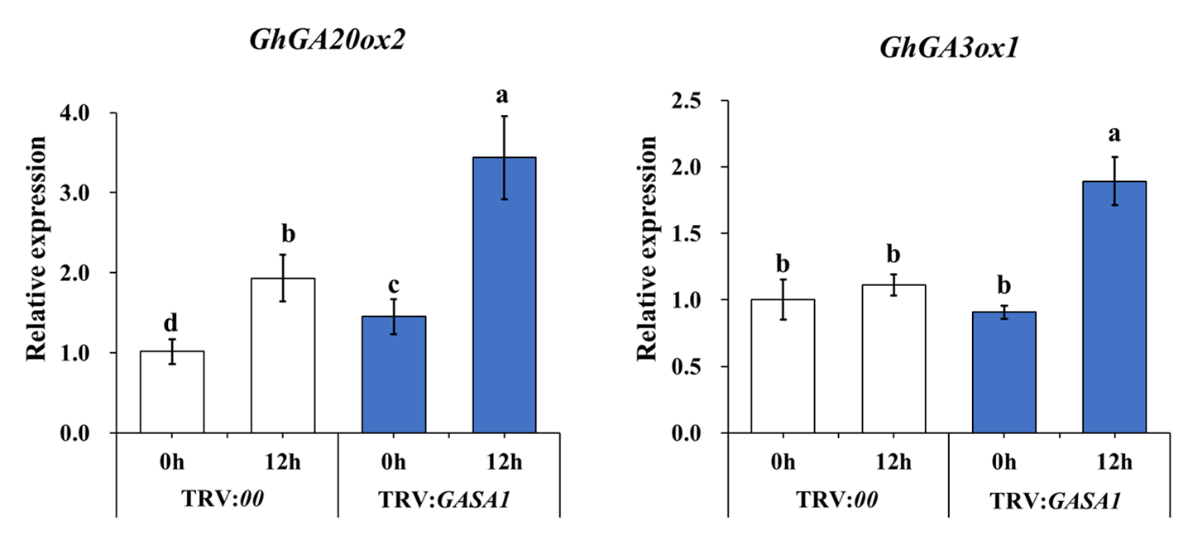


**Fig. S4 The transcript-level of GA-related genes between both parents in germination under salt stress.**

*GhGA20ox1*, *GhGA20ox2*, *GhGA3ox1*, were GA-related genes encoding active GAs. *GhGA2ox1* and *GhGA2ox2* were GA-related genes encoding inactive GAs. GhSLR1was a DELLA protein. The seeds were treated with 0.3% NaCl and sampled at 0 h, 6 h, 12 h, 1 d, 3 d, 5 d and 7 d and the water treatment as the control to calculate the relative value. Different letters at the top of each column indicate significant differences, as determined by ANOVA (*p <* 0.05). The data are presented as the means ± SEs.

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**Fig. S5 DAB staining of H2O2 in *GhADC2*-overexpressing *Arabidopsis* after salt stress.**

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**Fig. S6 The expression levels of genes related to GAs biosynthesis in TRV:*GASA1* after salt stress.**

Different letters at the top of each column indicate significant differences at *P* < 0.05 (*n* = 3 biological replicates) by the Student’s *t*-test. Error bars indicate s.e.m.