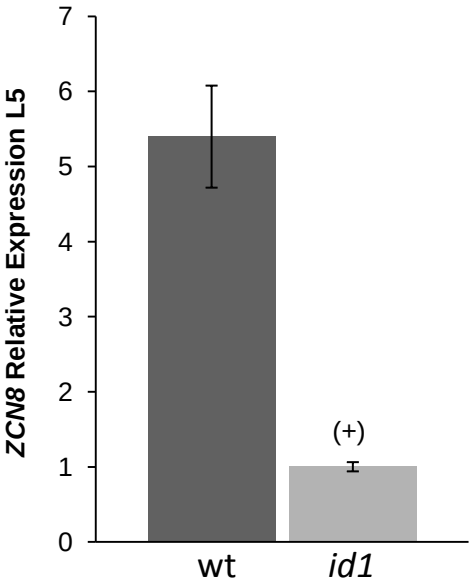


Figure S1. qRT-PCR analysis of *ZCN8* expression level in mature leaf five of V7 wild type (wt) plants relative to *id1* mutants at the same developmental stage. (+) denotes statistical significance based on a *t*-test ($P < 0.05$, $n = 5$). Error bars represent SD.

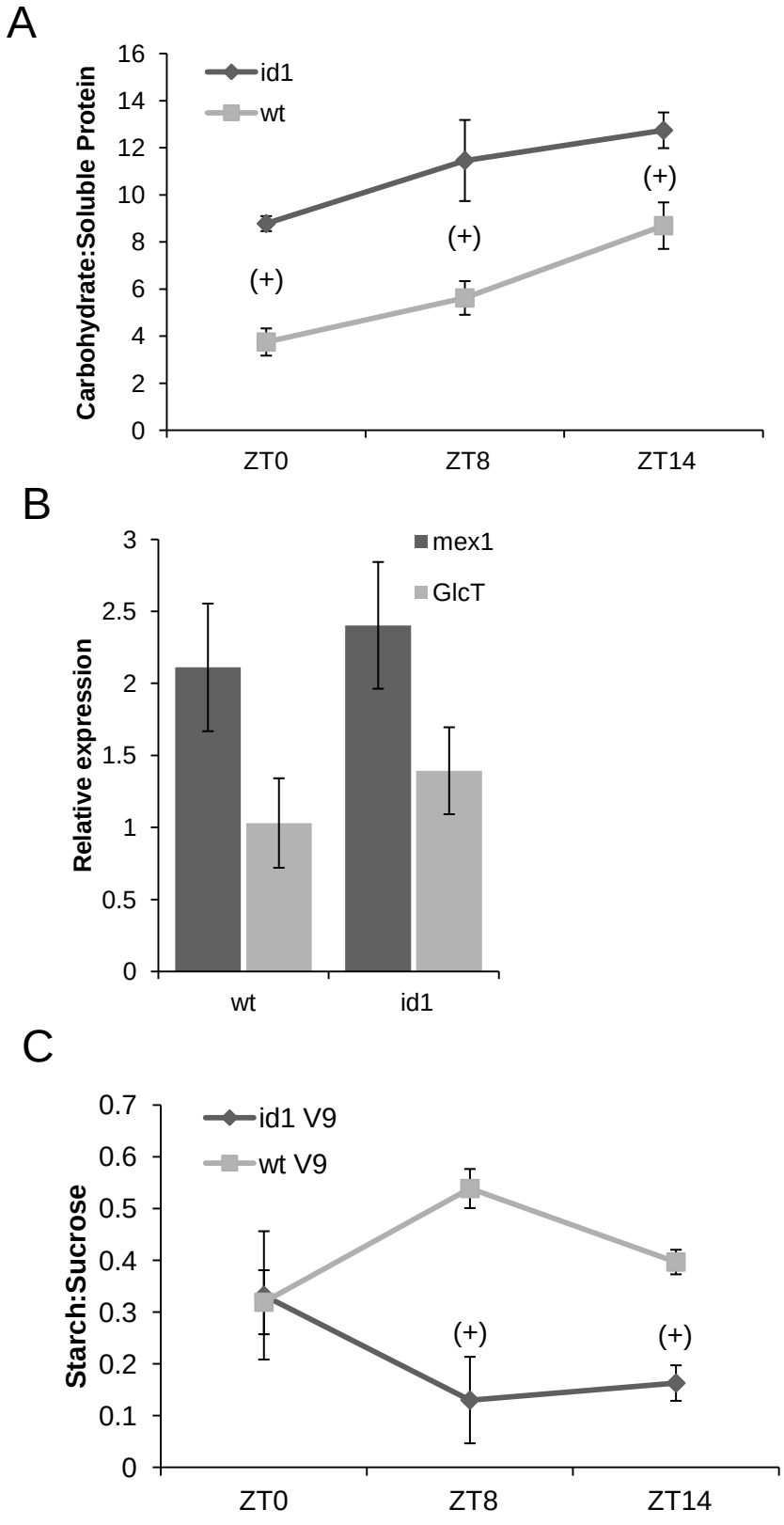
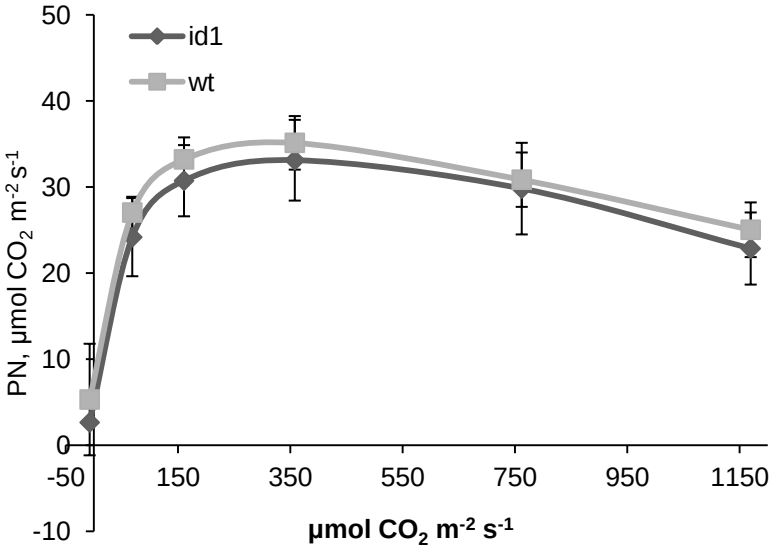


