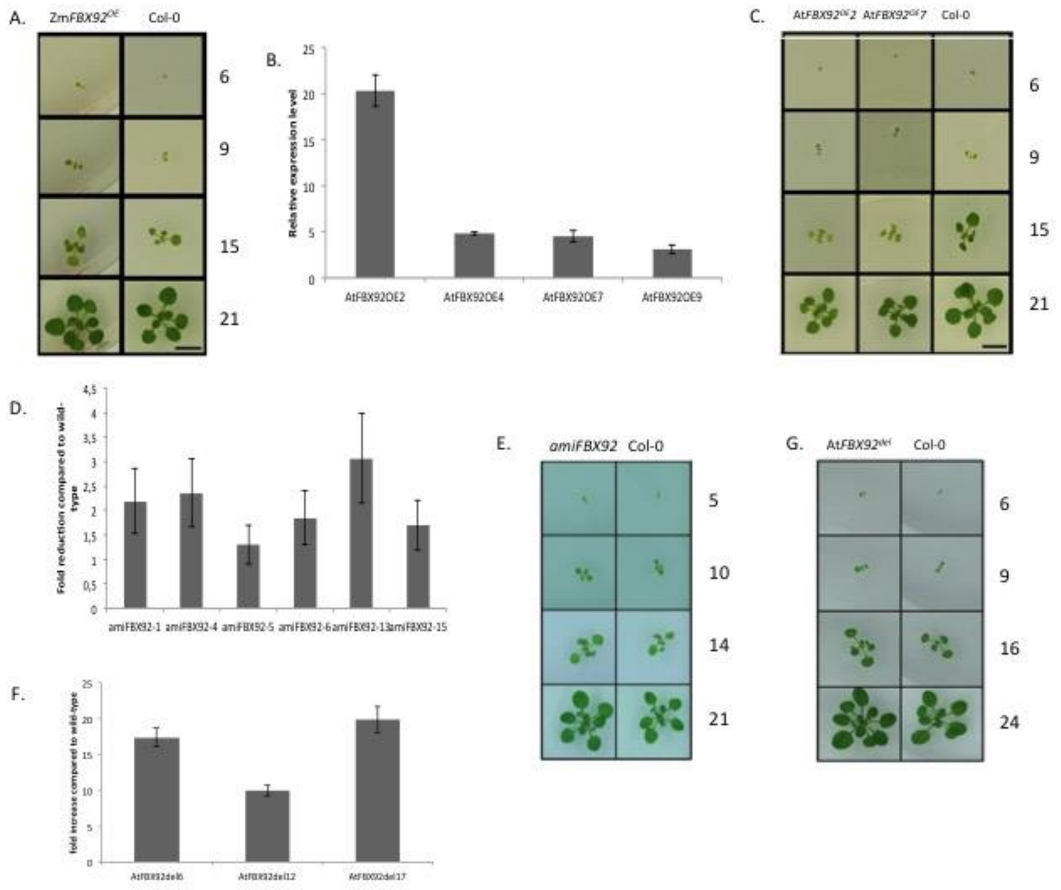
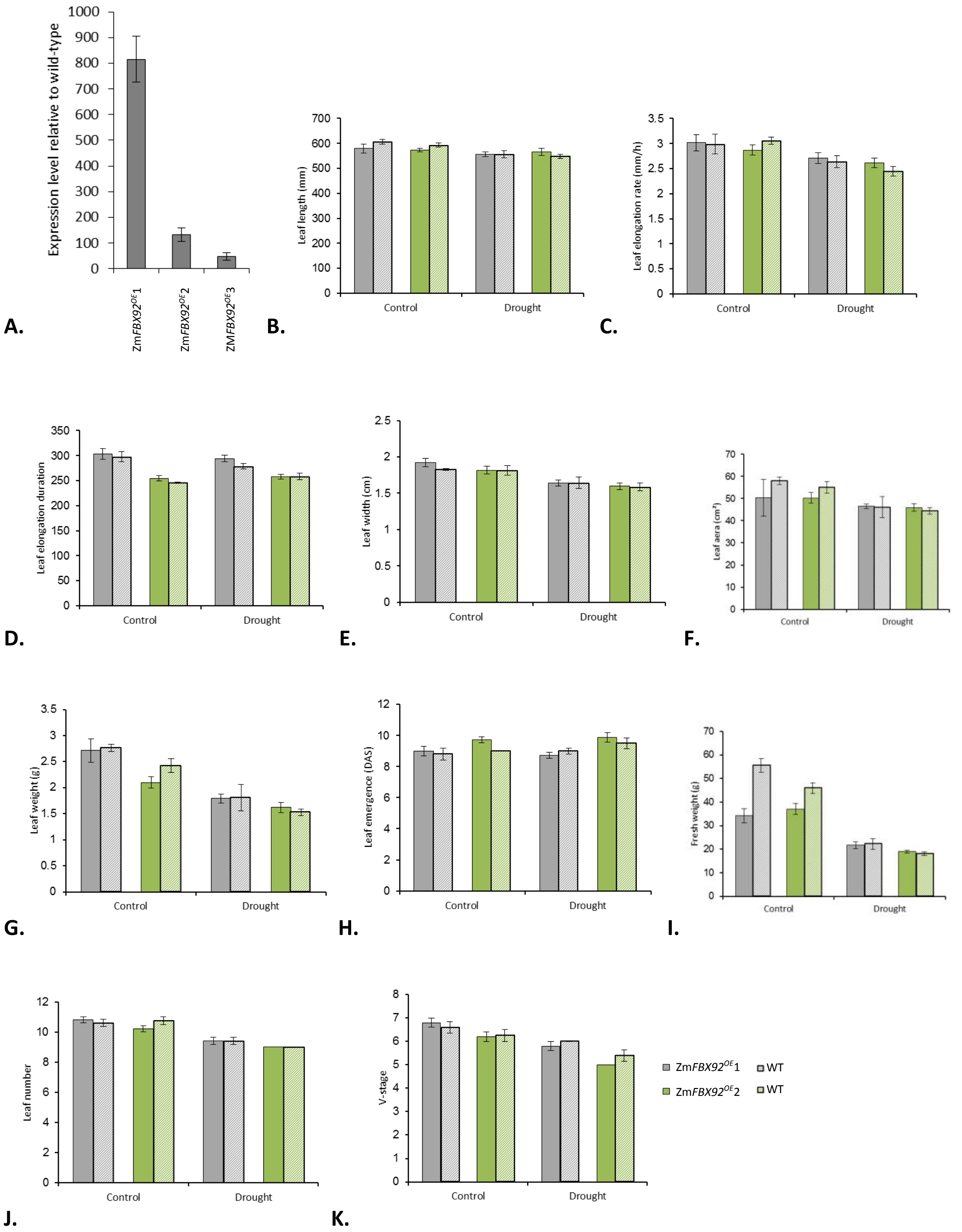
SUPPLEMENTARY DATA

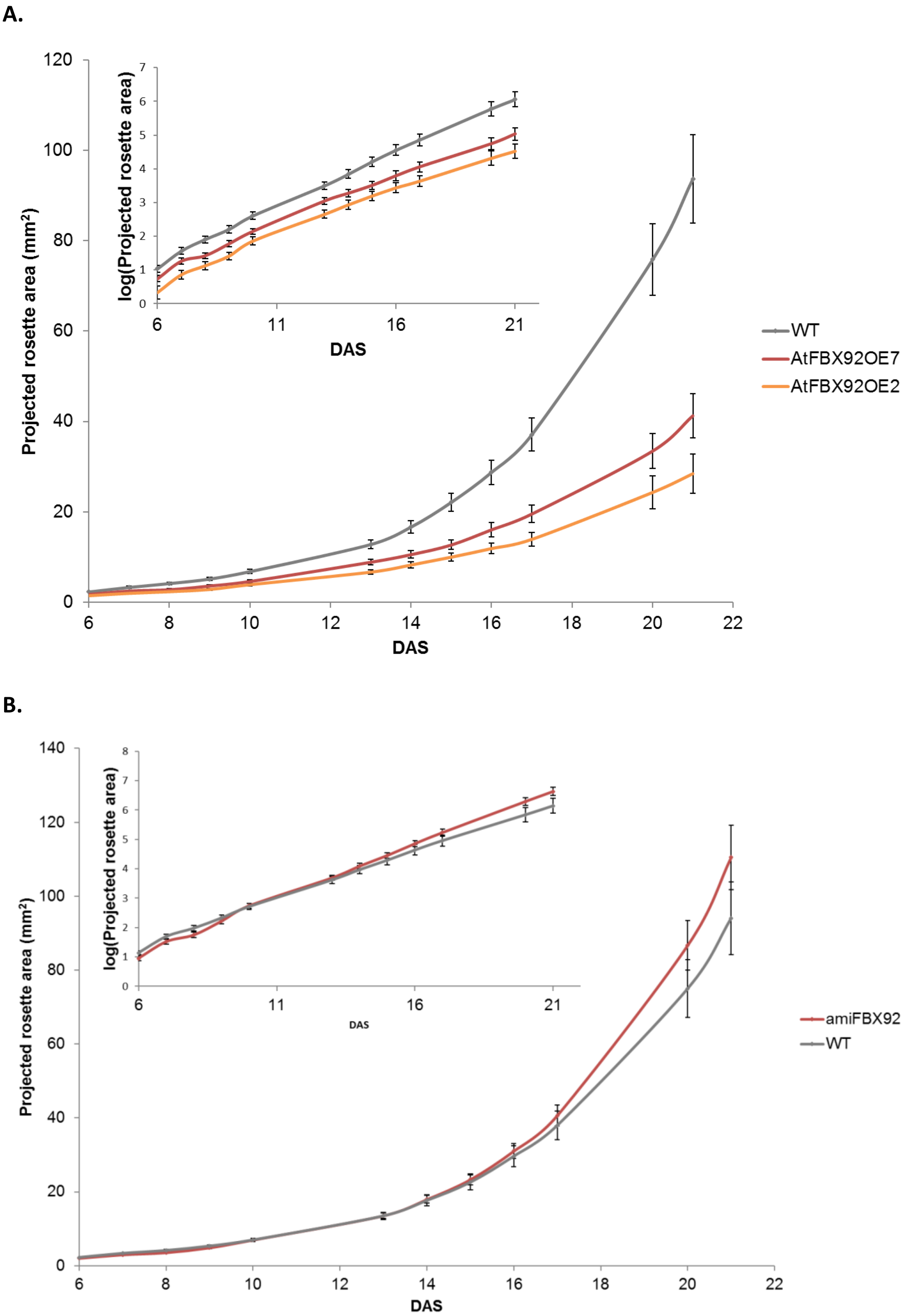


Supplementary Fig. S1. Representative pictures of Zm*FBX92*^{OE}, At*FBX92*^{OE}, *amiFBX92*, At*FBX92*^{del} and Col-0 grown *in vitro* and expression levels in mature leaves. (A) Pictures of Zm*FBX92*^{OE} and Col-0 plants grown *in vitro* at 6, 9, 15 and 21 DAS. Scale bar 1 cm. (B) qRT-PCR analysis of the At*FBX92* expression in mature leaves of four At*FBX92*^{OE} lines relative to wild type. (C) Pictures of At*FBX92*^{OE} and Col-0 plants grown *in vitro* at 6, 9, 15 and 21 DAS. Scale bar 1 cm. (D) qRT-PCR analysis of the At*FBX92* expression in mature leaves of six *amiFBX92* lines relative to wild type. (E) Pictures of *amiFBX92* and Col-0 plants grown *in vitro* at 5, 10, 14 and 21 DAS. Scale bar 1 cm. (F) qRT-PCR analysis of the At*FBX92* expression in mature leaves of three At*FBX92*^{del} lines relative to wild type. (G) Pictures of At*FBX92*^{del} and Col-0 plants grown *in vitro* at 6, 9, 16 and 24 DAS. Scale bar 1cm.



Supplementary Fig. S2. Effect of Zm*FBX92* overexpression on maize leaf size and shoot weight under control and mild drought conditions. (A) Expression level of Zm*FBX92* in mature leaves of Zm*FBX92*^{OE}plants relative to wild type as determined by qRT-PCR. Values were normalized against expression levels of housekeeping genes. Data are average fold change (transgenic versus wild-type plants) ± SE ($n_{transgenic}$ = 3 and $n_{wild\text{-}type}$ = 9-20). (B to H) Measurement of final leaf 4-related parameters: length (B), elongation rate (C), elongation duration (D), width (E), area (F), weight (G), and emergence

(H). Data are average ± SE ($n_{transgenic}$ = 20 and $n_{wild\text{-}type}$ = 20. (I to K) Measurement of shoot-related parameters at seedling stage: fresh weight (I), leaf number (J) and V-stage (K). Data are average ± SE ($n_{transgenic}$ = 20 and $n_{wild\text{-}type}$ = 20).



