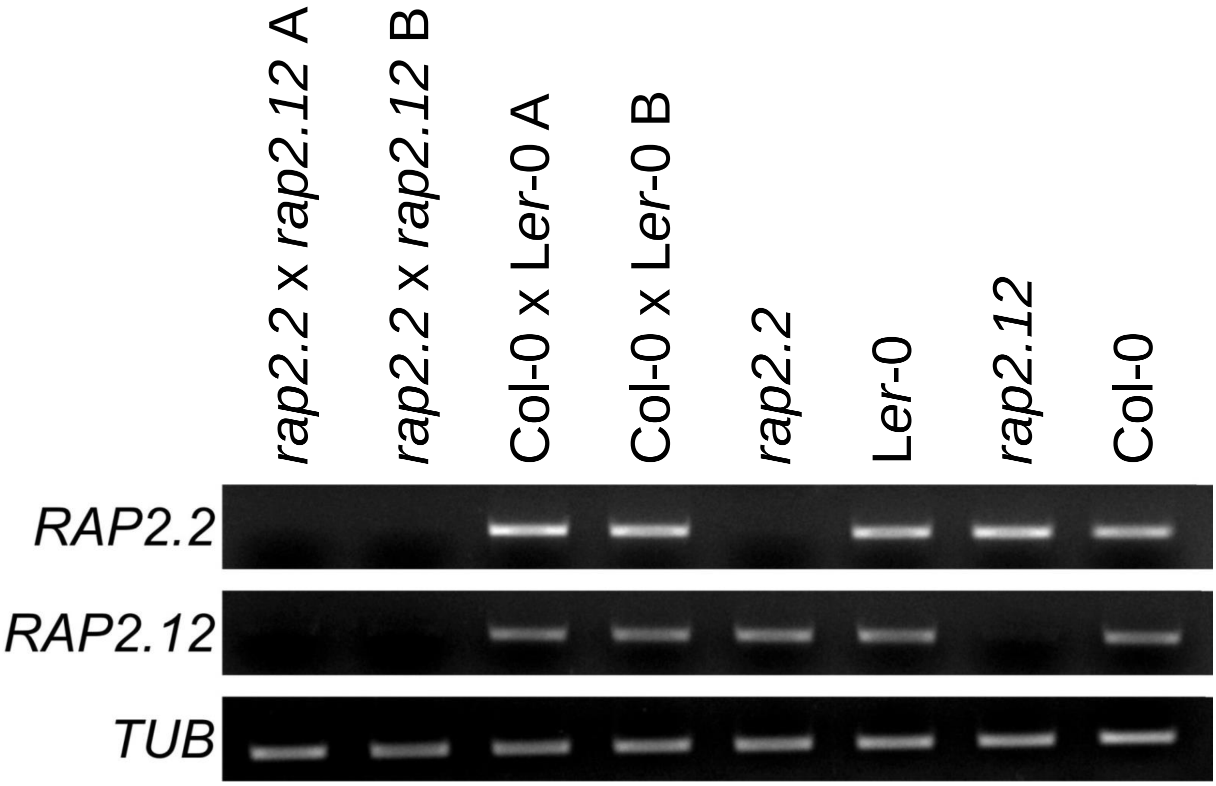
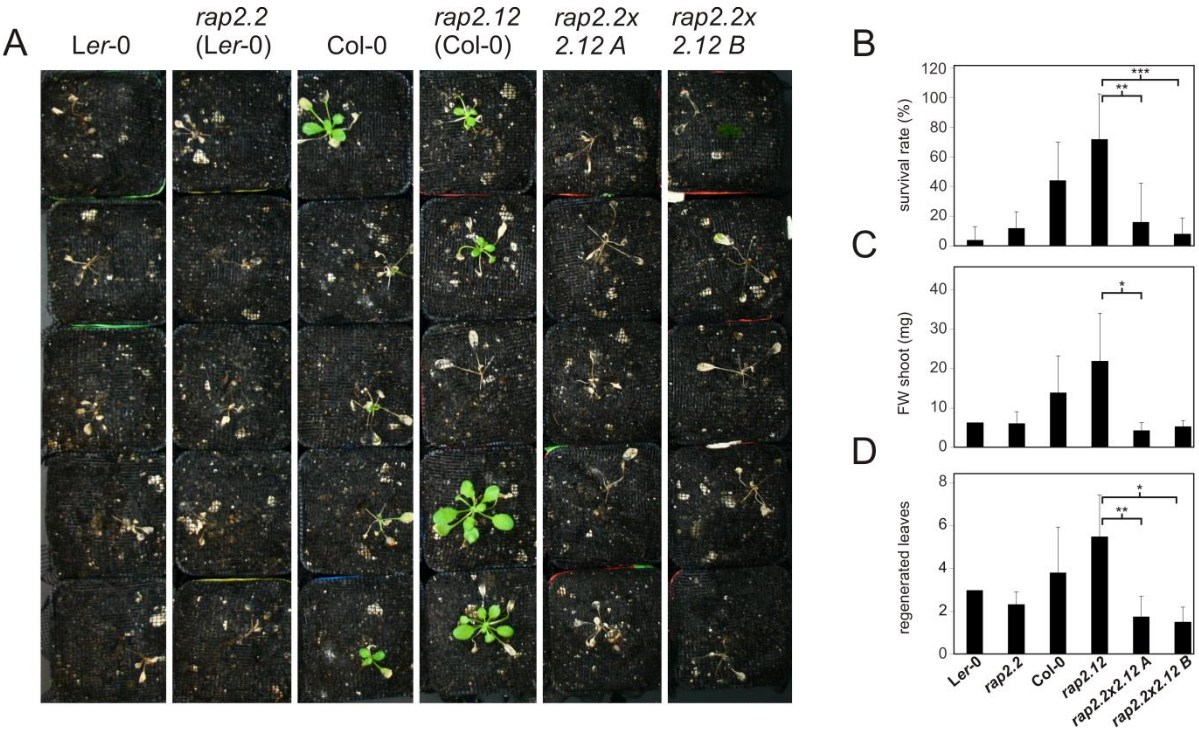


