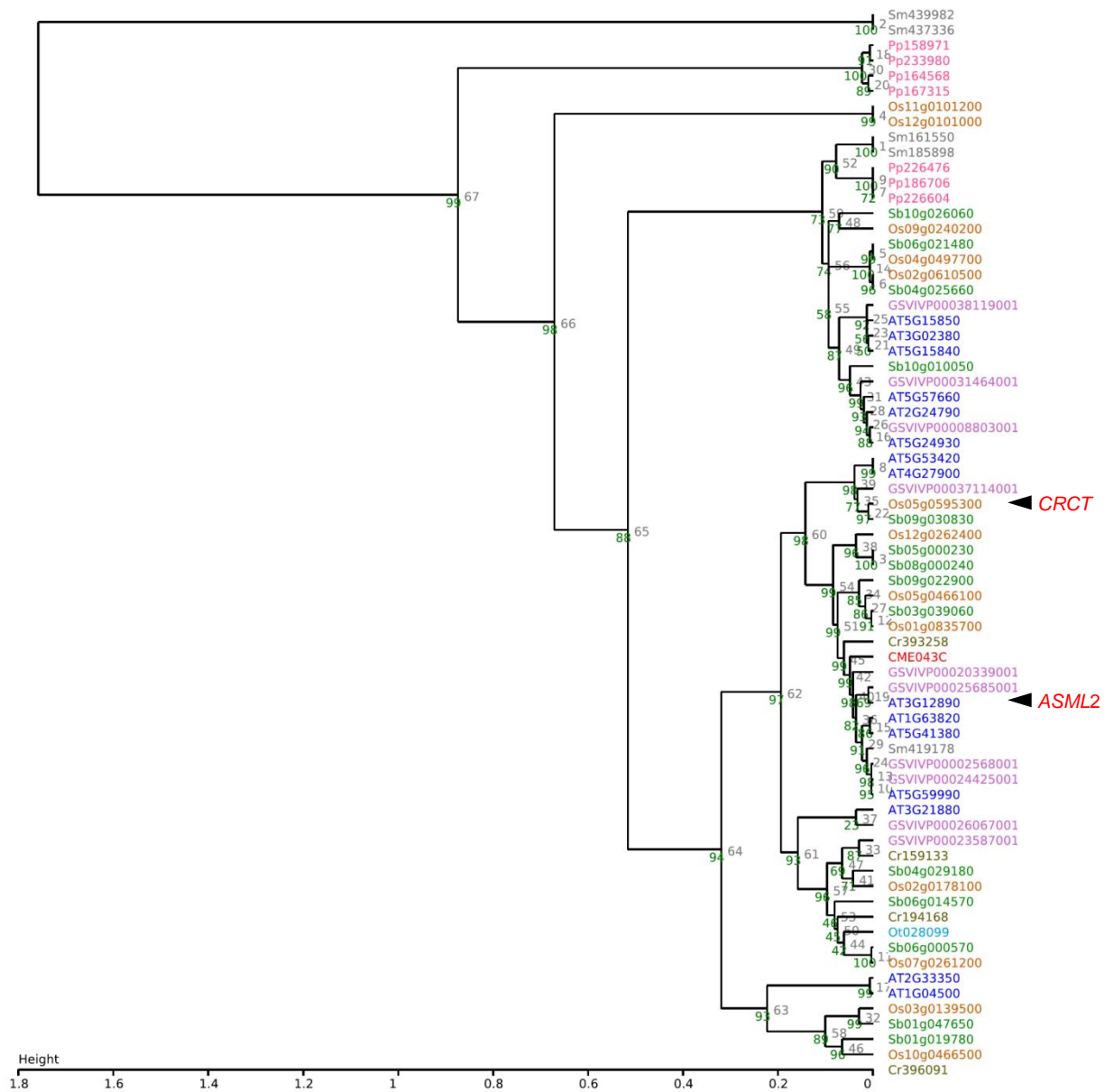
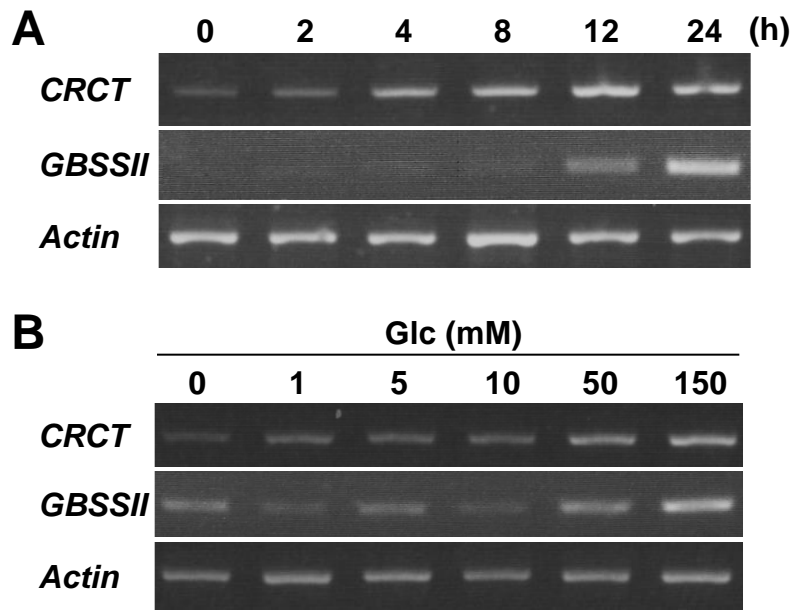


