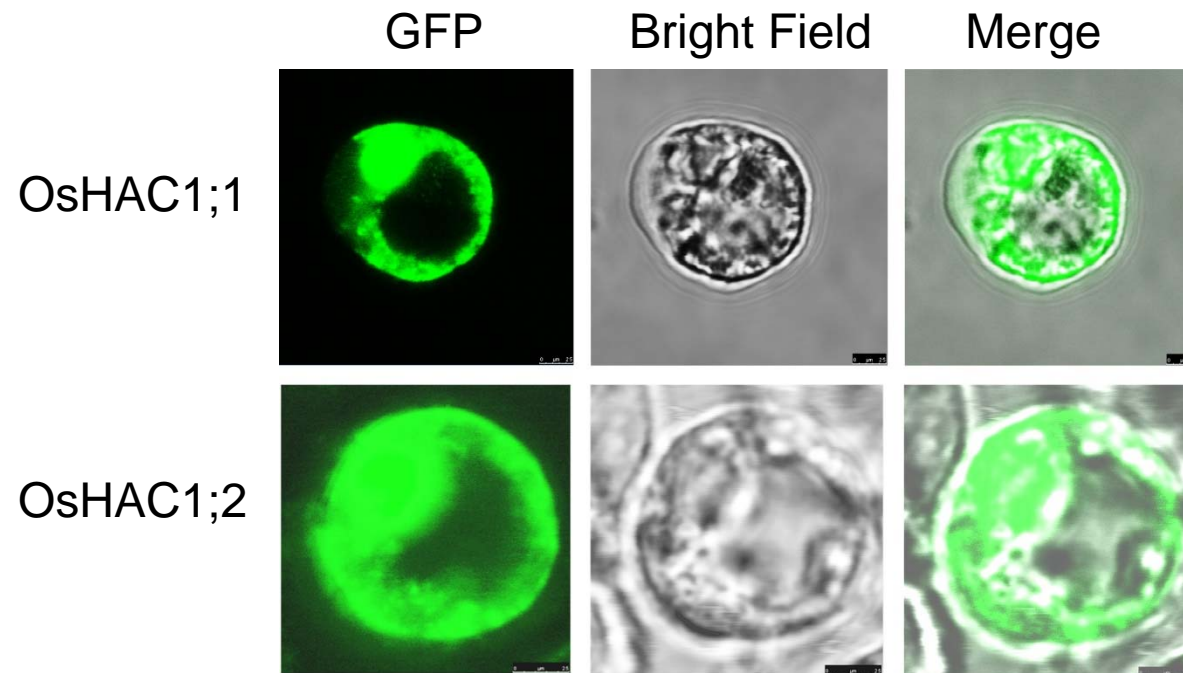
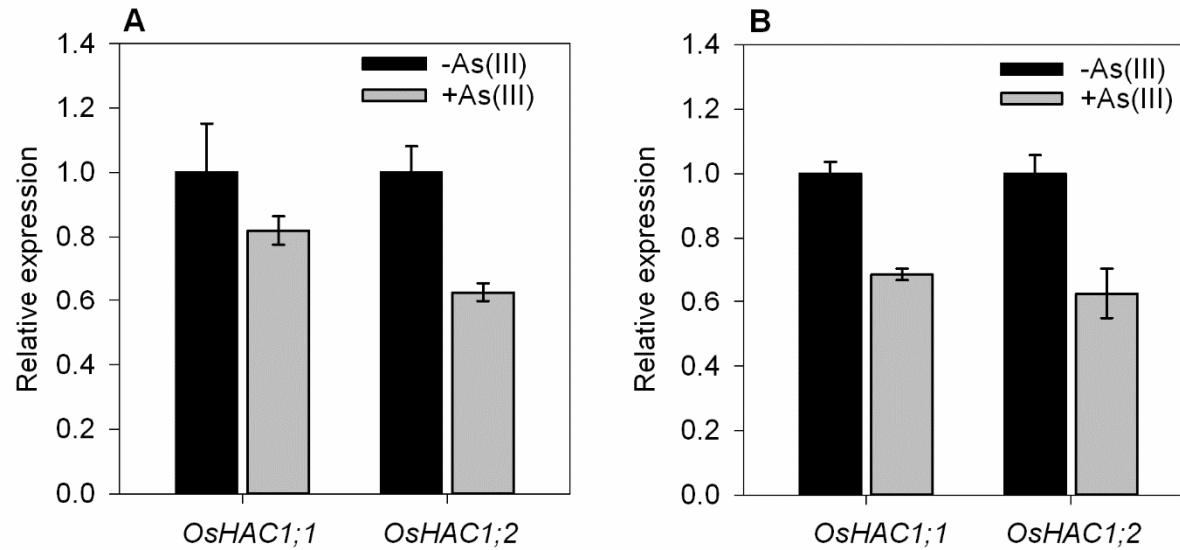


**Supplemental Figure S1.** Sequence analysis of *HAC* genes in rice and *Arabidopsis thaliana*. Phylogenetic analyses were conducted using MEGA version 6 (Tamura et al., 2013). Protein sequences were aligned using MUSCLE with UPGMB as clustering method. The tree was constructed using the Neighbor Joining (NJ) method. Bootstraps were carried out with 1,000 replications.



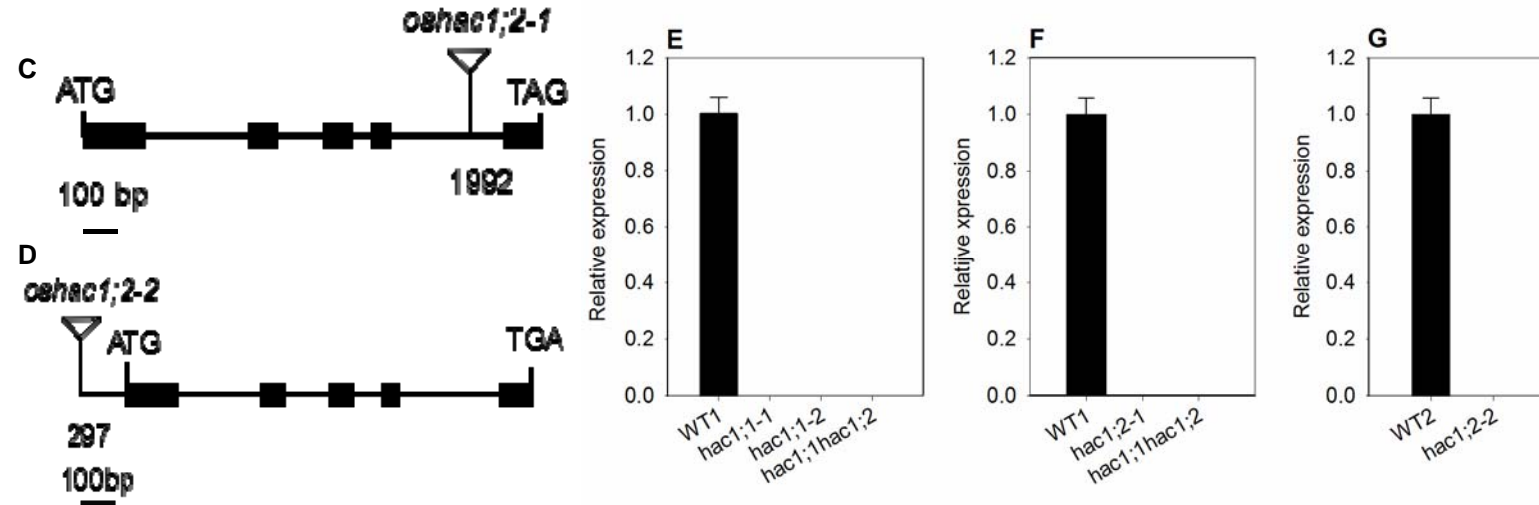
**Supplemental Figure S2.** Subcellular localization of OsHAC1;1 and OsHAC1;2. Protoplasts were isolated from the roots of transgenic rice plants expressing *pHAC1;1:OsHAC1;1-GFP* or *pHAC1;2:OsHAC1;2-GFP*. Top panel, scale bar=100  $\mu\text{m}$ . Bottom panel, scale bar = 25  $\mu\text{m}$ .