Supplemental Figure 1: T-DNA insertion mutations studied were null alleles (transcript undetectable).
Representative result of standard RT-PCR with *RAP2.2*- and *RAP2.12*-specific primers in L*er*-0 and Col-0 ecotypes and respective T-DNA insertion lines. Quality and relative quantity of cDNA was verified by reference gene *TUBULIN* (*TUB*).



Supplemental Figure 2: Submergence phenotypes of *rap2.2* and *rap2.12* single and double mutants.

(A) Representative phenotype after 3-week-old plants were submerged for 3 days in darkness and recovered for two weeks under SD conditions.

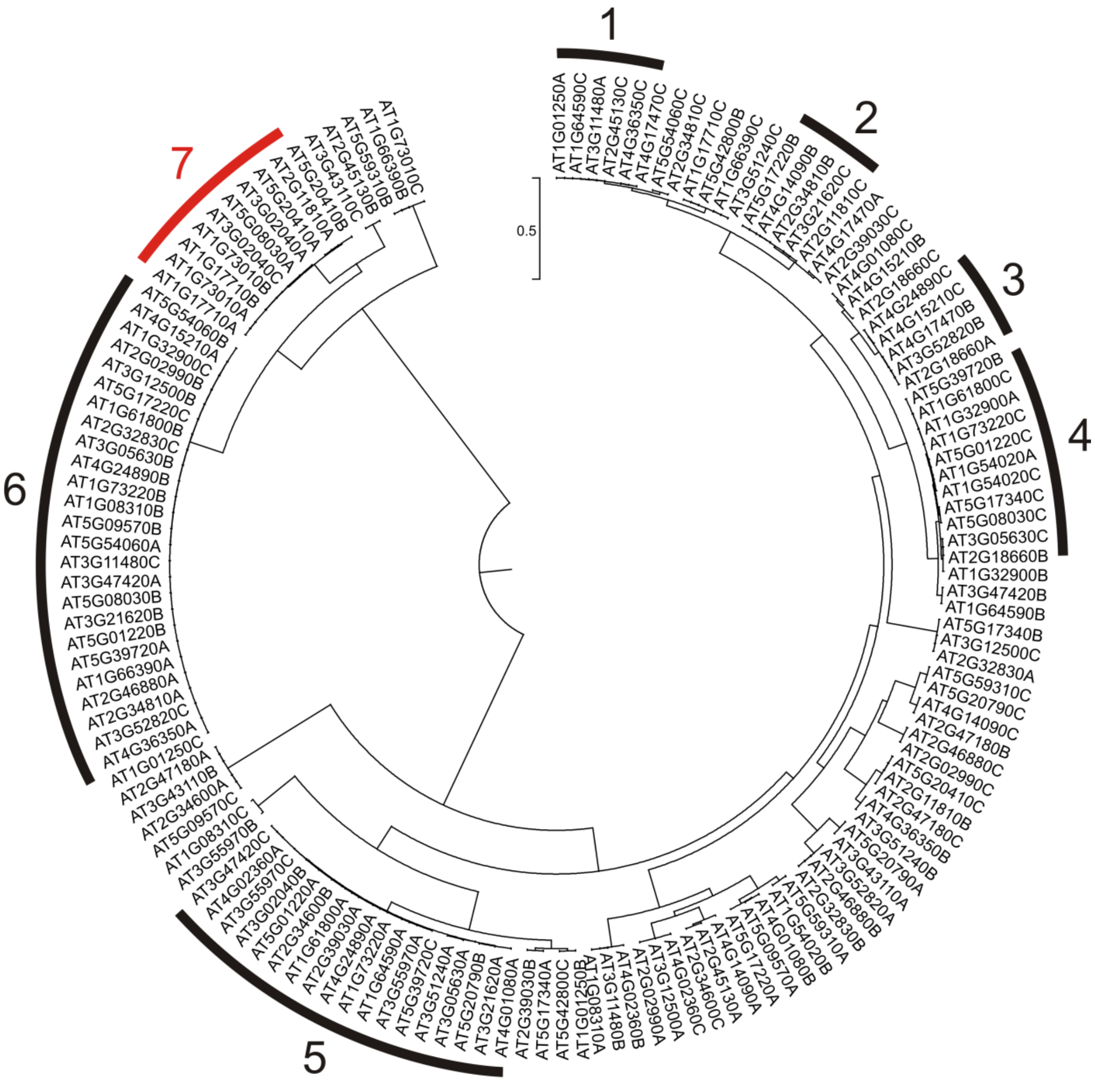
(B) Mean survival rate +/- SD [%] of 25 individuals out of 5 replicates. ** indicates significant differences at $p<0.01$ and *** at $p<0.001$ (Tukey HSD test).

