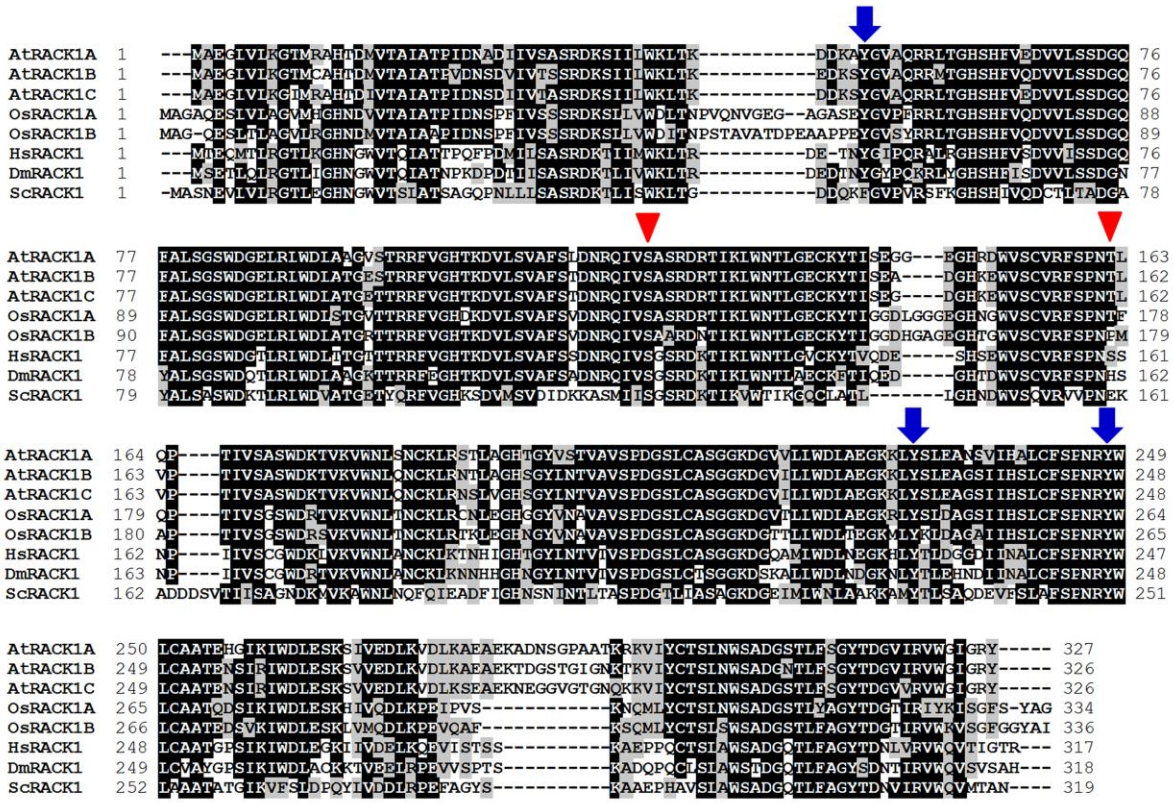
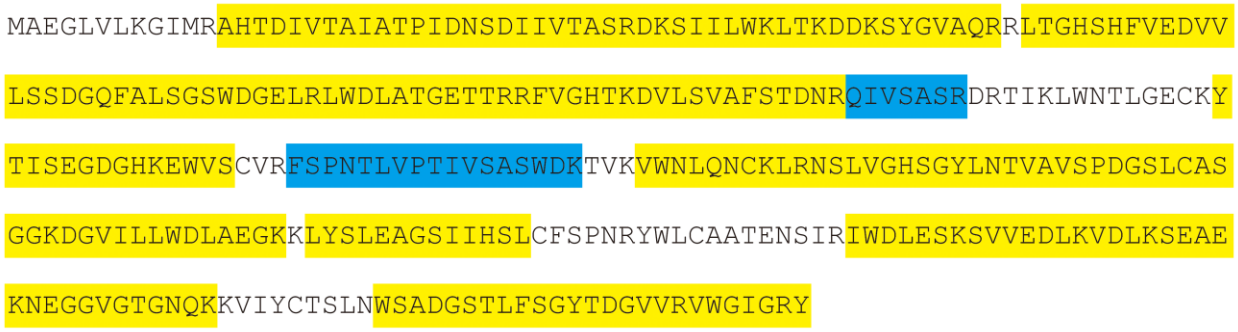
SUPPLEMENTAL DATA

