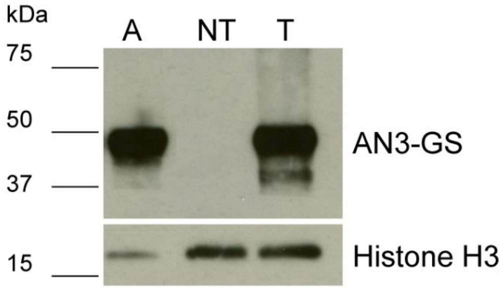
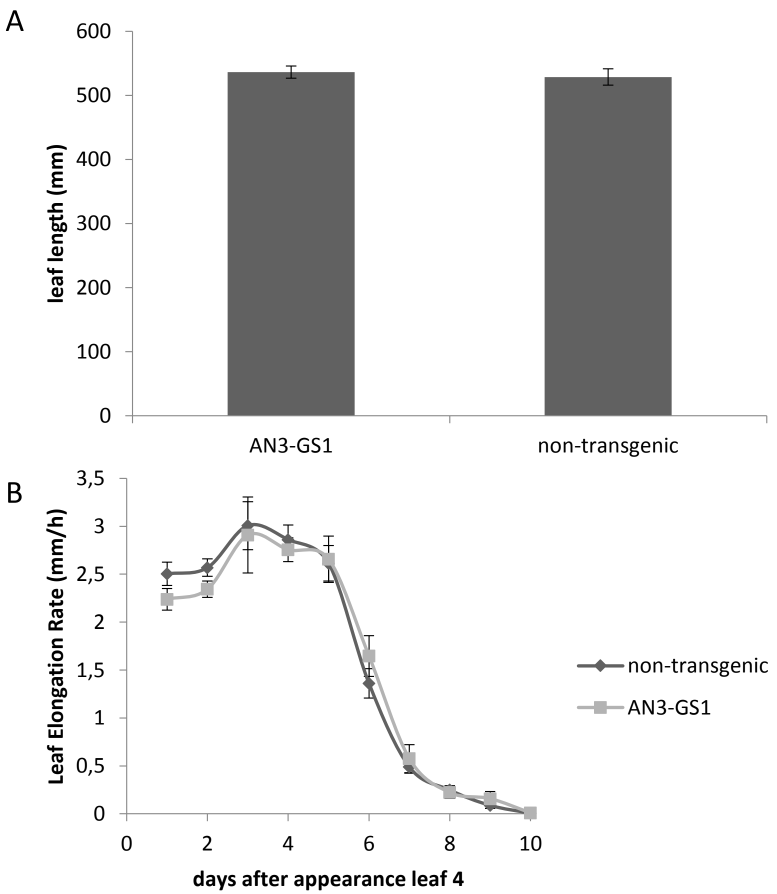