Supplementary Fig. S3. Effect of perturbed At*FBX92* expression on rosette growth under mild osmotic stress conditions. (A) PRA of At$FBX92^{OE}$ lines and WT over time from 6 until 21 DAS. Plants were grown *in vitro* on medium containing 25 mM mannitol. Inset: PRA in log scale. Values represent the mean ± SE ($n_{\text{transgenic lines}}$ = 26-32, n_{WT} = 40). (B) PRA of *amiFBX92* and WT over time from 6 until 21 DAS. Plants were grown *in vitro* on medium containing 25 mM mannitol. Inset: PRA in log scale. Values represent the mean ± SE (n = 29).

```
                                  10        20        30
ZmFBX92   -----------------MAEAAGGGPLLPEELVIWEILTRLPAKPLLRCR
                                ::   :::. .: .: .:::   . :
AtFBX92   MASEKSFKKRKITDDVDGVGVGGGLESLPED-IIADIFSRLPISSIARLM
                  10        20        30         40

            40        50        60        70        80
ZmFBX92   AVCLSWRRRLTSDAKFLLAHHRRQPSLPLLTQGDRSTEDRRIDALDYRTG
           :: :::  ::   .  :.     :. : :     :     .  ::
AtFBX92   FVCRSWRSVLTQHGR--LSSSSSSPTKPCLLLHCDSPIRNGLHFLDLSEE
            50        60          70        80        90

                90       100       110          120
ZmFBX92   E-RLPVARTTGRTAANADDLNVLASCDGLLVL---IANGGLHICNPATRQ
          : :.   . : : :..  . .:. ::.::: :   . :  :.. :: :
AtFBX92   EKRIKTKKFTLRFASSMPEFDVVGSCNGLLCLSDSLYNDSLYLYNPFTTN
          100       110       120       130       140

        130            140       150       160       170
ZmFBX92   RAPLA----LLHGASCISALYPYRPSGSYRVAGALLLRESRGRPRRVPRA
             :       :    .     .  .  :.:   .  : :      . :
AtFBX92   SLELPECSNKYHDQELVFGFGFHEMTKEYKVLKIVYFRGSSSNNNGIYRG
          150       160       170       180       190

                180       190       200       210       220
ZmFBX92   HRRV----ARAQVRRRTSRAVGVRRRGDGDADDVVLSPARRGRQQDLLAA
            :.    .  :.   .:.             :  ::    :.     :
AtFBX92   RGRIQYKQSEVQILTLSSKTT-----------DQSLSWRSLGK-----AP
          200       210                  220            230

                230       240       250
ZmFBX92   GKAARRQREGQQHARVRYSDRVLPATAVAPARGGPLP*------------
           :  .:  :   . :. .  :        : :  :
AtFBX92   YKFVKRSSEALVNGRLHFVTR--------PRRHVPDRKFVSFDLEDEEFK
                240       250               260       270


ZmFBX92   --------------------------------------------------

AtFBX92   EIPKPDCGGLNRTNHRLVNLKGCLCAVVYGNYGKLDIWVMKTYGVKESWG
              280       290       300       310       320


ZmFBX92   --------------------------------------------------

AtFBX92   KEYSIGTYLPKGLKQNLDRPMWIWKNAENGKVVRVLCLLENGEILLEYKS
              330       340       350       360       370


ZmFBX92   ---------------------------------------------

AtFBX92   RVLVAYDPKLGKFKDLLFHGLPNWFHTVVHAGTLSWFDTPLDLW*
              380       390       400       410
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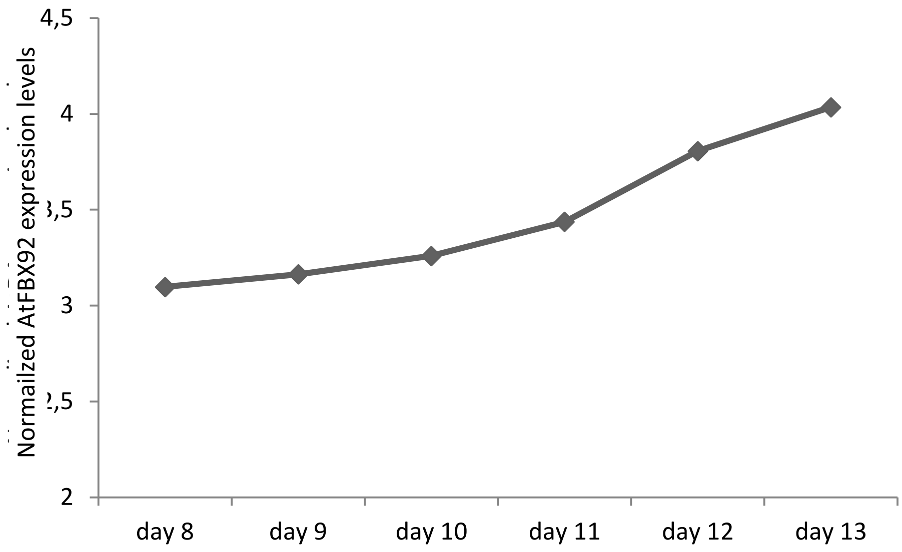
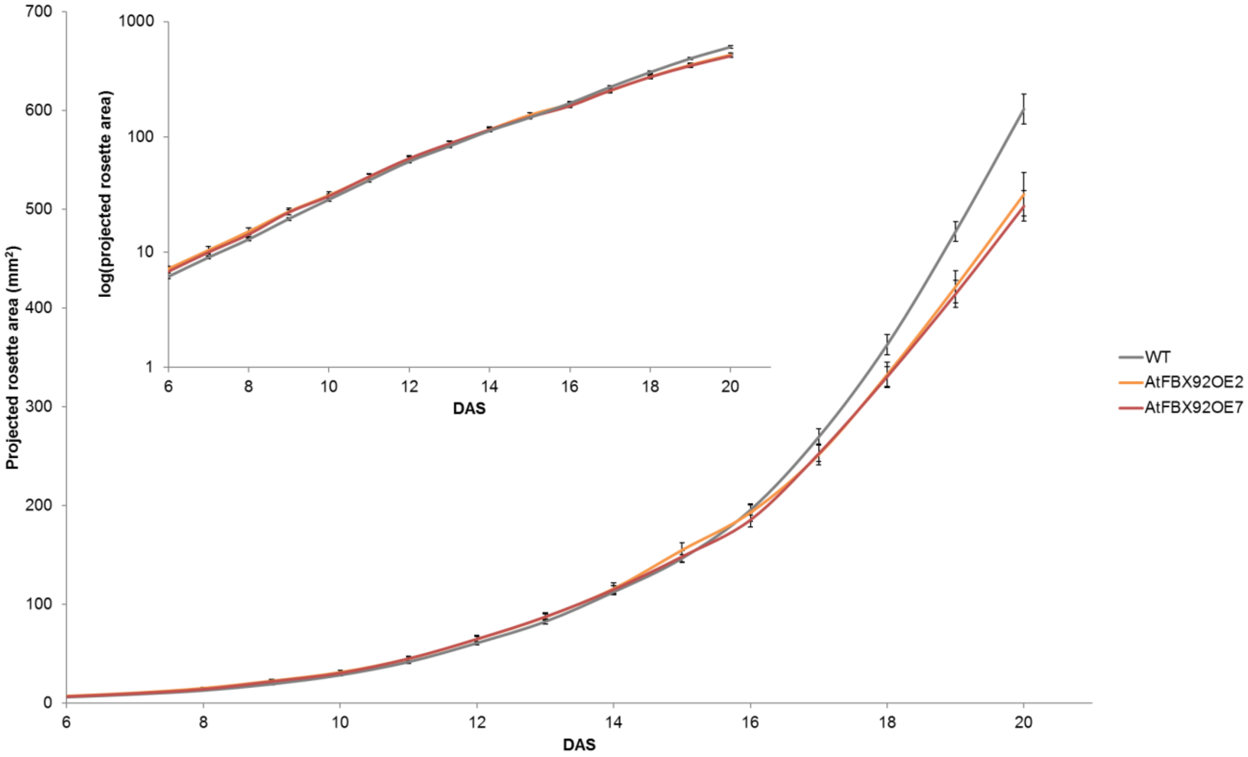
Supplementary Fig. S4. Amino acid alignment of the Zm*FBX92* and At*FBX92* proteins using EMBOSS Needle. Protein domains were determined using the Pfam database (Finn et al., 2014). The F-box domains are indicated in yellow, the F-box associated domain of At*FBX92* in red. Identical amino acids are indicated by “:”, similar amino acids by “.”.