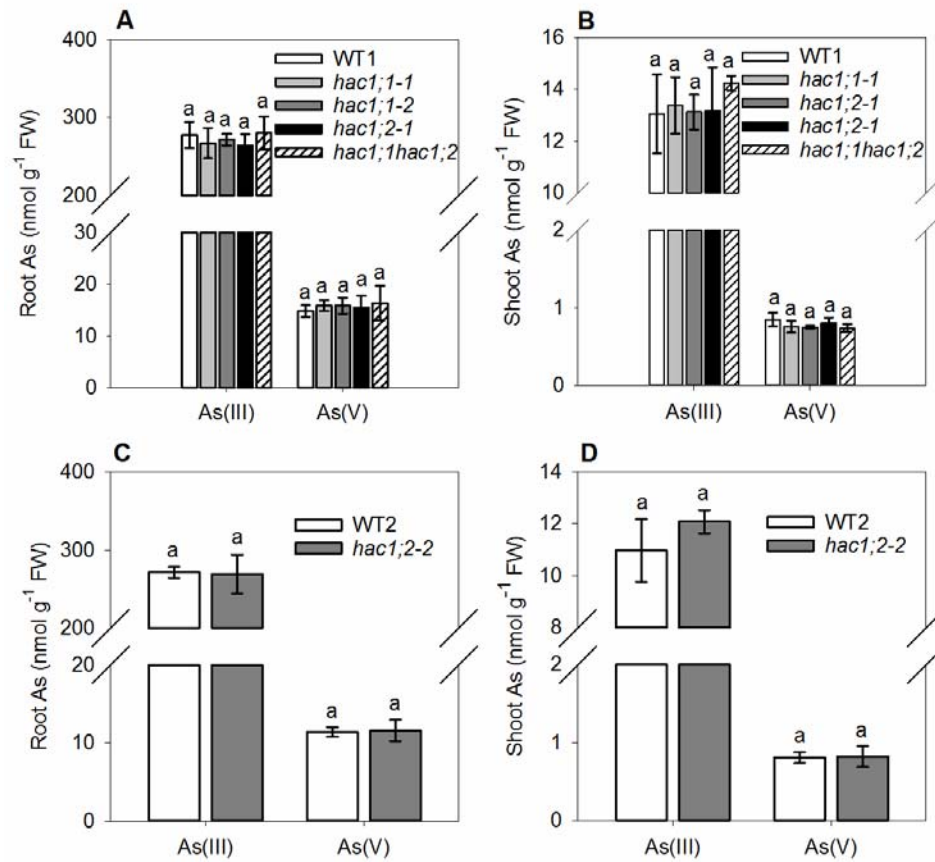
**Supplemental Figure S3.** Exposure to As(III) decreases the expression of *OsHAC1;1* and *OsHAC1;2*. The expression of *OsHAC1;1* and *OsHAC1;2* in roots (A) and shoots (B) after plants (cv Nipponbare) were exposed to 10  $\mu$ M As(III) for 24 h. The expression levels were determined using quantitative real-time PCR with *Actin* as the internal standard. Data represents means  $\pm$  S.D. ( $n=3$  biological replicates).