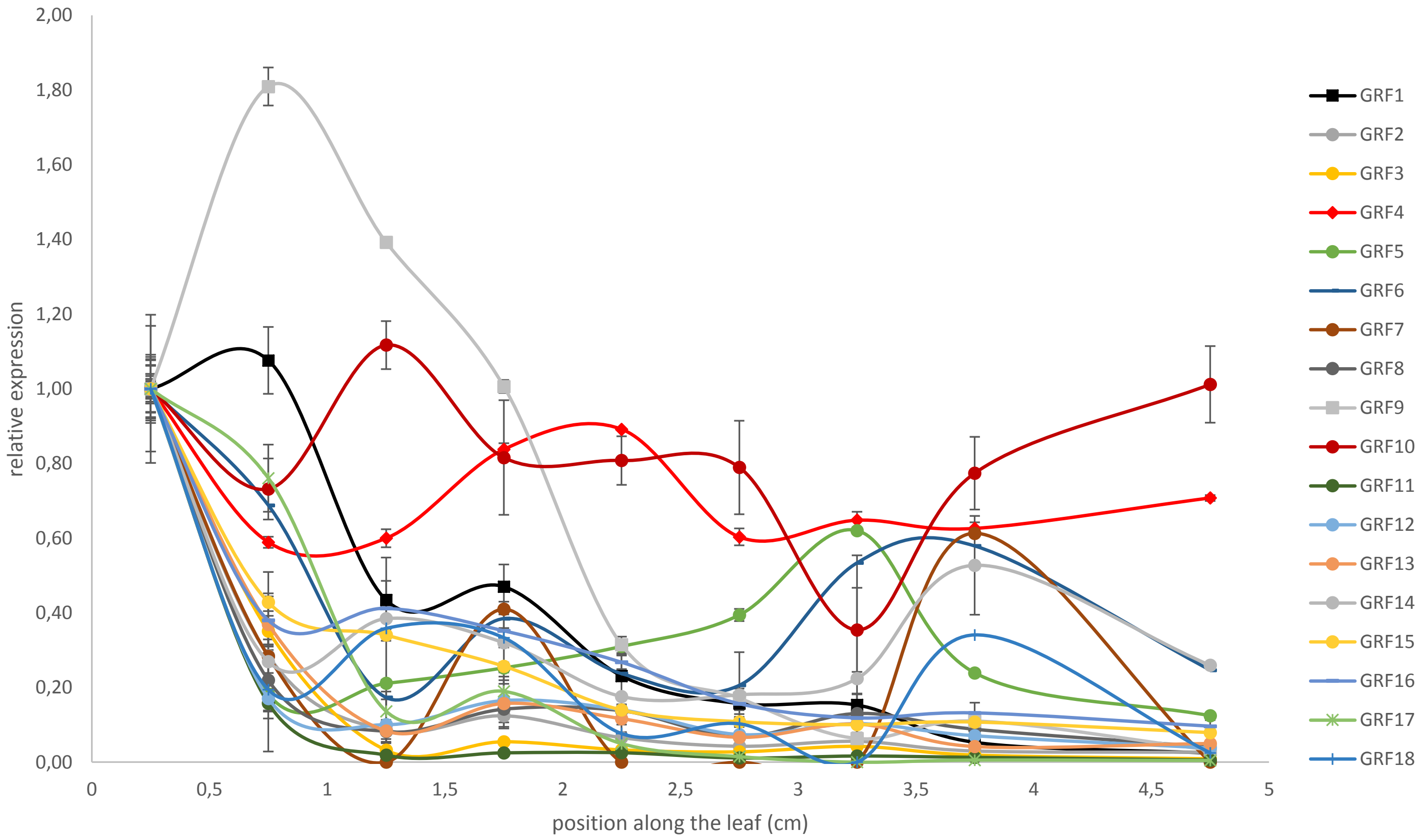
Supplemental Figure 1. Expression Analysis of the *AN3-GS1* maize line that was used for TAP. NT: protein extract from non-transgenic siblings from the segregating *AN-GS1* population; T: protein extract from transgenic siblings from the segregating *AN-GS1* population; A: protein extract from *Arabidopsis PSB-D* cell cultures transformed with the Ath_AN3 bait fused to the GS TAP-tag; Histone H3 immunodetection was used as a protein loading control.



C

days after sowing to reach developmental stage	germination	leaf2	leaf4	tassel
non-transgenics	5,64	8,43	10,93	60,20
AN3-GS1	5,60	8,40	10,40	67,60
p-value	0,82	0,88	0,03	0,25

Supplemental Figure 2. Phenotype of the *AN3-GS1* Plants Compared to Their Non-Transgenic Siblings. Final length of leaf 4 **(A)**, leaf elongation rate of leaf 4 **(B)** and plant development over time **(C)**. ≥10 plants were used per analysis. DAS: days after sowing. Error bars represent standard error.



Supplemental Figure 3. Expression levels of the GRF genes over the maize leaf growth zone in B104 at steady state growth of leaf 4. Error bars represent standard error.

Raw data for Supplemental Figure 3: Expression levels of the *GRF* genes over the maize leaf growth zone in B104 at steady state growth of leaf 4. Error bars represent standard error (SE).