Supplementary Fig. S5. Amino acid sequence comparison of the ZmFBX92 and AtFBX92 proteins. Schematic representation of the protein domains in Zm*FBX92*, At*FBX92* and At*FBX92*^{del} drawn to scale.

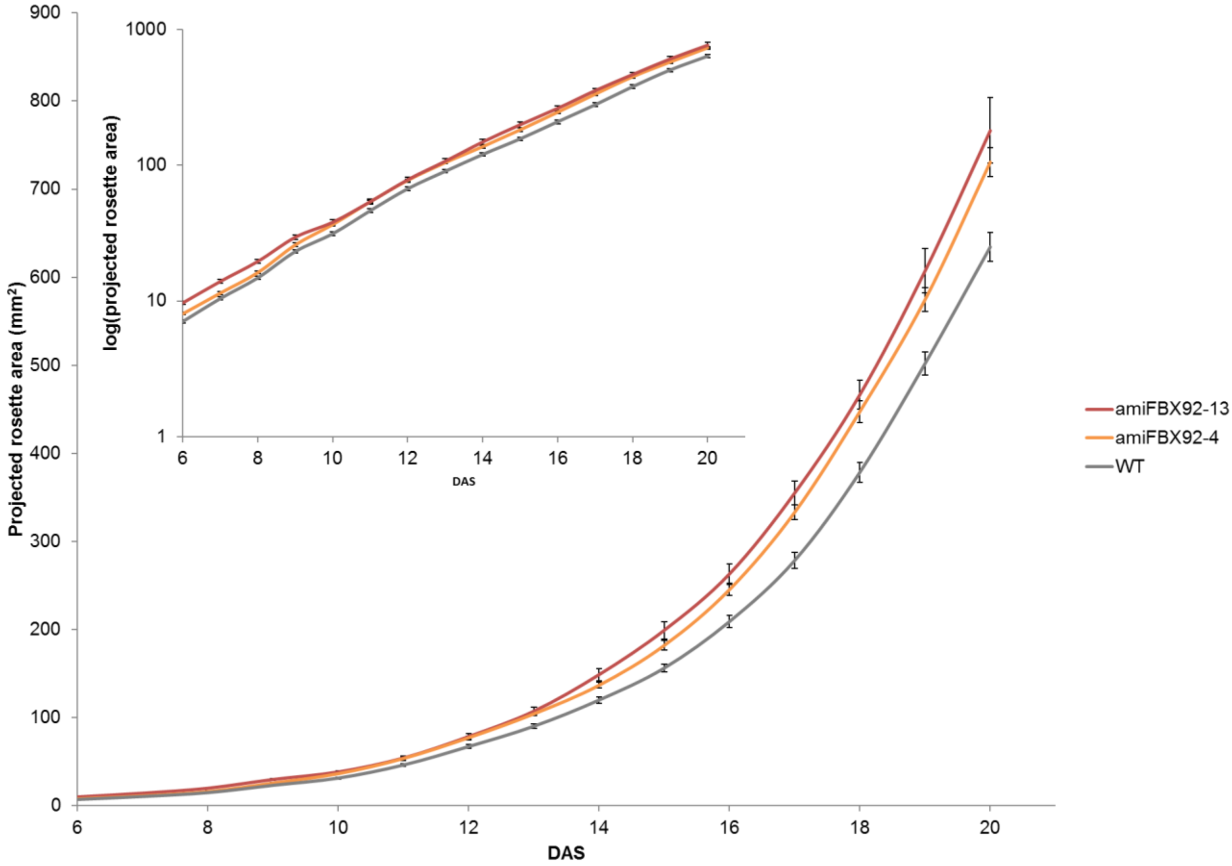


Supplementary Fig. S6. At*FBX92* expression levels in leaf 3 during the subsequent phases of leaf development. Normalized expression levels as calculated from AGRONOMICS1 tiling arrays by Andriankaja et al. (2012).