(C) Mean fresh weight from regenerated shoots ± SD [mg] of 1 to 18 surviving individuals per genotype out of 5 replicates. * indicates significant difference at $p<0.05$ (Tukey HSD test).

(D) Mean leave number (leaf size > 1 mm^2) from regenerated shoots ± SD of 1 to 18 individuals per genotype out of 5 replicates. * indicates significant difference at $p<0.05$ and ** at $p<0.01$ (Tukey HSD test).

Supplemental Figure 3 (next page): Comparative phylogenetic footprinting can detect expected *cis*-elements.

Tree shows phylogenetic footprints for each of 49 highly low phosphate-responsive genes from *A. thaliana* shoots (Bustos et al., 2010), grouped by similarity to seven distinct clusters (Clusters1-7). Clusters were defined as groups of at least five motifs with a branch length of less than 0.01 between two nodes, representing one consensus sequence. Sequence logos display consensus sequences and names of known matching cis-elements are indicated. Cluster 7 represents the well-characterized *PHR1* promoter-binding site (P1BS).


1
2
3
4
5
6
7
0.5
AT1G01250A
AT1G64590C
AT3G11480A
AT2G45130C
AT4G36350C
AT4G17470C
AT5G54060C
AT2G34810C
AT1G17710C
AT5G42800B
AT1G66390C
AT3G51240C
AT5G17220B
AT4G14090B
AT2G34810B
AT3G21620C
AT2G11810C
AT4G17470A
AT2G39030C
AT4G01080C
AT4G15210B
AT2G18660C
AT4G24890C
AT4G15210C
AT4G17470B
AT3G52820B
AT2G18660A
AT5G39720B
AT1G61800C