average	**GRF1**	**GRF2**	**GRF3**	**GRF4**	**GRF5**	**GRF6**	**GRF7**	**GRF8**	**GRF9**	**GRF10**	**GRF11**	**GRF12**	**GRF13**	**GRF14**
0,25	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00
0,75	1,08	0,28	0,35	0,59	0,18	0,69	0,28	0,22	1,81	0,73	0,16	0,17	0,37	0,27
1,25	0,43	0,09	0,03	0,60	0,21	0,17	#DIV/0!	0,08	1,39	1,12	0,02	0,10	0,08	0,38
1,75	0,47	0,12	0,05	0,84	0,25	0,38	0,41	0,14	1,01	0,82	0,03	0,16	0,16	0,32
2,25	0,23	0,07	0,03	0,89	0,31	0,24	#DIV/0!	0,14	0,31	0,81	0,03	0,14	0,12	0,18
2,75	0,16	0,04	0,03	0,60	0,39	0,21	#DIV/0!	0,07	0,17	0,79	0,01	0,07	0,07	0,18
3,25	0,15	0,06	0,04	0,65	0,62	0,53	#DIV/0!	0,13	0,06	0,35	0,02	0,10	0,10	0,22
3,75	0,05	0,03	0,02	0,63	0,24	0,58	0,61	0,09	0,11	0,77	0,01	0,07	0,04	0,53
4,75	0,02	0,03	0,01	0,71	0,12	0,25	#DIV/0!	0,04	0,03	1,01	0,01	0,04	0,05	0,26
SE	**GRF1**	**GRF2**	**GRF3**	**GRF4**	**GRF5**	**GRF6**	**GRF7**	**GRF8**	**GRF9**	**GRF10**	**GRF11**	**GRF12**	**GRF13**	**GRF14**
0,25	0,03	0,06	0,04	0,03	0,00	0,04	0,08	0,06	0,04	0,08	0,00	0,09	0,20	0,17
0,75	0,09	0,07	0,04	0,01	#DIV/0!	0,05	0,04	0,08	0,05	0,08	0,02	0,05	0,05	0,24
1,25	0,05	0,02	0,02	0,02	0,01	0,03	#DIV/0!	0,03	0,01	0,06	0,00	0,09	0,08	0,16
1,75	0,06	0,02	0,01	0,02	0,01	0,02	#DIV/0!	0,03	0,02	0,15	0,00	0,08	0,06	0,11
2,25	0,01	0,01	0,00	0,00	0,01	0,00	#DIV/0!	0,01	0,02	0,06	0,00	0,04	0,04	0,11
2,75	0,01	0,02	0,01	0,02	0,02	0,04	#DIV/0!	0,03	0,03	0,13	0,00	0,06	0,05	0,11
3,25	0,03	0,02	0,02	0,02	0,01	0,04	#DIV/0!	0,05	0,00	0,11	0,00	0,04	0,02	0,33
3,75	0,01	0,01	0,01	0,02	0,01	0,01	#DIV/0!	0,03	0,02	0,10	0,00	0,02	0,03	0,13
4,75	0,00	0,01	0,00	0,01	0,00	0,04	#DIV/0!	0,01	#DIV/0!	0,10	0,00	0,00	0,00	0,00

Supplemental Table 1: Tandem Affinity Purification with ZmAN3 as bait. Additional proteins for which no orthologous interaction in *Arabidopsis* or human could be detected. cm1 corresponds to dividing cells, cm4 to expanding cells.