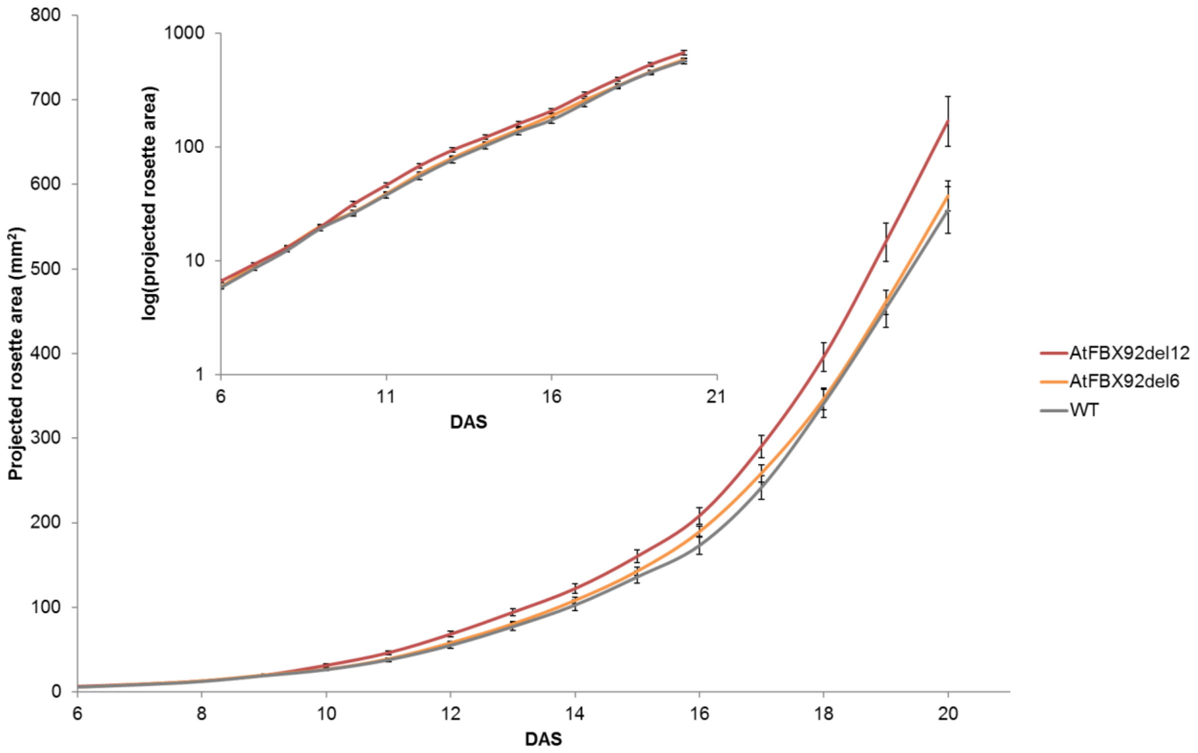
A.


Projected rosette area (mm²)
700
600
500
400
300
200
100
0
6
8
10
12
14
16
18
20
DAS
log(projected rosette area)
1000
100
10
1
6
8
10
12
14
16
18
20
DAS
WT
AtFBX92OE2
AtFBX92OE7

B.

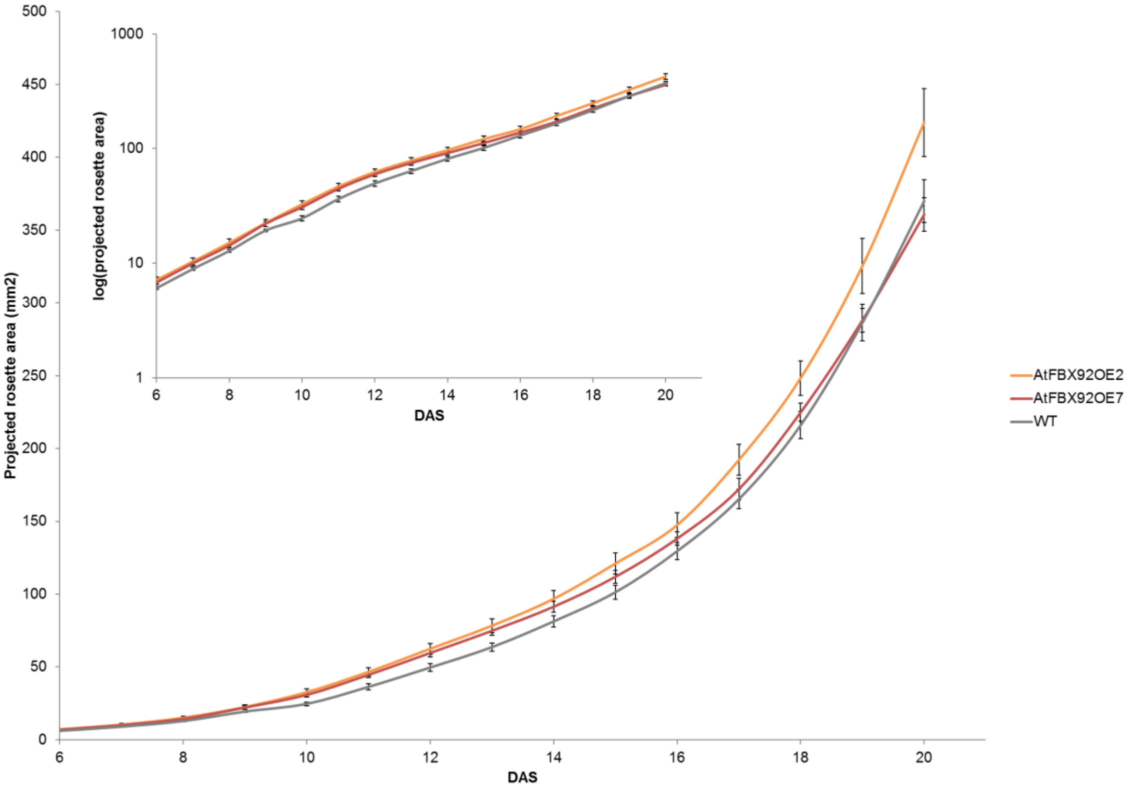

Projected rosette area (mm²)
900
800
700
600
500
400
300
200
100
0
6
8
10
12
14
16
18
20
DAS
log(projected rosette area)
1000
100
10
1
6
8
10
12
14
16
18
20
DAS
amiFBX92-13
amiFBX92-4
WT

C.