AT1G32900A
AT1G73220C
AT5G01220C
AT1G54020A
AT1G54020C
AT5G17340C
AT5G08030C
AT3G05630C
AT2G18660B
AT1G32900B
AT3G47420B
AT1G64590B
AT5G17340B
AT3G12500C
AT2G32830A
AT5G59310C
AT5G20790C
AT4G14090C
AT2G47180B
AT2G46880C
AT2G02990C
AT5G20410C
AT2G11810B
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AT4G36350B
AT3G51240B
AT5G20790A
AT3G43110A
AT3G52820A
AT2G46880B
AT2G32830B
AT5G59310A
AT1G54020B
AT4G01080B
AT5G09570A
AT5G17220A
AT4G14090A
AT2G45130A
AT2G34600C
AT4G02360C
AT3G12500A
AT2G02990A
AT4G02360B
AT3G11480B
AT1G08310A
AT1G01250B
AT5G42800C
AT5G17340A
AT2G39030B
AT4G01080A
AT3G21620A
AT5G20790B
AT3G05630A
AT3G51240A
AT5G39720C
AT3G55970A
AT1G64590A
AT1G73220A
AT4G24890A
AT2G39030A
AT1G61800A
AT2G34600B
AT5G01220A
AT3G02040B
AT3G55970C
AT4G02360A
AT3G47420C
AT3G55970B
AT1G08310C
AT5G09570C
AT2G34600A
AT3G43110B
AT2G47180A
AT1G01250C
AT4G36350A
AT3G52820C
AT2G34810A
AT2G46880A
AT1G66390A
AT5G39720A
AT5G01220B
AT3G21620B
AT5G08030B
AT3G47420A
AT3G11480C
AT5G54060A
AT5G09570B
AT1G08310B
AT1G73220B
AT4G24890B
AT3G05630B
AT2G32830C
AT1G61800B
AT5G17220C
AT3G12500B
AT2G02990B
AT1G32900C
AT4G15210A
AT5G54060B
AT1G17710A
AT1G73010A
AT1G17710B
AT1G73010B
AT3G02040C
AT5G08030A
AT3G02040A
AT5G20410A
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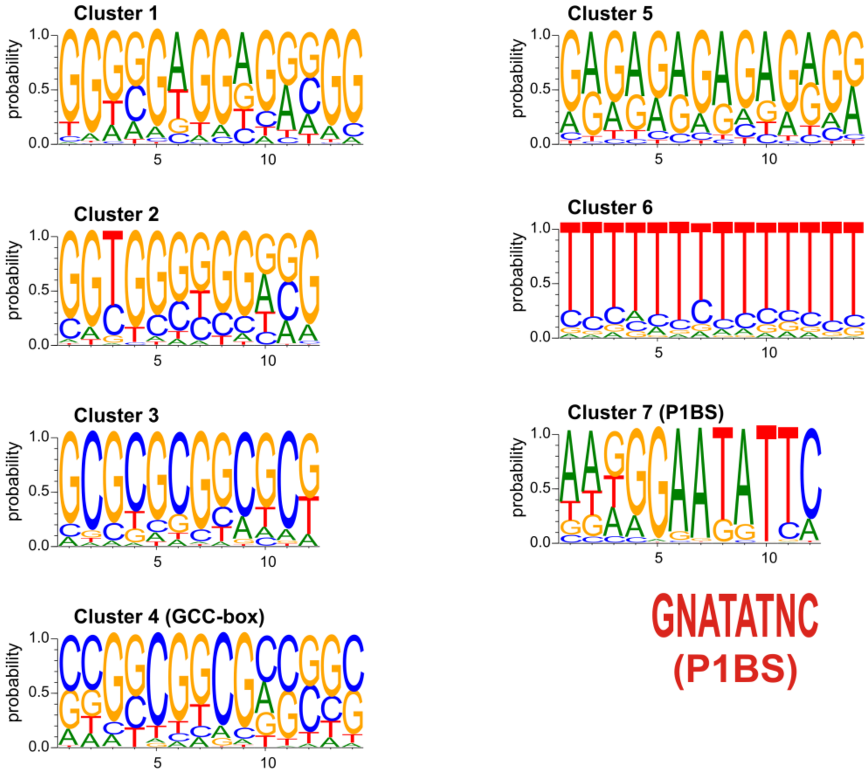
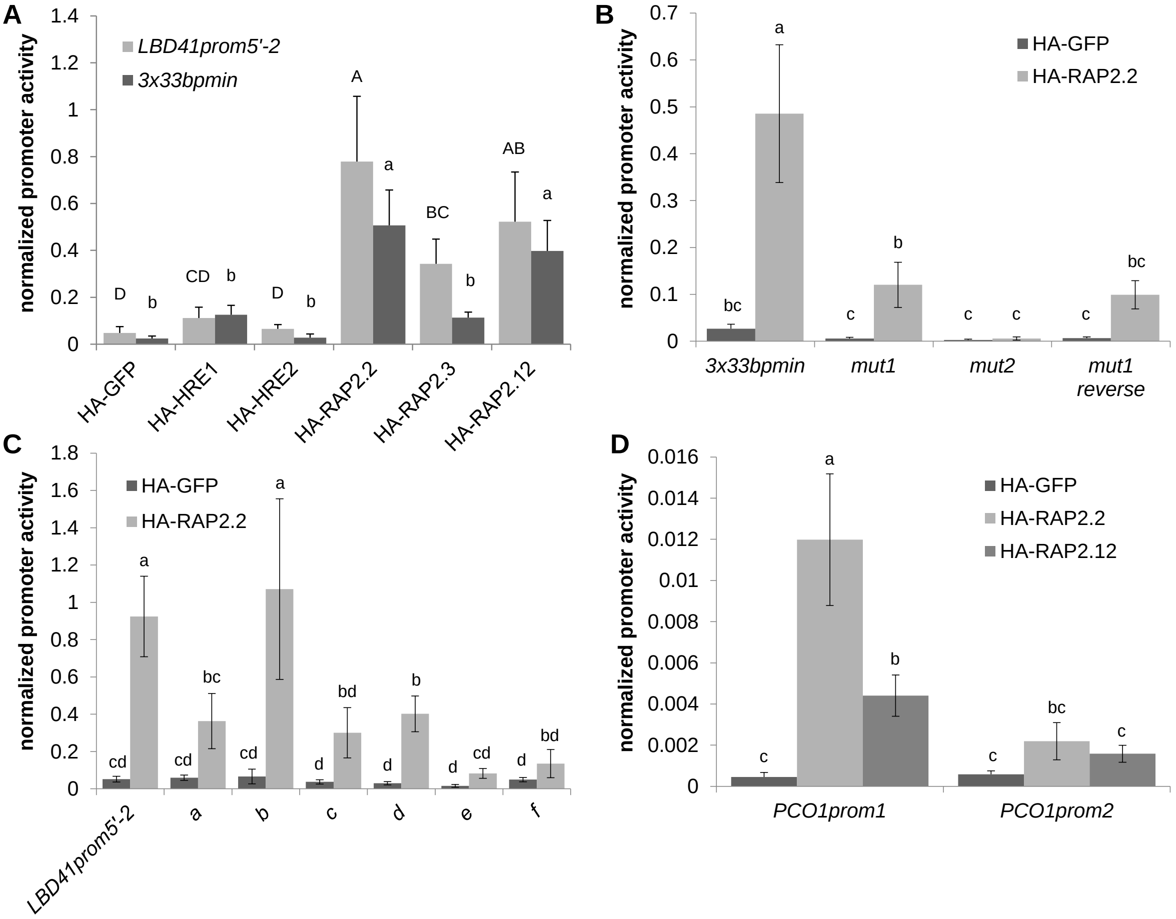
AT1G66390B
AT1G73010C