Leading protein ID	**Description**	**LEAF entire growth zone**	**LEAF division zone**	**LEAF expansion zone**	**EAR**	**At ortholog (BHIF)**	***Arabidopsis* TAP**	
		# 4cm Exps with id (in 2 Exps)	**# cm1 Exps with id (in 4 Exps)**	**# cm4 Exps with id (in 4 Exps)**	**# Exps with id (in 6 exps)**			
GRMZM2G138419	Osmotin-like protein	2	4	4	5	AT2G28790		additional proteins
GRMZM2G084767	Importin subunit beta-1	2	4	3	6	AT3G08947		
GRMZM2G441753	TRIBOA-glucoside O-methyltransferase BX7	2	4	4	2	(AT4G35160)		
GRMZM2G116079	putative zinc finger protein30	1	4	1	5	AT3G15680		
GRMZM2G030144	AP-1 complex subunit gamma	1	3	1	5	AT1G60070		
GRMZM2G139643	ribonucleoprotein A1, A2/B1 homolog	0	2	1	6	AT3G13224		
GRMZM2G020940	hydroxyproline-rich glycoprotein family protein	1	3	0	3	AT2G39050		
GRMZM2G347105	0	2	1	4	0	0		
GRMZM2G325131	synthase component 2	1	3	2	0	AT5G57890		
GRMZM5G895313	COLD SHOCK DOMAIN PROTEIN 1	1	4	0	0	AT2G21060		
GRMZM2G031545	elongation factor 1-delta 1	0	3	2	0	AT2G18110		
GRMZM2G078274	Auxin response factor	0	3	0	0	AT5G37020		
GRMZM2G023214	15-cis-phytoene desaturase	1	1	1	0	AT5G14060		
GRMZM5G881775	40S ribosomal protein S19	0	0	0	6	0		
GRMZM2G389768	Cold shock	0	0	0	6	AT4G36020		
GRMZM5G832672	FRIGIDA-like protein 4b	0	0	0	6	AT3G22440		
GRMZM2G057448	histone-arginine methyltransferase CARM1	0	0	0	6	AT5G49020		
GRMZM2G067624	SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8	0	0	0	6	AT1G53160		
GRMZM2G042992	TOPLESS	0	0	0	6	AT1G15750		
GRMZM2G334216	tract-binding protein homolog 3	0	0	0	6	AT1G43190		
GRMZM2G099860	trehalose-6-phosphate synthase	0	0	0	6	AT1G68020		
GRMZM5G866100	Uridine kinase-like protein 2, chloroplastic	0	0	0	6	AT3G27190		
GRMZM2G549512	WRKY transcription factor 4	0	0	0	6	AT1G13960		
GRMZM2G064993	annexin p33	0	0	0	5	AT5G10230		
GRMZM2G159028	RNA binding protein	0	0	0	5	AT5G66010		
GRMZM2G136831	Serine/threonine-protein kinase WNK-related	0	0	0	5	AT1G60060		
GRMZM2G073750	Auxin response factor	0	0	0	4	AT1G30330		
GRMZM2G026556	Regulatory protein NPR6	0	0	0	4	AT2G41370		
GRMZM2G073792	transposable element	0	0	0	4	0		
GRMZM2G094497	vacuolar ATP synthase subunit B	0	0	0	4	AT4G38510		
GRMZM2G119499	glutathione transferase11	0	0	0	3	AT3G03190		
GRMZM2G589579	Protein argonaute	0	0	0	3	AT2G27040		
GRMZM2G163406	Salt stress-induced protein	0	0	0	3	AT1G19715		
GRMZM2G154007	Alcohol dehydrogenase class-3	0	0	0	2	AT5G42250		
GRMZM2G018950	Carboxypeptidase Y homolog A	0	0	0	2	AT3G45010		
GRMZM2G020146	Carboxypeptidase Y homolog A	0	0	0	2	AT3G45010		
GRMZM2G430027	damage-binding protein 1	0	0	0	2	AT4G05420		
GRMZM2G348666	Isoleucine--tRNA ligase	0	0	0	2	AT4G10320		
GRMZM2G112074	licensing factor MCM7	0	0	0	2	AT4G02060		
GRMZM2G166355	mRNA 3-UTR binding protein	0	0	0	2	AT1G17370		
GRMZM2G133764	Protein piccolo	0	0	0	2	0		
GRMZM2G119219	stem-specific protein TSJT1	0	0	0	2	AT5G19140		

Supplemental Table 2: Co-purified proteins in TAP experiments on *Arabidopsis* cell cultures transformed with 35S::AN3-GS and analyzed with Orbitrap mass spectrometry

AGI code	Name	Total/4 exps
AT1G18450	ARP4	4
AT1G20670	BRD1	4
AT1G21700	SWI3C	4
AT1G43850	SEU	4
AT2G28290	SYD	4
AT2G32700	LUH	4
AT2G46020	BRM	4
AT3G01890	SWP73A	4
AT3G03460	unknown protein	4
AT3G60830	ARP7	4
AT4G17330	G2484-1	4
AT4G25520	SLK1	4
AT4G34430	SWI3D	4
AT4G35550	HB-4, WOX13	4
AT5G07980	dentin sialophosphoprotein-related	4
AT5G14170	SWP73B	4
AT5G17510	GLTSCR	4
AT5G28640	AN3, GIF	4
AT5G55040	BRD13	4
AT5G55210	unknown protein	4
AT5G62090	SLK2	4
AT1G76380	BRD2	3
AT3G22990	LFR	3
AT5G07940	dentin sialophosphoprotein-related	3
AT5G07970	dentin sialophosphoprotein-related	2

