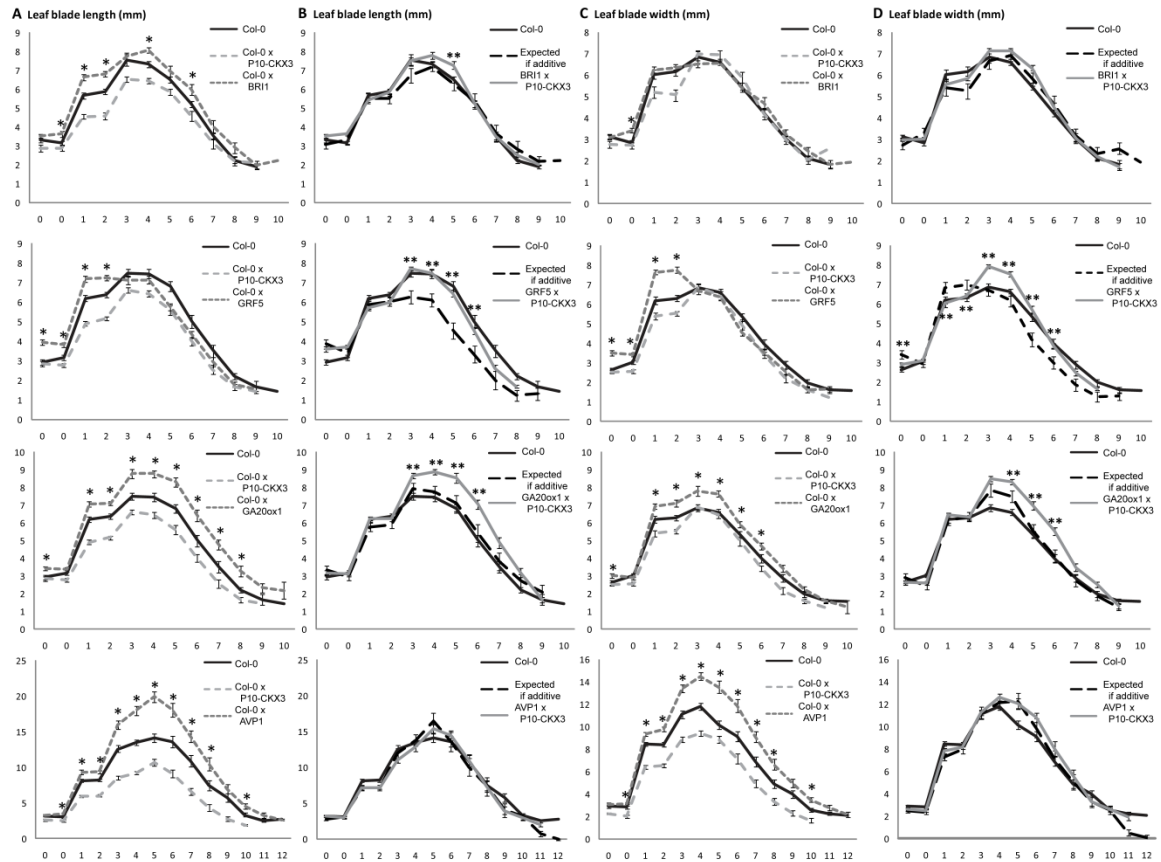**Supplemental Figure S1.** Leaf parameters for wild-type (Col-0) and *P10-CKX3* plants calculated from leaf series made at 21 DAS from plants grown in vitro.

A, Blade length. B, Blade width of cotyledons (0) and leaves 1 to 9. *, Significantly different from the wild type (P < 0.05, Student's *t* test). Error bars are SE (n ≥ 14).

Supplemental Figure S2. Leaf parameters of *P10-CKX3* plants crossed with *BRI1*, *GRF5*, *GA20ox1* and *AVP1*-overexpressing plants, respectively, for cotyledons (0) and leaves 1 to 10 or 12.