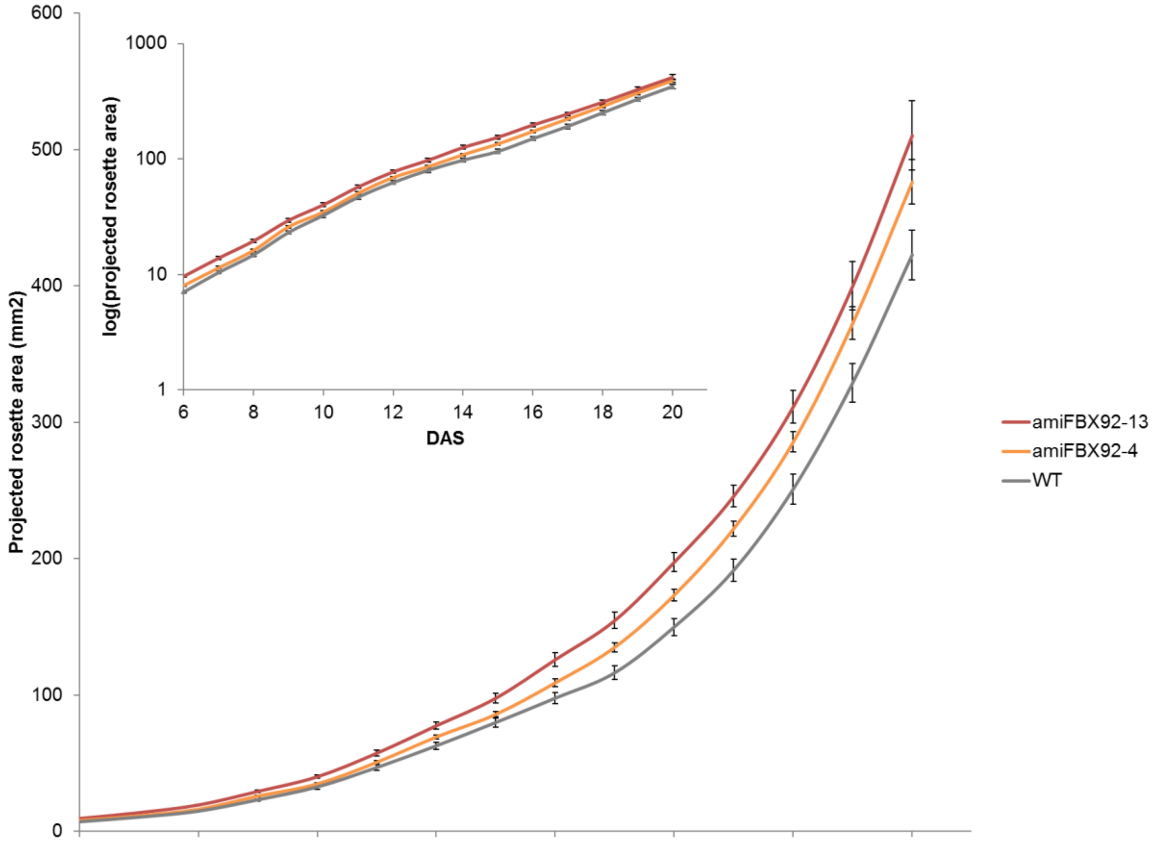


Supplementary Fig. S7. Effect of At*FBX92* perturbation on rosette growth under standard conditions in soil. (A) PRA of At*FBX92*^{OE} and WT plants grown in soil from 6 until 20 DAS. Plants were grown in standard. Inset: PRA in log scale. Values represent the mean ± SE (n = 16). (B) PRA of *amiFBX92* and WT plants grown in soil from 6 until 20 DAS. Plants were grown in standard conditions. Inset: PRA in log scale. Values represent the mean ± SE (n = 16). (C) PRA of At*FBX92*^{del} and WT plants grown in soil from 6 until 20 DAS. Plants were grown in standard conditions. Inset: PRA in log scale. Values represent the mean ± SE (n = 16).

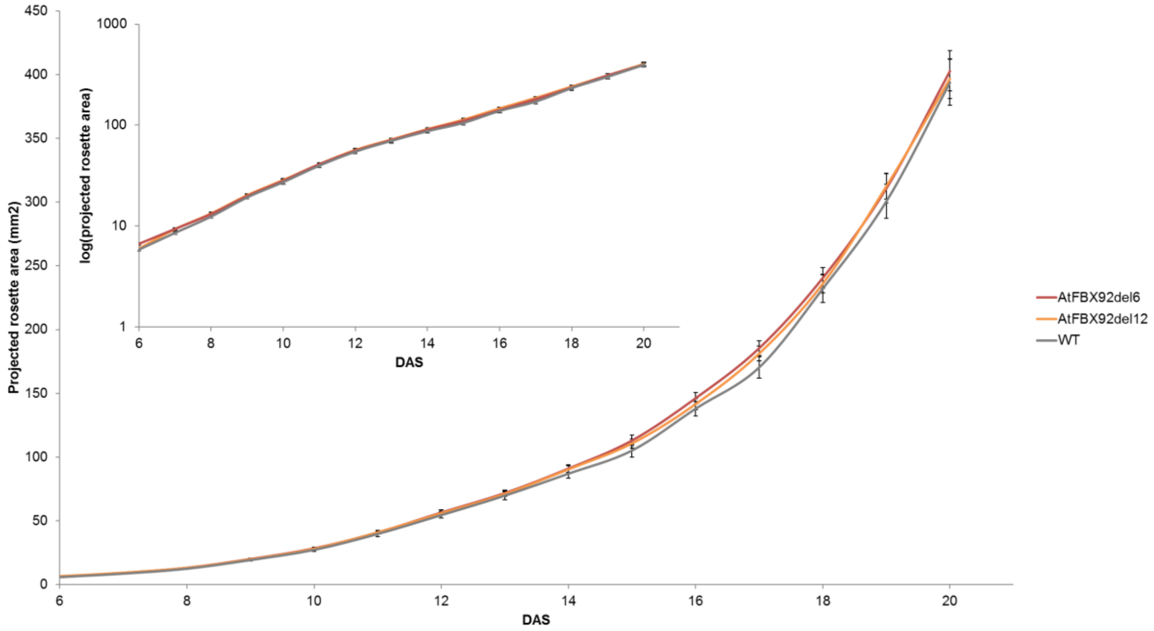
A.


Projected rosette area (mm2)
500
450
400
350
300
250
200
150
100
50
0
6
8
10
12
14
16
18
20
DAS
log(projected rosette area)
1000
100
10
1
6
8
10
12
14
16
18
20
DAS
AtFBX92OE2
AtFBX92OE7
WT

B.