Supplemental Table 3: Comparison of the core components between *Arabidopsis* and maize

protein	Arabidopsis	maize	remarks
G2484-1	1	2	both maize proteins were identified in TAP
SWI3D	1	2	both maize proteins were identified in TAP
SWI3C	1 out of 3	2 out of 5	AT1G21700 was identified using AN3 as bait and the other two were identified in reverse TAP experiments using SWP73B as bait in *Arabidopsis* cell culture. In maize, two of the five SWI3C homologous proteins were identified
BRD	3	2 out of 6	
SWP73	2	1	
SYD		misannotated	two genes (GRMZM2G387890 and GRMZM2G467799) were initially identified as SYD homologs and peptides matching both were identified in the TAP experiments, both genes are located 30-kb apart on the same chromosome and encode peptides that correspond to distinct parts of the *Arabidopsis* SYD homolog. Analysis of RNAseq data showed that these gene models were most likely misannotated and should be considered as a single gene with a

Supplemental Table 4: Significantly changing proteins between the division zone and the expansion zone. t-test analysis results from the Perseus software on a set of four independent TAP experiments on both dividing and expanding leaf tissue, analyzed by Orbitrap Velos and relative label-free quantification (MaxLFQ) with the MaxQuant software, as presented in Supplemental Data Set 1.

Leading protein ID	**Plaza ID**	**Description**	**At ortholog (BHIF)**	**Background**	**Significant[1]**	**Test statistic[2] (y-axis in Figure 2)**	**Difference[3] (x-axis in Figure 2)**
GRMZM2G066460	ZM06G01850	60S acidic ribosomal protein P0	AT3G09200	y	+	4,28	2,80
GRMZM2G119499	ZM01G02590	glutathione transferase11	AT3G03190		+	4,08	4,00
GRMZM2G067303	ZM09G24710	S ribosomal protein S20 Fragment (S2	AT3G47370	y	+	4,02	3,18
GRMZM5G850129	ZM06G15600	GRF7	AT3G13960		+	3,98	6,57
GRMZM2G090422	ZM01G53160	60S ribosomal protein L13a	AT5G48760	y	+	3,78	3,33
GRMZM2G178261	ZM01G51610	GRF15	AT2G22840		+	3,18	6,00
GRMZM2G119359	ZM09G06280	GRF12			+	3,13	4,89
GRMZM5G895313	ZM10G24580	OLD SHOCK DOMAIN PROTEIN 1 (CSDP1	AT2G21060		+	3,13	4,83
GRMZM2G112210	ZM02G19410	dirigent			+	2,19	5,13
GRMZM2G041223	ZM02G05420	GRF6	AT3G13960		+	2,07	5,11
GRMZM2G034876	ZM05G37690	GRF1	AT3G13960		+	2,00	5,71
GRMZM2G124566	ZM04G21130	GRF17	AT2G36400		+	1,93	6,10

[1] Significant: This column indicates which data points were significant in the two groups test.

[2] Test statistic: -log10 p-value, taking into account FDR=0.01 and S0=0.9

[3] Difference: log2 (LFQratio(division/expansion)) = log2 average LFQ intensity (group1, division) - log2 average LFQ intensity (group2, expansion); calculated from the Proteingroups file (Supplemental Data Set 1) with the Perseus software (as described in the methods section, briefly: LFQ intensities were logged; missing values were imputated from a normal distribution around the detection limit of the mass spectrometer; average log2 LFQ intensity was calculated for each identification in both groups: division (cm1, green columns) and expansion (cm4, red columns); for each identification, the difference in average log2 LFQ intensity between the 2 groups is