Figure S1



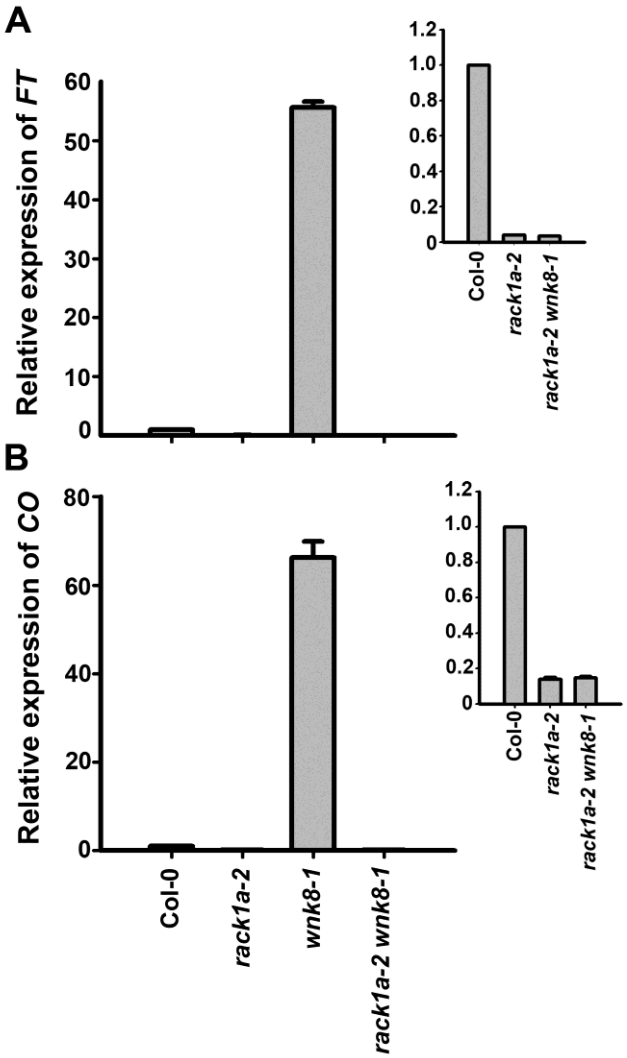
Supplemental Figure S1. Alignment of RACK1 amino acid sequences. The amino acid sequences were aligned by CLUSTALW multiple alignment using BioEdit (http://www.mbio.ncsu.edu/bioedit/bioedit.html). Amino acids that are identical or similar are shaded with black or gray, respectively. Gaps are shown as dashed lines. The proteins aligned are (name of species and accession number in parentheses): AtRACK1A (*Arabidopsis thaliana*, NP_173248), AtRACK1B (*Arabidopsis thaliana*, NP_175296), AtRACK1C (*Arabidopsis thaliana*, NP_188441), OsRACK1A (*Oryza sativa*, NP_001043910), OsRACK1B (*Oryza sativa*, NP_001056254), HsRACK1_Hs (*Homo sapiens*, NP_006089), DmRACK1 (*Drosophila melanogaster*, NP_477269), ScRACK1 (*Saccharomyces cerevisiae*, NP_013834). Arabidopsis RACK1 phosphorylation sites (Ser122; Thr 162 of AtRACK1A and Thr161 of AtRACK1B and AtRACK1C) identified in this study are indicated by red arrow heads on the top of amino acids. Human RACK1 phosphorylation sites (Tyr52, Tyr228 and Tyr246 of HsRACK1) are indicated by blue arrows on the top of amino acids.

Figure S2



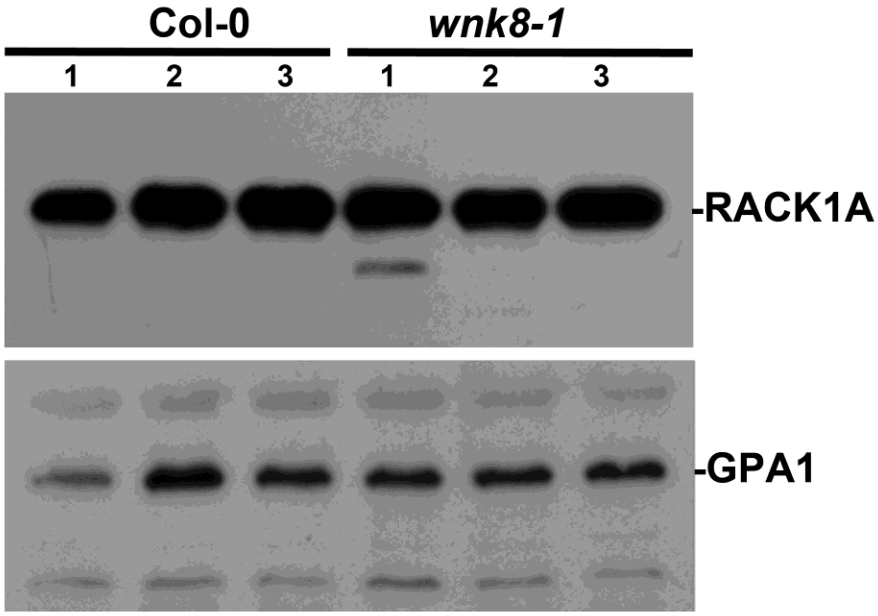
Supplemental Figure S2. Peptides detected in mass spectrometry analysis. The amino acid sequence of RACK1C is shown. Non-phosphorylated peptides detected are marked in yellow. Peptides containing phosphorylation sites are marked in blue.

Figure S3



Supplemental Figure S3. Quantitative RT-PCR analysis of the transcript level of flowering marker genes *FT* (A) and *CO* (B) and. RNA was isolated from fully-expanded rosette leaves of plants that had been grown for 51 days under 8/16 photoperiod. Insets illustrate the difference in transcript levels between Col-0, *rack1a-2* single mutant and *rack1a-2 wnk8-1* double mutant. Shown are means of three replicates ± s.e.

Figure S4



Supplemental Figure S4. Immunoblot analysis of RACK1A protein in *wnk8* mutant and Col-0 wild-type background. Total proteins were extracted from one-week old Arabidopsis seedlings grown in ½ MS liquid media. Anti-RACK1A peptide antibodies were used for immunoblot analysis. The same membrane was blotted with anti-GPA1 peptide antibodies as a loading control. Three biological replicates were used for each genotype.