A and B, Blade length. C and D, Blade width. Blade length and width were calculated from leaf series made at 21 DAS from plants grown in vitro or at 22 DAS from plants grown in soil (*AVP1×P10-CKX3*). Blade length (A) and width (C) of wild type and the heterozygous parents. Blade length (B) and width (D) of wild type and the crosses and the expected values for an additive effect. Values expected if additive were calculated as the sum of the single heterozygous lines minus wild type. * and **, Significantly different from the wild type and the value expected for an additive effect, respectively (P < 0.05, Student's *t* test). Error bars are SE (n ≥ 14).
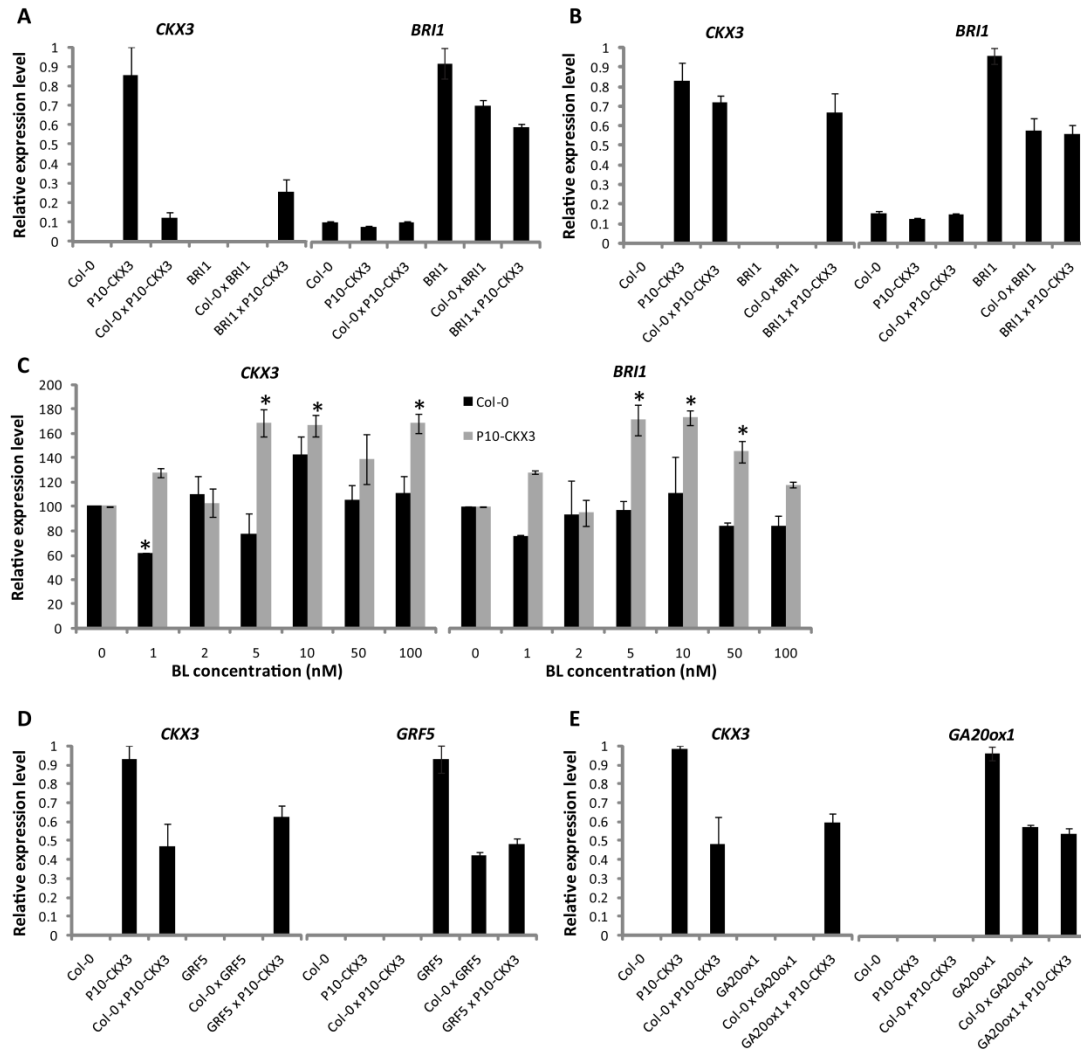
Supplemental Figure S3. Relative mRNA levels of *CKX3*, *BRI1*, *GRF5* and *GA20ox1* determined by qRT-PCR.

A and B, Expression levels of *CKX3* and *BRI1* in wild type (Col-0), *P10-CKX3*, *BRI1*, *BRI1×P10-CKX3* and the heterozygous control plants in (A) the shoot of plants at 14 DAS and (B) in roots of 9-day-old seedlings. C, *CKX3* and *BRI1* Expression levels in wild-type and *P10-CKX3* plants treated with 1 to 100 nM brassinolide (BL) relative to mock-treated controls (0 nM BL) for each line at 11 DAS. *, Significantly different from mock-treated control (P < 0.05, Mixed-model based *t* test). D and E, Relative expression levels in wild type seedlings, homo- and heterozygous parents and crossed seedlings at 5 DAS. D, *CKX3* and *GRF5* expression. E. *CKX3* and *GA20ox1* expression. Error bars are SE (n = 6 for crosses or n = 2).