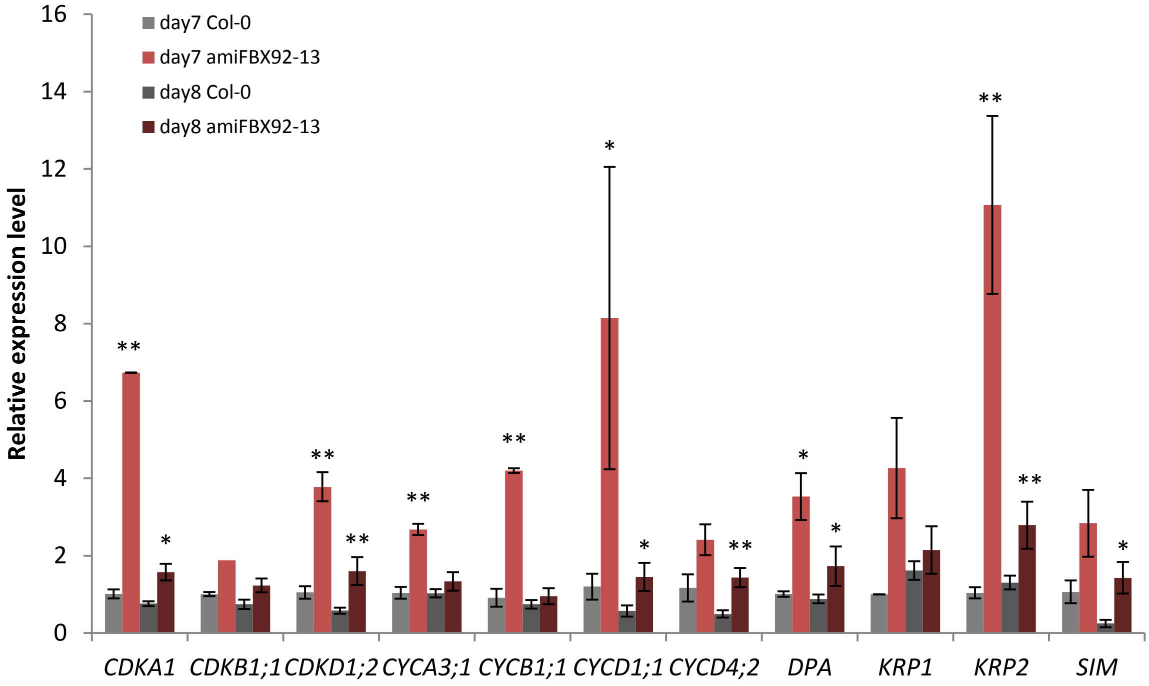

Projected rosette area (mm2)
600
500
400
300
200
100
0
6
8
10
12
14
16
18
20
DAS
log(projected rosette area)
1000
100
10
1
6
8
10
12
14
16
18
20
DAS
amiFBX92-13
amiFBX92-4
WT

C.

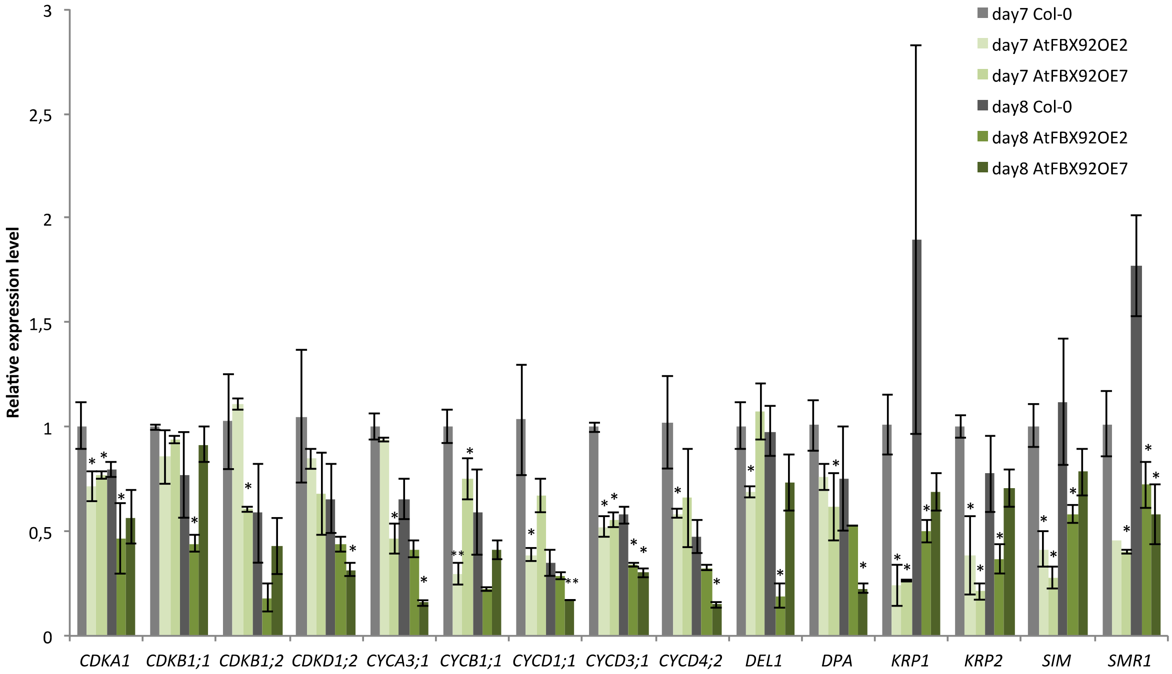


Supplementary Fig. S8. Effect of At*FBX92* perturbation on rosette growth under mild drought conditions in soil. (A) PRA of At*FBX92*^{OE} and WT plants grown in soil from 6 until 20 DAS. Plants were grown under mild drought conditions from 10 DAS onwards. Inset: PRA in log scale. Values represent the mean ± SE (n = 16). (B) PRA of *amiFBX92* and WT plants grown in soil from 6 until 20 DAS. Plants were grown under mild drought conditions from 10 DAS onwards. Inset: PRA in log scale. Values represent the mean ± SE (n = 16). (C) PRA of At*FBX92*^{del} and WT plants grown in soil from 6 until 20 DAS. Plants were grown under mild drought conditions from 10 DAS onwards. Inset: PRA in log scale. Values represent the mean ± SE (n = 16).

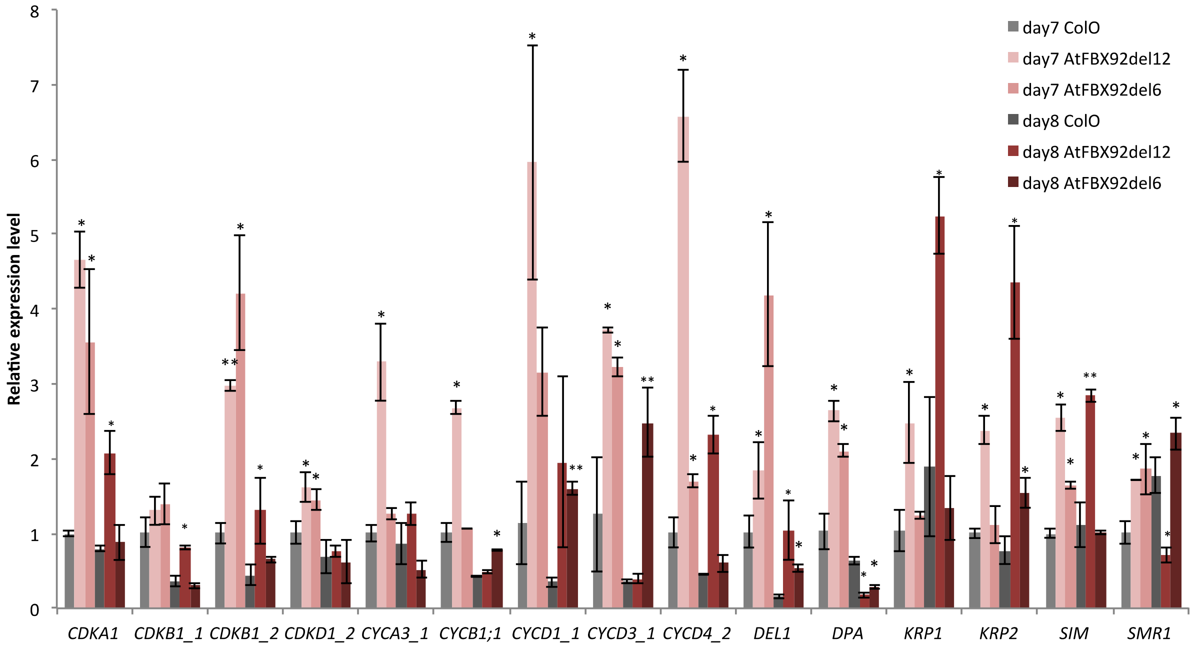
A.