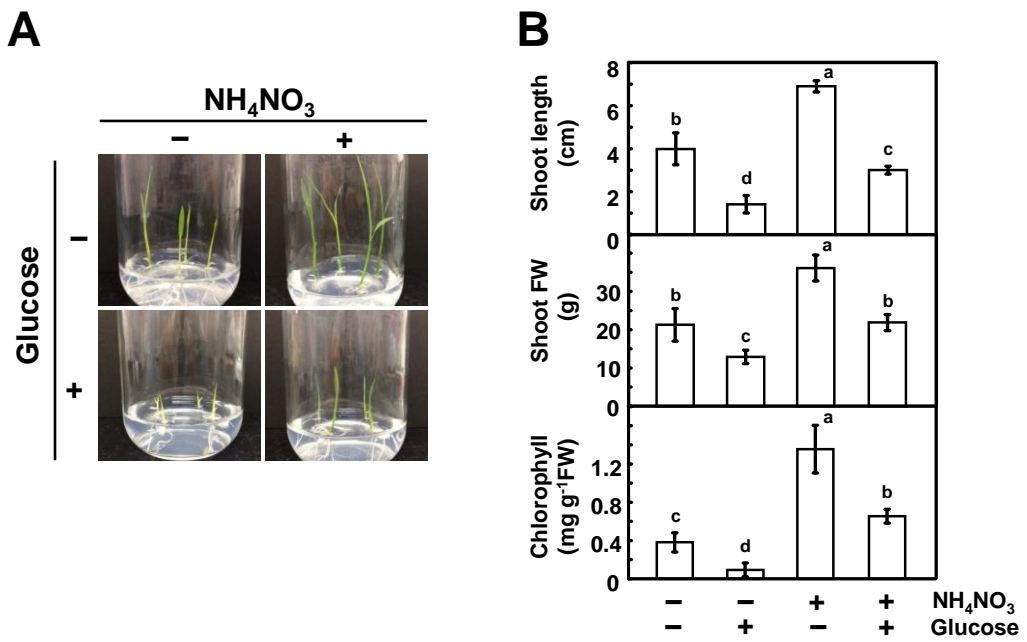
Supplemental Figure S1. Gene structures of CCT domain containing proteins. Domain structures of *Arabidopsis* TOC1 (At5g61380), ZML (At3g21175), CONSTANS (At5g15840) and ASML2 (At3g12890) from *Arabidopsis* and CRCT (Os05g0595300) from rice are indicated. The CCT domain is commonly observed in these proteins. REC, tify, ZnF-GATA and BBOX are domains containing Zinc finger motif. White boxes indicate motifs of unknown function common to some CCT domain containing proteins, referenced to the Surveyed Conserved motif ALignment diagram and the Associating Dendrogram (SALAD) database.



