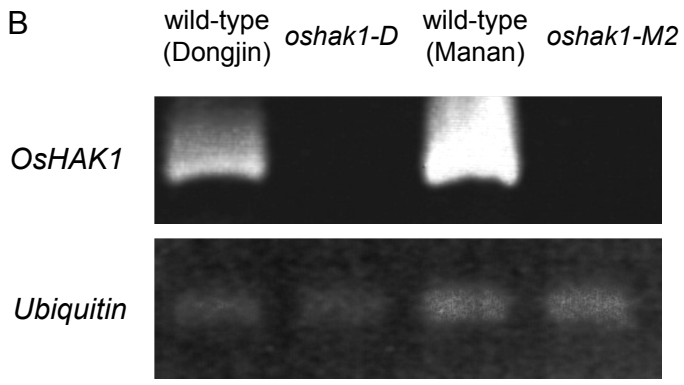
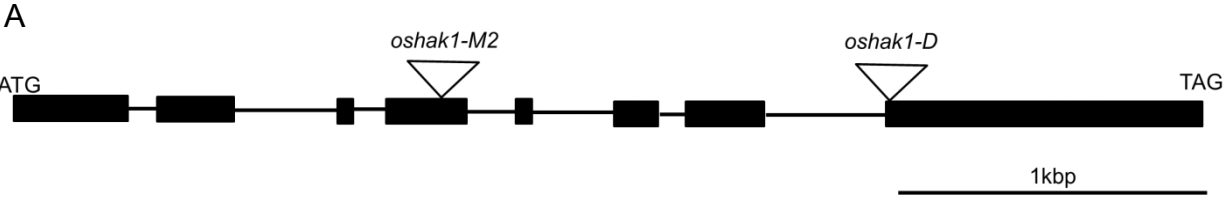


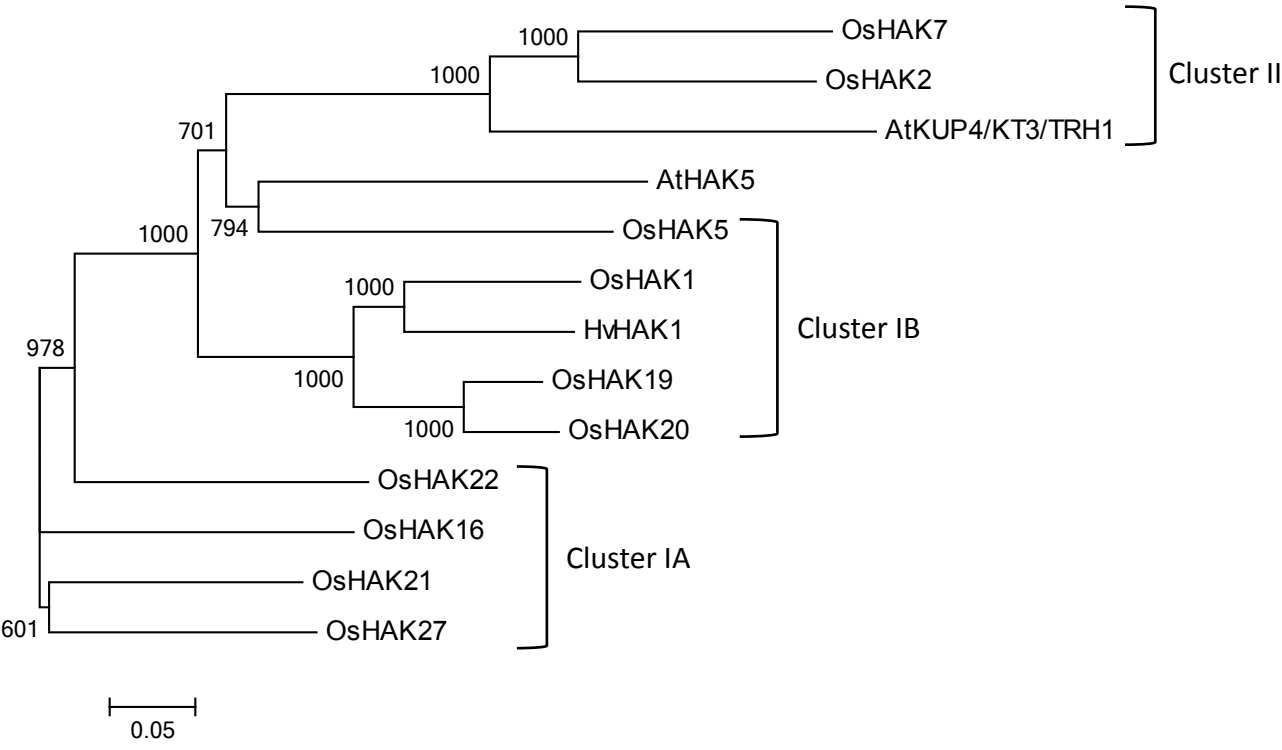
# Supplemental Figure 1.



## Supplemental Figure 1.

Isolation of two homozygous T-DNA insertion mutants in the *OsHAK1* gene. (A) *OsHAK1* gene structure; eight exons are boxed; black box shows the open reading frame. The triangles show the T-DNA insertion positions. (B) RT-PCR using cDNA from wild-type (cultivars Dongjin and Manan) and two T-DNA insertion lines (*oshak1-D* and *oshak1-M2*). PCR primers were designed using sequence information from the 5' UTR and 3' UTR surrounding the T-DNA insertion site to amplify a partial cDNA. *Ubiquitin* primers were also used as an internal control.

# Supplemental Figure 2.



Supplemental Figure 2. Phylogenetic relationship of HAK transporters in cluster I. The tree was generated using the neighbor-joining method by using MEGA6 program. Three HAK transporters in cluster II were used as the outgroup for comparison of the aligned entities. Bootstrap values from 1,000 replicates are indicated at each branch.

Supplemental Figure 2. Tomoyuki Okada