Figure S2. A, Total carbohydrate (sucrose plus starch) to soluble protein ratio in *id1* and wt mature leaf 5 at V7. B, Relative expression levels of a putative maize maltose transporter gene (*maltose excess1*, *mex1*) and a glucose translocator gene (*GlcT*) in wt and *id1* mature leaves. C, Starch to sucrose ratio in source leaves of *id1* and wt plants after the floral transition (V9).
Bars represent SD (n = 5) and statistical significance (+) is evaluated at the $P < 0.05$ level.

A



B

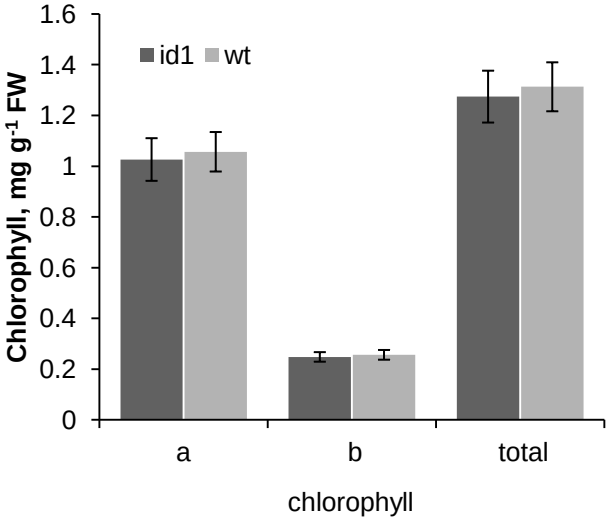


Figure S3. A, Carbon dioxide (CO_2) response curve for photosynthesis of *id1* and wt leaf five at the V7 stage. B, Chlorophyll quantification of *id1* and wt leaf five at the V7 stage. Bars represent SD (n = 5) and statistical significance (+) is evaluated at the $P < 0.05$ level.

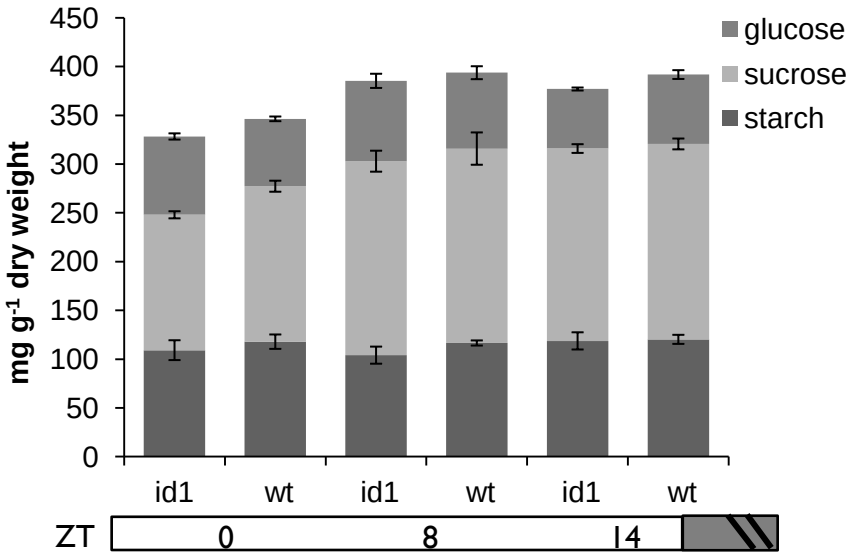


Figure S4. Comparison of starch, sucrose, and glucose levels in immature sink leaves of id1 mutants relative to normal-flowering V7 maize plants.