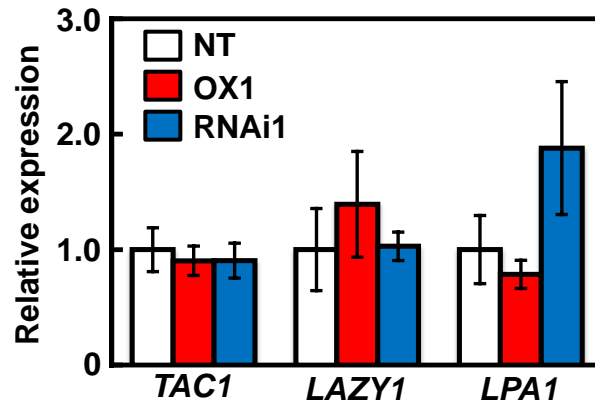
Supplemental Figure S2. Phylogenetic tree based on motif of amino acid sequence among CCT domain containing proteins in plants. Phylogenetic tree was constructed and obtained from SALAD database. Bootstrap value and node number are indicated in green and black, respectively, on each node. Related genes of rice (orange), *Arabidopsis* (blue), sorghum (green), grape (light purple), *Selaginella moellendorffii* (silver), *Physcomitrella patens* (pink), *Chlamydomonas reinhardtii* (gold), *Cyanidioschyzon merolae* (red), *Ostreococcus tauri* (light blue) are shown. CRCT and ASML2 are indicated by arrowhead.



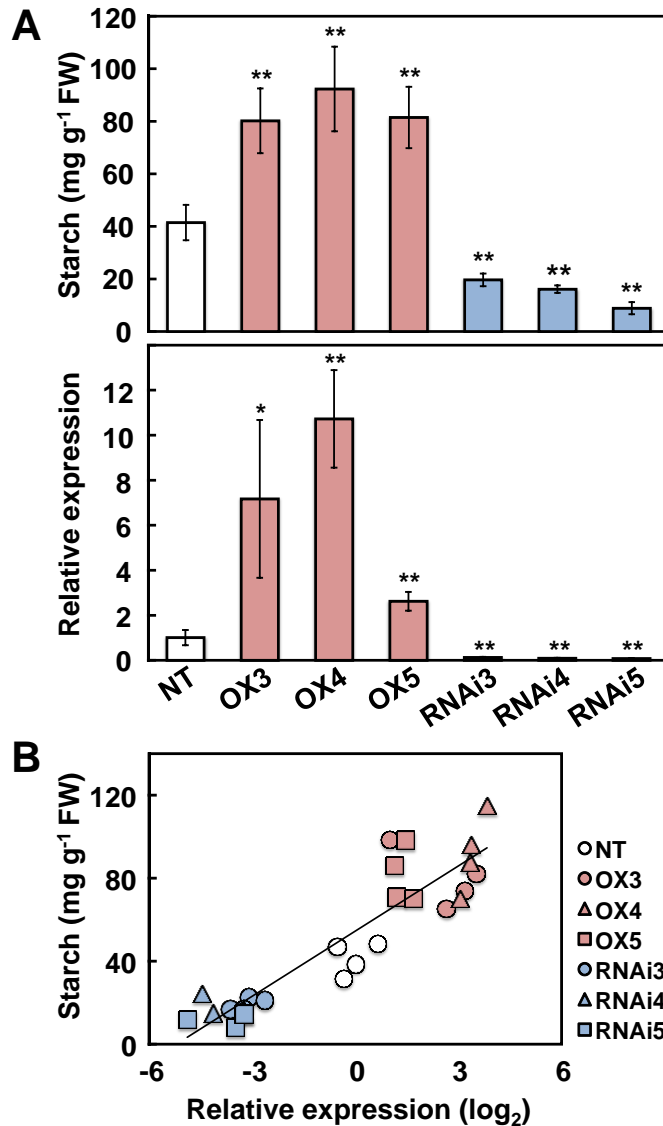
Supplemental Figure S3. Effects of glucose on the expression of *CRCT*. Plants were kept in darkness for 2 days. Then, the uppermost fully expanded leaves were harvested and floated on solutions containing 50 mM glucose for 0-24 h (A) or different concentrations of glucose (Glc) for 8 h (B). The expression of *CRCT* was analyzed by RT-PCR. *GBSSII* was shown as known sugar inducible gene (Dian et al., 2003). *Actin* was used as internal control.