Cluster 1
Cluster 2
Cluster 3
Cluster 4 (GCC-box)
Cluster 5
Cluster 6
Cluster 7 (P1BS)
probability
1.0
0.5
0.0
5
10
GNATATNC
(P1BS)



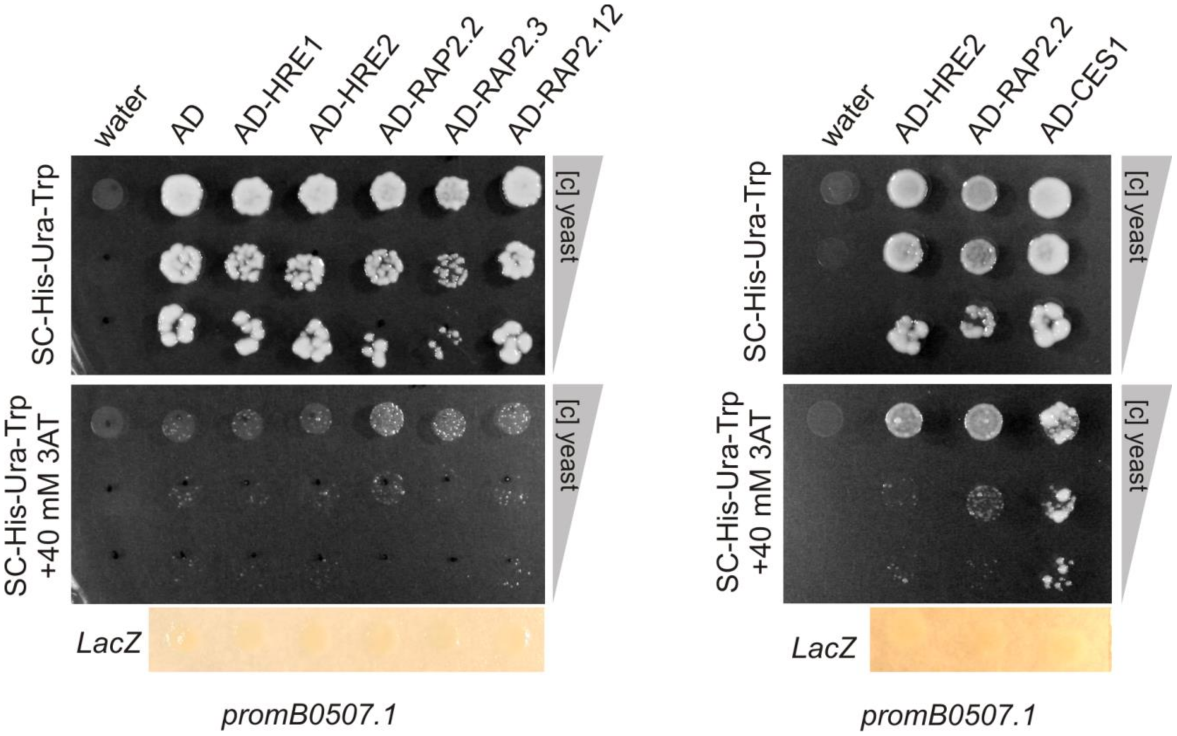
Supplemental Figure 4: Normalized promoter activities for Figures 5 and 6.
(A) Comparison of LUC activity from the 589 bp long *LBD41prom5'-2:LUC* with the *3x33bpmin:LUC* reporter construct in the presence of transiently expressed HA-ERF-VIIs.

(B) Comparison of HA-RAP2.2-induced LUC activity of wild type and mutated versions of *3x33bpmin:LUC*.

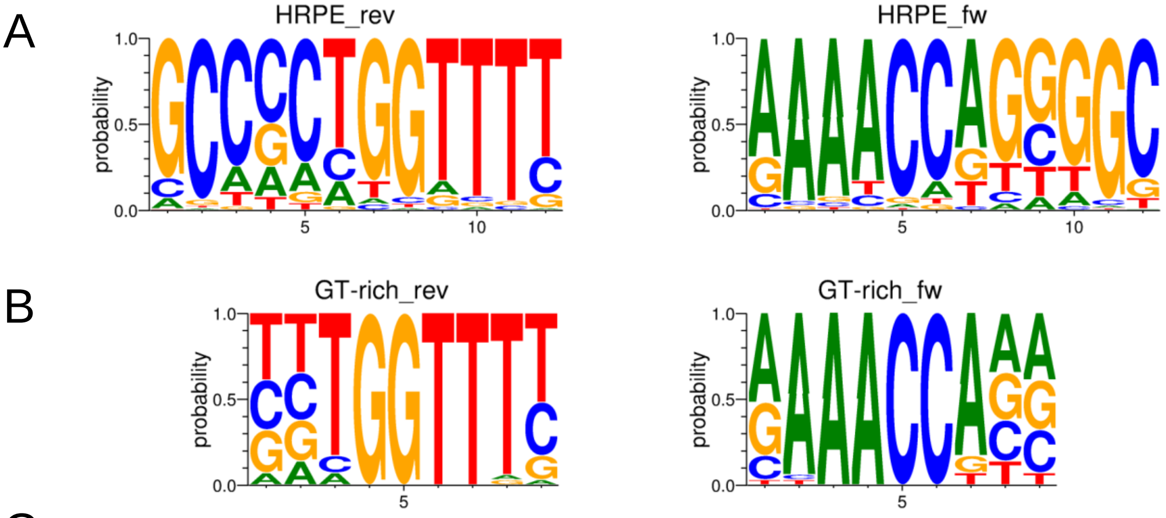
(C) Comparison of HA-RAP2.2-induced LUC activity of the 589 bp *LBD41prom5'-2:LUC* reporter and point mutations in two C9motifs.