A ZH11 1 ATGGCGCCTCCTATGAAACCAGGTCAGTCAGATCA 36  
*oshac1;1-1* 1 ATGGCGCCTCT-----AGGTCAGTCAGATCA 26

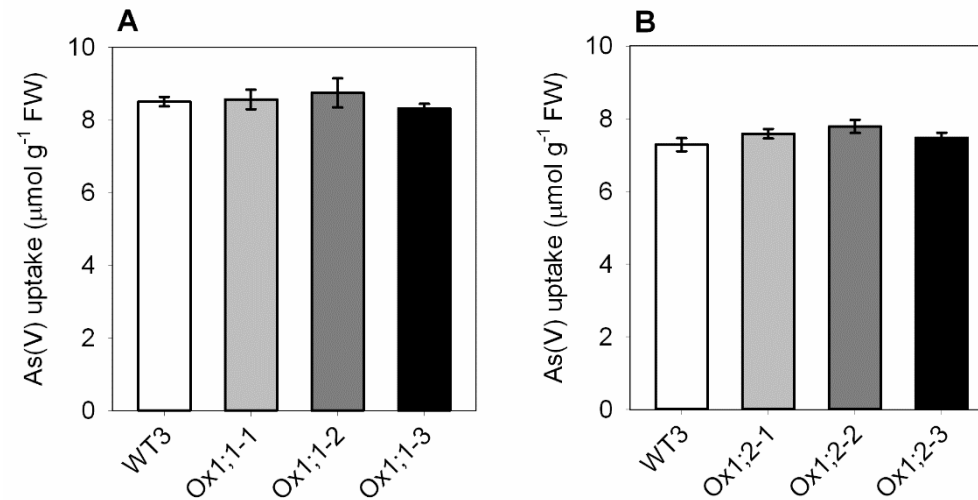
B ZH11 1 ATGGCGCCTCCCTATGAAACCAGGTCAGTCAGATCA 36  
*oshac1;1-1* 1 ATGGCGCCTAGATA-----GTCAGTCAGATCA 27



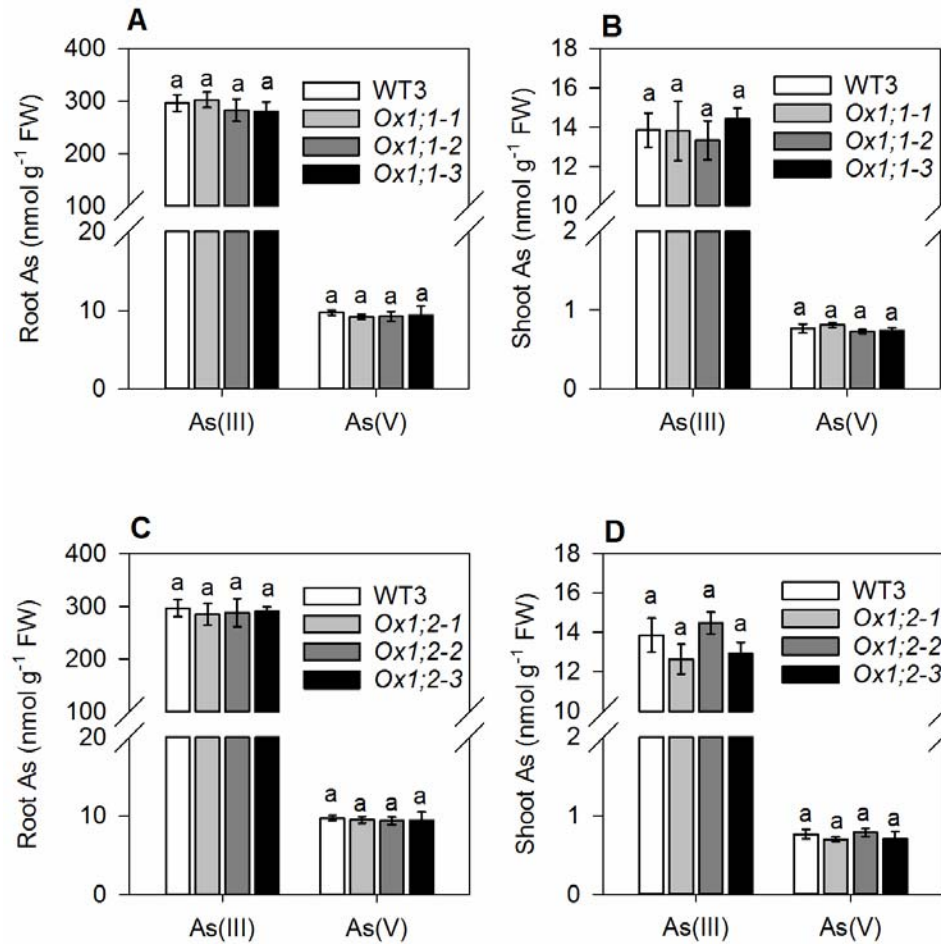
**Supplemental Figure S4.** Knockout mutants of *OsHAC1;1* (*hac1;1-1*, *hac1;1-2*), *OsHAC1;2* (*hac1;2-1*, *hac1;2-2*) and double mutant of *OsHAC1;1* and *OsHAC1;2* (*hac1;1hac1;2*). (A, B) Two independent knockout mutants of the *OsHAC1;1* in the cv. Zhonghua 11 (ZH11) background generated by CRISPR-Cas9. (C, D) Two independent T-DNA insertion mutants of *OsHAC1;2* in the Zhonghua 11 (C) or Dongjin (D) background. The black boxes stand for exons, the lines stand for introns, and the triangle indicates the T-DNA insertion. (E, F, G) The expression levels of *OsHAC1;1* (E) and *OsHAC1;2* (F, G) in wild-type (WT1, Zhonghua 11; WT2, Dongjin) and mutants by quantitative real-time PCR with *Actin* as the reference gene.



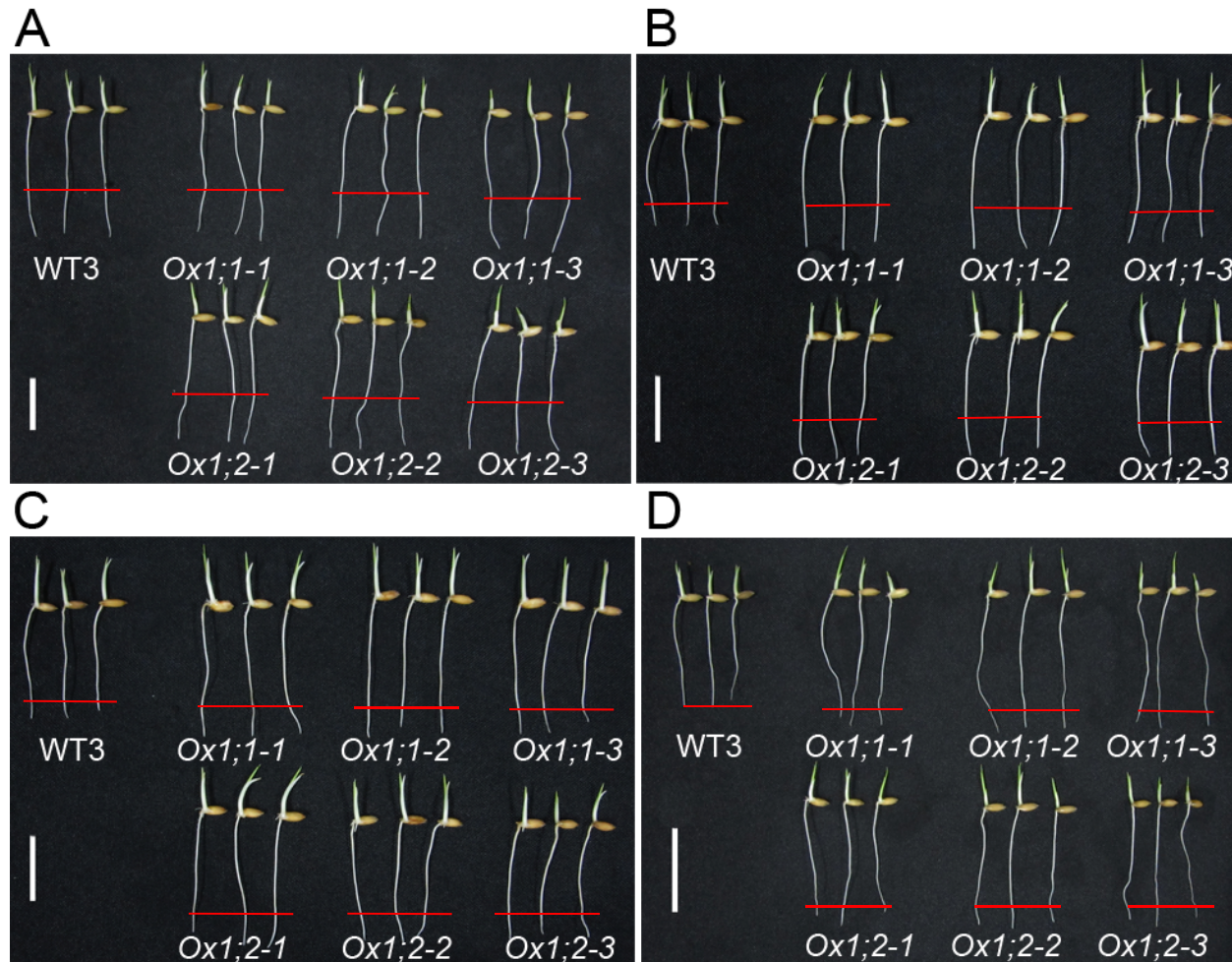