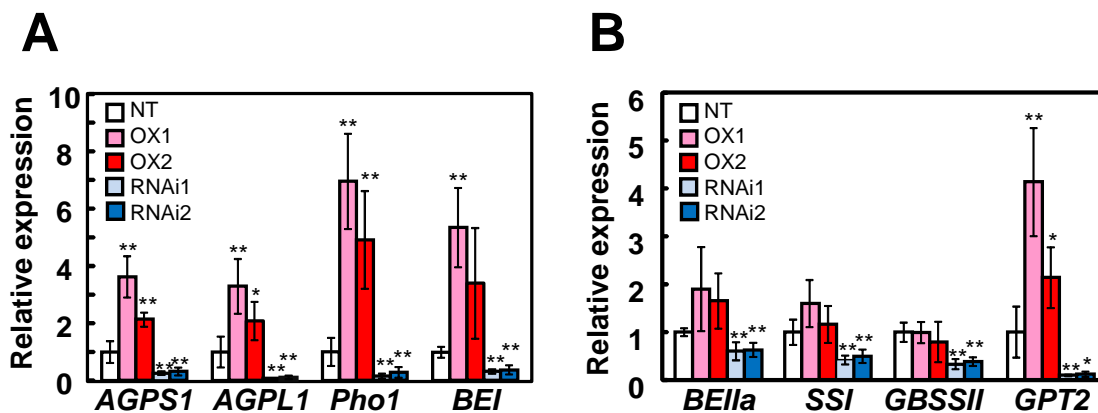
Supplemental Figure S4. Effects of carbon and nitrogen on growth of rice. A, Effects of carbon and nitrogen on growth of rice. Rice seedlings were grown on media for 5 days with or without 450 mM glucose and 30 mM NH_4NO_3 . B, The shoot length, shoot fresh weight (FW) and chlorophyll contents determined at 5 days after germination. Data represent mean \pm SD of four biological replicates. Different letters indicate significant difference by Tukey's test ($P < 0.05$).



Supplemental Figure S5. Expression of tiller angle related genes in stem base of transgenic rice. Plants were grown in a growth chamber. In vegetative stage, tillar bases were sampled at middle of daytime. The expression of tillar angle related genes were analyzed by real-time PCR. Expression data are normalized by the expression levels of *Actin*. Data represent mean \pm SD of four replicates. Expression levels of these genes in transgenic lines were not significantly different from those in nontransgenic (Student's t-test at $P < 0.05$). NT, non-transgenic rice; OX1, *CRCT* overexpression lines; RNAi1, *CRCT* knockdown lines.