Supplemental Table 5. Sequence of the qPCR primers

gene	*accession number*	*forward primer*	*reverse primer*
GRF1	GRMZM2G034876	CCACTGATCGGTTGTCTG	GTTCCTGCCTTTCTTCGG
GRF1	GRMZM2G034876	CAGCTACTCCTACGCAGCTC	GCCACTGGCTCTCTATCGAC
GRF2	GRMZM2G099862	AGACATCTTAACTGACCATT	CTGCTAGACATTTGTAGGA
GRF3	GRMZM2G105335	CCGAATGAAACCTCCAGAA	GCGAAGCAATACAGAGTAATAC
GRF4	GRMZM2G004619	AAGTACTGCGAACGCCACAT	GGGAGCAGATTTTGAGCCTGA
GRF5	GRMZM2G129147	GCCTTATGTAACGCTATT	TCACTGAGTACAAAGAAAC
GRF6	GRMZM2G041223	CTAGTATCATGCTCCTGGA	CCACGCAGAACATACAAT
GRF7	GRMZM5G850129	AGCCAAAGACTCCACTTTCA	AACAATGATGAAGCGGCAG
GRF8	GRMZM2G033612	CTTCTGGATACGGCTGTA	TTCTGTCAATCAAAGTGGTT
GRF9	GRMZM5G893117	TGTCTATAGCCTTGTAGGT	CCGCTCATCATCATCATC
GRF10	GRMZM2G096709	TCACCTCGTCTTCCCGGTAT	CGTCCTCCAGGAAAACCATCT
GRF11	GRMZM2G067743	CAAGCAGCAATAGGACTCTA	GTCACACCGAACAACAAC
GRF12	GRMZM2G119359	AATCGCATTAAGAACAGAAC	CATGGTCGGTACTACAAC
GRF13	GRMZM2G018414	TCTGAATCTGGCTGTATCT	GGACCACTGAAGTTTCTG
GRF14	GRMZM2G098594	CAGCTCTCCATCTCCATC	GCAGCGAACAGAATCAAG
GRF15	GRMZM2G178261	ACCTCTCGATGCTGACTTCC	CATACTCTGTGAGCCGAGCA
GRF16	GRMZM5G853392	GCAATATAGCAGGGAACTGGC	TGGAAGTCAGCATCGAGACAT
GRF17	GRMZM2G124566	GGTTATTACTGTGTCGTG	TAAACAGCAGAATCAACG
GRF18	GRMZM2G045977	GCCGTTCAAGAAAGCCTGTG	CTGTGGGCGAGGAGGAC

Supplemental Table 6. MaxQuant search parameters

Group specific parameters	
General	
type	standard
multiplicity	1
variable modifications	Acetyl (Protein N-term), Oxidation (M)
digestion mode	specific
enzyme	Trypsin/P
max missed cleavages	2
instrument type	orbitrap
Label free quantification	
label free quantification	LFQ
LFQ min ratio count	1
fast LFQ	TRUE
LFQ min number of neighbors	3
LFQ av number of neighbors	6
First search	
separate var modifications first search	FALSE
separate enzyme first search	FALSE
Advanced	
main search ppm	4,5
max number of mod per peptide	5
max charge	7
individual pept mass tolerances	TRUE
Global parameters	
General	
Fasta files	ZmB73_5a_WGS_translationsplus.fas
fixed modifications	Carbamidomethyl (C)
re-quantify	TRUE
match between runs	TRUE
matching time window	0,5
alignment time window	20
match unidentified features	FALSE
Sequences	
decoy mode	revert
special AAs	KR
include contaminants	TRUE
I=L	FALSE
Identification	
PSM FDR	0,01
Protein FDR	0,01
Site Decoy Fraction	0,01
min Pep Length	7
min peptides	1
min Razor+Unique peptides	1
min Unique peptides	1
min score unmodified peptides	0
min score modified peptides	40
min Delta score unmodified peptides	0
min Delta score modified peptides	17
base FDR calculations on Delta score	FALSE
filter labeled AA	TRUE
second peptides	TRUE
dependent peptides	FALSE
Protein Quantification	
min ratio count	1
peptides for quantification	Unique
use only unmodified peptides and	TRUE
modifications used in quantification	Acetyl (Protein N-term), Oxidation (M)
card unmodified counterpart peptides	TRUE
Site Quantification	
mode	Use Least Modified Peptide
use for occupancies	Normalized Ratios
Label free quantification	
separate LFQ in parameter groups	FALSE
LFQ stabilize large ratios	TRUE
LFQ require MSMS	TRUE
Advanced	
calc peak properties	FALSE
mass difference search	FALSE
top x window	100
max peptide mass	4600
min time	NaN
max time	NaN
in peptide length for unspecific search	8
ax peptide length for unspecific search	25
min peak length	2