**Supplemental Figure S5.** Knocking out *OsHAC1;1* or *OsHAC1;2* has no significant effect on As(III) uptake and As accumulation in rice. A-D, As speciation in roots (A, C) and shoots (B, D) after wild-type and knockout mutant plants were exposed to 10  $\mu$ M As(III) for 48 h. WT1, cv Zhonghua 11; WT2, cv Dongjin. Data are means  $\pm$  S.E. ( $n=4$  biological replicates).



**Supplemental Figure S6.** Overexpression of *OsHAC1;1* or *OsHAC1;2* has no significant effect on As(V) uptake. As(V) uptake by overexpressing lines of *OsHAC1;1* (A) and *OsHAC1;2* (B) and wild-type (Nipponbare) plants from nutrient solution containing 10  $\mu\text{M}$  As(V) for 48 h. *Ox1;1-1*, *Ox1;1-2*, *Ox1;1-3* represent independent overexpression lines of *OsHAC1;1*. *Ox1;2-1*, *Ox1;2-2*, *Ox1;2-3* represent independent overexpression lines of *OsHAC1;2*. Data represents means  $\pm$  S.E. ( $n=4$  biological replicates).



**Supplemental Figure S7.** Overexpression of *OsHAC1;1* or *OsHAC1;2* has no significant effect on As(III) uptake and As accumulation in rice. A-D, As speciation in roots (A, C) and shoots (B, D) after wild-type and knockout mutant plants were exposed to 10  $\mu$ M As(III) for 48 h. WT3, cv Nipponbare. *Ox1;1-1*, *Ox1;1-2*, *Ox1;1-3* represent independent overexpression lines of *OsHAC1;1*. *Ox1;2-1*, *Ox1;2-2*, *Ox1;2-3* represent independent overexpression lines of *OsHAC1;2*. Data represents means  $\pm$  S.E. ( $n=4$  biological replicates).



**Supplemental Figure S8.** Root elongation of *OsHAC1;1* and *OsHAC1;2* overexpression lines and wild-type plants exposed to different concentrations of As(V): 0 μM (A), 2.5 μM (B), 3 μM (C) and 4 μM (D), for 24 h. WT3 represent wild-type plants (Nipponbare). *Ox1;1-1*, *Ox1;1-2*, *Ox1;1-3* represent independent overexpression lines of *OsHAC1;1*. *Ox1;2-1*, *Ox1;2-2*, *Ox1;2-3* represent independent overexpression lines of *OsHAC1;2*. The red line indicates root length at the beginning of As(V) treatment. Scale bars = 2 cm.