(D) Effect of HA-RAP2.2 and HA-RAP2.12 on C9motif-containing and C9motif-less *PCO1* promoter versions.

All data are means ± SD of 6 replicates, different letters indicate significant differences at $p<0.05$ (Tukey HSD test). Normalized promoter activity is LUC activity normalized to *p35S:RUC* activity. Data are the basis for calculation of fold-change in Figure 5B and Figure 6C-E.



Supplemental Figure 5: ERF-VIIs do not activate unrelated Y1H reporters.
Yeast-one-hybrid (Y1H) assays with stable *promB0507:HIS promB0507:LacZ* yeast strain transiently expressing Activation Domain (AD)-ERF-VII fusions (baits). Water and an AD-only expressing vector were used as negative controls. *AD-CES1* was used as positive control. Panels show equally concentrated yeast transformants and 1:10 and 1:100-fold dilutions after 5 d of growth on selective medium in the absence and presence of 40 mM of the *HIS* gene inhibitor 3-aminotriazole (3AT).



C

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AtLBD41_C9_A          1  ------------AAATCCAGGGGC-------- 12
AtLBD41_C9_B          1  ------------AAAACCAGGAGC-------- 12
AtLBD41_C9_C          1  ------------AAAAACAGCGGC-------- 12
AtADH C9_RSAT rev     1  ------------AATACTAGGGGC-------- 12
ZmADH C9_RSAT         1  ------------AAAACCACGGTC-------- 12
ZmLBD41 C9_RSAT       1  ------------GAAACCACAGGC-------- 12
ARE_MAIZE_sub1 rev    1  ----------GCGAAACCGGGGCTGCAGCC-- 20
ARE_MAIZE_sub2 rev    1  -----GGGCAAGCAAACCACGGCGCGGC---- 23
ARE_ATH               1  AGAGAACAAGGCAAAACCAAATACGCCCCTAG 32
```

Supplemental Figure 6: Comparison of the HRPE and AREs.
(A) Graphical display of the HRPE in both orientations.
(B) Graphical display of the GT-rich region from the At ARE (Hoeren et al., 1998).
(C) Alignment of predicted HRPEs from At *LBD41*, At *ADH1*, Zm *LBD41* and Zm *ADH1*, and previously identified Zm *Adh1* ARE subregions. The GC pair that is important for TF binding (Figure 6D) is highlighted in red.

Yellow: HRPE motifs predicted by RSAT
Italic: 5'UTR
Magenta: ATCTA element
Underlined: ARE region
Green: ARE GC-rich subregion (Walker et al., 1987; Dolferus et al., 1994)
Blue: ARE GT-rich subregion (Walker et al., 1987; Dolferus et al., 1994)
ATG: start codon

>AtADH1
ATAATACTATTAAAGAGCTATTTAAGATGAAACCGCCCGAAACCAAAAGCATTCGATGGGTA
CACCGATTACTGCTTTTAGCAACACCACGGCGTGACCATCAAGACTAATTAACTAAGACCAC
ATTTTAAAAAAACTATTAATAATTACTACAATTTGTAATTAAAAAGATCAACGAGAAATGCC
ACGTGGACGAATACTAGCAACGCCAAGTGGAAAGAGCGTTCGAGAGAACAAGGCAAAACCAA
ATACGCCCCTAGTATTCTACAGATGTCGACTGGATAATTACAAAAGATTTCAATAAACAGTA
CTAATTAATTTCTAGTGGTGAGTTTTTGTAAATA*TCTACTTCTTCCAATTACCAGCTGCTAT*
ATAAATCCCCTTCTCTGTTTCTCTTTTCTTACATCACAATCACACAAAACTAACAAAAGATC
*AAAAGCAAGTTCTTCACTGTTGATA*ATG

>ZmADH1
GCGCGGCGCATCCGACGGCCACGACAGCGCAGTGCCGTCCTCCGCCGCCACCGCTTGGCGAT
TGTCCGCACCCCACCAGTCCACCACCTCCCCCACGAGCGAAAACCACGGTCCACGGACCACG