Relative expression level
0
2
4
6
8
10
12
14
16
day7 Col-0
day7 amiFBX92-13
day8 Col-0
day8 amiFBX92-13
CDKA1
CDKB1;1
CDKD1;2
CYCA3;1
CYCB1;1
CYCD1;1
CYCD4;2
DPA
KRP1
KRP2
SIM

B.


Relative expression level
0
0,5
1
1,5
2
2,5
3
day7 Col-0
day7 AtFBX92OE2
day7 AtFBX92OE7
day8 Col-0
day8 AtFBX92OE2
day8 AtFBX92OE7
CDKA1
CDKB1;1
CDKB1;2
CDKD1;2
CYCA3;1
CYCB1;1
CYCD1;1
CYCD3;1
CYCD4;2
DEL1
DPA
KRP1
KRP2
SIM
SMR1

C.



Supplementary Fig. S9. Relative expression levels of cell cycle genes in the first leaf pair of *amiFBX92-13* (A), At*FBX92*^{OE}*2* and At*FBX92*^{OE}*7* (B) and At*FBX92*^{del}*12* and At*FBX92*^{del}*6* (C) compared to WT at 7 and 8 DAS as determined by qRT-PCR. Values were normalized against the expression level of the housekeeping gene and represent mean expression levels of indicated transcripts of three technical repeats ± SE. Significant differences (Student's *t*-test): *, $P < 0.10$; **, $P < 0.01$ relative to WT.

Supplementary Table S1. Primer Sequences.

Construct	**Application**	**Forward primer**	**Reverse primer**
Zm*FBX92*^{OE}	cloning	AAAAAGCAGGCTTCATCTCTCCCAGATCCGATC	GAAAGCTGGGTCCCGCTGTTCATCTGAAACAG
Zm*FBX92*	qRT-PCR	GATGCCGATGATGTTGTG	CTGTTGCTGGAAGGACTC
18S rRNA	qRT-PCR	ACCTTACCAGCCCTTGACATATG	GACTTGACCAAACATCTCACGAC
At*FBX92*^{OE}	cloning	AAAAAGCAGGCTATGGCTTCAGAG	GAAAGCTGGGTCGAAGATGTACCC
At*FBX92*^{del}	cloning	AAAAAGCAGGCTATGGCTTCAGAG	GAAAGCTGGGTCTTAGACAAGTTCTTGGTCG
amiFBX92	cloning	gaTACTAGTCTATGGTTGGGCCGtctctcttttgtattcc	gaCGGCCCAACCATAGACTAGTAtcaaagagaatcaatga
amiFBX92	cloning	gaCGACCCAACCATACACTAGTTtcacaggtcgtgatatg	gaAACTAGTGTATGGTTGGGTCGtctacatatatattcct
pAt*FBX92*	cloning	AAAAAGCAGGCTAAAATGTCTTGCAGCTG	GAAAGCTGGGTCCTAGCTCCTCGAATGAAGAGAATCAGAAG
At*FBX92*	qRT-PCR	GCGCGGTCGTTTATGGTAAC	GCTTTAGCCCCTTTGGCAAG
At*FBX92*^{del}	qRT-PCR	GCAACGGTCTTCACTTCCTC	TGGTCGTGGTACTTGTTGGA
CDKA1	qRT-PCR	TGATCAGCCAAAAGCCCTTA	ACGGAGTTCCCATGATTCTG
ACTIN1	qRT-PCR	GTTGACTACGAGCAGGAGATGG	ACAAACGAGGGCTGGAACAAG
CDKB1;1	qRT-PCR	GCATTGCTTCATATCTTCAGGTT	CAGTCACGCAGTGTGGAAAC
CDKB1;2	qRT-PCR	CCAATGAAGAAGTATACCCATGAG	AATGGGTGGCACCAAGAAG
CDKD1;2	qRT-PCR	CAGATTCCAGCTTCCAAAGG	TGAATCCTTCAGGACCCATC
CYCA3;1	qRT-PCR	GCCGACGAAAAAGAGAACTG	CTTTGTCTATTGCCGCTTCC
CYCB1;1	qRT-PCR	GCTTCTGCAATCTACGCAGC	CCAACAGCTTTGCACAGTCC
CYCD1;1	qRT-PCR	GCGAACGAGTTACCTTCTCTATCC	GCTCAATCCGTCACACCAAGTC
CYCD3;1	qRT-PCR	CGAAGAATTCGTCAGGCTCT	ACTTCCACAACCGGCATATC
CYCFBX92;2	qRT-PCR	CCTAGTGGAAAAGCTTGGACTG	TTAGCCTCAAACACGAACATGG
DEL1	qRT-PCR	TGATGACGCTGCAAAATTACTG	CATAAAGCCGCCTCACTTTAGTT
DPA	qRT-PCR	GCAAGAACAGAAGCAAGAACAGAAC	CGGTCAGCGAGTATCAATGGATC
KRP1	qRT-PCR	GTGGAAGCAATGAATATAAGAAGAAA	CGACGTTTCAGTGTCACCAT
KRP2	qRT-PCR	CGTGGATTTACGATGATTTGAA	GCGGCGAGACTCTACATCTT
SIM	qRT-PCR	CCCACTTCTTCCGACCACAA	GCCGAGAGACGACGGTGT
SMR1	qRT-PCR	GCTACGCCGGCTCTGATG	CGGAGGAGAAGAAACGGTCA