Supplemental Figure S6. Starch content and expression level of *CRCT* in leaf sheath of different transgenic lines used in Figs 3-9. A, Starch content and expression level of *CRCT* analyzed by real-time PCR. Expression data are normalized by the expression levels of *Actin*. Data represent mean \pm SD of four biological replicates. * and ** indicate significant difference between nontransgenic rice and transgenic lines by Student's t-test at $P < 0.05$ and $P < 0.01$, respectively. B, Relationship between the content of starch and the expression level of *CRCT*. The relative expression level of *CRCT* is expressed as \log_2 . Regression line ($r = 0.912$) is shown. NT, non-transgenic rice; OX3, OX4 and OX5, *CRCT* overexpression lines; RNAi3, RNAi4 and RNAi5, *CRCT* knockdown lines.



Supplemental Figure S7. Expression analysis of genes related to starch synthesis by real-time PCR. A, Genes related to starch synthesis showing significant difference in the expressions between non-transgenic rice and transgenic rice by microarray. B, Other representative genes functioning in starch synthesis in vegetative organs. Expression data are normalized by the expression levels of *Actin*. Data represent mean \pm SD of four biological replicates. * and ** indicate significant difference between nontransgenic rice and transgenic rice by Student's t-test at $P < 0.05$ and $P < 0.01$, respectively. NT, non-transgenic rice; OX1 and OX2, *CRCT* overexpression lines; RNAi1 and RNAi2, *CRCT* knockdown lines.

IKHHAETFPV FSEPHFSPLK AYHATAKSVL DTLIMNWNAT YDYYDRTNVK **QAYYLSMEFL** 60
QGRALTNNAV NLELTGQYAE ALQQLGHSLE DVATQEPDAA LGNGGLGRLA SCFLDSLATL 120
 NYPAWGYGLR YKHGLFKANH TKDQEEVAE NWLEMGNPWE IVRTDVSYPV KFYGKVVVEGT 180
 DGRMHWIGGE NIKVVAHDIP IPGYKTKTTN NLRLWSTTVP SQDFDLEAFN AGDHASAYEA 240
 HLNAEKICHV LYPGDESPEG KVLRLKQQYT LCSASLQDII ARFERRAGDS LSWEDFPSKV 300
AVQMNDTHPT **LCIPELMRIL** IDVKGLSWNE AWSITERTVA **YTNHTVLPEA** **LEK**WSLDIMQ 360
 KLLPR**HVEII** **EKID**GELMNI IISKYGTEDT SLLKKKIKEM RILDNIDLDP SIAKLFVKPK 420
 EKKE**SPAKLK** EKLLVKSLEP SVVVEEKTVS KVEINEDSEE VEVDSEEVVE AENEDSEDEL 480
 DPFVKSDPKL PRVVRMANLC VVGHHSVNGV AAHSEIVKE DVFNSFYEMW PAKFQNKTN 540
 VT**PRR**WIRFC NP**ELSAI**ISK WIGSDDWVLN TDKLAE**LK**KF ADDEDLQSEW RAAK**KANKVK** 600
 VVSLIREKTG YIVSPDAMFD VQVKRIHEYK **RQLLNILGIV** **YRYK**MKKEMS AKDRINSFVP 660
 RVCIFGG**KAF** **ATYVQAK**RIV KFITDVAATV NHDPEIGDLL KVVFI**PDY**NV SVAEALIPAS 720
 ELSQHISTAG MEASGTSNMK FAMNGCILIG TLDGANVEIR EEVGEENFFL FGAEAEHIAG 780
 LRKERAQ**GK**F VPDP**RFE**EVK RFVRS**GV**FGT YNYDDLMGSL EGN**EYGRAD** **YFLV**G**KDFPS** 840
YIECQEKVDK AYRDQKLWTR MSILNTASS KFN**SDRT**IHE YAKDIWDIKP VILP 900

Supplemental Figure S8. Amino acid sequence of Pho1 and detected peptides of unknown band found on SDS-PAGE of soluble protein extracted from leaf sheath of *CRCT* overexpression line OX1 by LC-MS analysis. Amino acid sequence (Os03g0758100) was obtained from The Rice Annotation Project Database. Tryptic fragments identified by LC-MS analysis and subsequent MASCOT search were shown in red. Sequence coverage was 10.3%.