GCTATGTTCCACTCCAGGTGGAGGCTGCAGCCCCGGTTTCGCAAGCCGCGCCGTGGTTTGCT
TGCCCACAGGCGGCCAAACCGCACCCTCCTTCCCGTCGTTTCCCATCTCTTCCTCCTTTAGA
GCTACCACTATATAAATCAGGGCTCATTTTCTCGCTCCTC*ACAGGCTCATCTCGCTTTGGAT*
CGATTGGTTTCGTAACTGGTGAGGGACTGAGGGTCTCGGAGTGGATTGATTTGGGATTCTGT
*TCGAAGATTTGCGGAGGGGGGCA*ATG

Supplemental Figure 7: Promoter of *ADH1* from *Arabidopsis* and maize with marked motifs, as described in the legend.

Yellow: HRPE motifs predicted by RSAT
Italic: 5'UTR
Magenta: ATCTA element
Underlined: primers used
ATG: start codon

>At3g02550 (LBD41)

TTCTCAAGTCTTTGTAAATTGTAATCTTGATAAATTCAAAATGCTTTGTATTATTCGAACAA
GCTTCCGTCTTTAGAGATTCTAATTGTCTTGTCTCTCTGGAATGGACAAGAGAAACGAAACG
GAAAATAATGCGAATGAAACGGAGCCATCAGCGTTGACTACGTAACTTGACACTTACGAATT
ACGTACGGTCTATTCAACGAACGAAGATTCCTTCAATATTGTCGTGAACAAGAACACTAATC
TCATGGACGCATTAAATGAATGGAAATAGTATTTGACTAGTTAATGTCGTTTAGAACTTAGT
AAATTTTGAACCAAACCCATGGATATGAATTGCAGTAGAATCATAATACCAATCGGAAATAC
TAGTTAATTATTTTTTACAACTCATTAAATTTTGAACCAAAGACATGAATATGAATTGATGT
ATGAAACGCTACATTTTTGTCTTTTTGCTACGTGGTTTGTTGTTAAATGTACATGTTTTTTT
AATAGAAAACAAGGATTTAACTCACGGTTTACCGCGGGCAATCGGTTTATTTGGTTTTTATA
CTAAATATTTGAGTAAATTTGATATCCTAAACTTATAAATATAAATTTTTTAATCAAACATA
ACTAAAAAATAATTTGGATTTTTTTTGTTGTTATTTAGTGATAAGAAGAATGTGTTAAAATG
TGATTAAATTTTTTTTGCTTGTTATTTATTTATTTTTGTTGAACGGTTTAGATTGAAGGGAA
TTAATTTTATTGAACGGTTTAGATTTAATCGAATCATATAAAGTTTAGAAGATTGTTAAGAC
CAAATTACCCTTAATGATTTTGAATAACAAAGAACAAAATCCAAATTTGAAATAAAAATTAA
GATCAAATTAGACAAAATTCAATTTGTACTTCCCTTATAATAATAAGAGGATACATAACAGA
ATCCACTAAACTCAAATCAAATGTGCTACAAAATGGGTCTCACAATATTGTAATGTAATCTG
GTACAAAGTTAAATTTAAGTGGATTACGTAAGAAAGAATATCAAAGCTGAGTTTTGGTTGTC
TGGATTAAACTATAAGGTGGGGAAAATAAGAATTAATCTAAAGGTGATTAAAGATAAAATTT
ATTAAGTAAAAGATGATTTAAGATTACGTTTTTTACGAAAGCGTCGGCTAACAGAGAGAGTC
ACAAAGATCCGCCCACAGGGAGAGAAGAAGAAAAGATCAAAAACCGGAAACCATAAAACCAG
AAACCAGTCAATAGTTTTGGACATAGTTGAAAGCAGTATTGTTAAAACAGATTCTTTTCCAG
AAAACCAGGAGCTAAGTGTGGGCCCCAGTTCTTCCAAATGCTCCTCAAATGACTCAAATCCC
ATCTGGATGACTTACGTGGCGATTCGACCAAATTTCTTACTCGCGAGCGTGGAGGCCACGTG
TCTTATCACAGTCTCTTCAAACACATTTAAGACAATTTAACCAAAATCCTACTCCATAGATA
CTCTGAATTGGTCAGATACTTTAATCAACAACCATATTAAATCGTTTTAGAACGAATTAGAT
TGTATAATCCAGAATTTATAGACTATTCACTAGTAATTAAAAAATGGTAACTTGATATGTCA
CGTGTATGACACGCGCATTGGATAGAGTGGGGACAAAAACATAACTTGGGGAAGAAACACAA
GAAGCAAAACCTTGAATCAGGGTGAAG*AAAAACAGCGGCGGTTCTGGGAAAATAAAGGAAGG*
ATTTTGTAATTAAAAGACAAAACAACCCTTGTCTTTAGAGAAAAACAGCTCTTCTTATCTTG
TTTTCTTTGTCTTCTGCCTTCTTCCCTTGGTTTTATAATCTCTCTCCGCTTCCCCCAAAAAT
CCAGGGGCTTCTTACACGCACACAATCCTTTAAAGCTATCGTCTTTCTTATATAATCAGTGA
ATCTTCATTAACACCTCCCACAAAATCTCAGAAATAACTTTCACAACAGAGTCAAAGAGTTC
CAAATCGTTTGTTTGTATTTTGTACGATCAAAGTTGTTGGTACTTGTAAGATAATCGAAACC
*AAAG*ATG

>At5g15120 (PCO1)

CTATTGATGTTTTAAGGGAAAGACAATTTTTTCAACATTTTGATTTTTTGCTTCTAATCTAG
TTCAGGAAATAAATAATTTCAGGGGTGAAAATGATTAAAAAAAAATTCTAATTTGTAAAGTT
ATTTTTTGTGTTATGAAAACAAGTTATATAAAGAGTAAGCCATAACAGCTGGTTCTTGTAAT
ACATAATTCACATTTTGTTTGTTAAACAACCAAAACTAAATCATCAAATACTTTTTTTTGGA
TTCAAATCTGCATAAAACATGCTGGTAAACAAAAATATAATGATAATGATATTAGAGGTTTT
TAGACATTATGATATGTTTTTCTTAATATCATATCATTAGAATCATATAATCAACATCTTCT
GATTTGTTATGTGCTTAATTGCTTTATTGTCAAAGATCTCAACTATAAATGACAATTATACT
GCATGACAAAAATAAGATATACACAAATAATATTGCCAAAGATAACAAGTGATACCAAAACA
AATATTTATCAATGAAAAGAGAAAAAGAAATAACAAAAACAAAGATTCCTAGTACTCATTCC

CATATAATCCGGTGAAGAAAAAAAGATTTCAGGGTCAAAGACGACATTTTTAAATTATGTAT
ATCAAAGTAAACAACACACAAAACAATCCTATGATTTTAACATATTTCAAATTAAATACATG
TATTTTTATTTGTCAAATTTATATAAATGAATCTATGAAATTGACAAATTATGAGTGAAATA
GTAATTCAGCCAGTGTAAGTAAATAAAACAAATCTAATAAACCGGCTATTTATAACCAACCG
GGTTAGAGTAAACCGATAAAACATATGATAATATTTTAATAAAGTGTATGTGTTTCCAAATT
TGCCCCTTTGCGAAGACCGAAACGGATAAAAAAAGAATCCGCTGTTTGAAAAAAACACAGCC
CATAGGAAACAAAAGAATGGCCCCTGGTTTTGTAATCGATAATGGTATAATCCTCTTTTCTT
ATTTTTCCCTGTTTTTATATCTCATTCTTATTCTTCTTAAATCC*ATTCCCAGATTCACACTT*
*TTGATTTCGTGATACACTGTTACATTTTATTTTTTTTTGTTGGGTTTGGTGAGACTTTT*ATG

Supplemental Figure 8: Promoters of *LBD41* and *PCO1* from *Arabidopsis* with marked motifs and underlined primers, as described in the legend.

Supplemental Table 1: Overview of group VII ERF T-DNA insertion lines used in the literature

Name of line	**ID of line**	**Ecotype**	**References**
hre1-1	SALK_039484	Col-0	Hess et al., 2011; Gibbs et al., 2014
hre1-2	SALK_018181	Col-0	Hess et al., 2011
hre1-3	SALK_023445	Col-0	Licausi et al., 2010
hre2-1	SALK_052858	Col-0	Licausi et al., 2010; Hess et al., 2011; Park et al., 2011, Gibbs et al., 2014
rap2.12-1	SALK_019873	Col-0	Zhao et al., 2012
rap2.12-2	SAIL_1215_H10	Col-0	Papdi et al., 2015; this paper
rap2.12-3	FLAG_525G09	WS	Bui et al., 2015
rap2.12-4	GK_503A1_11	Col-0	Gibbs et al., 2014 (named "rap2.12-1" in that publication)
rap2.2-1	SAIL_184_G12	Col-0	Hinz et al., 2010; Gibbs et al., 2014
rap2.2-2	SAIL_799_D10	Col-0	Hinz et al., 2010
rap2.2-3	SALK_010265	Col-0	Zhao et al., 2012
rap2.2-4	SAIL_18_G09	Col-0	Bui et al., 2015; Papdi et al., 2015
rap2.2-5	AY201781/ GT5337	L*er*-0	this paper
rap2.3-1			Ogawa et al., 2007; Gibbs et al., 2014; Papdi et al., 2015

Supplemental Table 2: Majority of C9motif containing core genes are early N-end rule targets.
P-values indicate hypergeometric distribution probability as a measure for overrepresentation of Cluster motif-containing core genes among indicated datasets in the promoter regions in comparison to the promoters of all *Arabidopsis* genes. The 3 kb upstream of the ATG start codon for the gene groups were screened for the 9 cluster motifs by use of RSAT, with a significance cutoff of > 4.5. Low P-values indicate enrichment of cluster motifs among the groups of genes.

Cluster motif	**Sample size**	**1**	**2 (Ibox)**	**3**	**4 (GCC-box)**	**5**	**6**	**7 (ABRE)**	**8**	**9 (HRPE)**
49-core genes (Mustroph et al., 2009)	49	0.91	0.10	0.0184	0.32	0.62	0.0042	0.20	0.02	7.65E-06
30 min, 1% vs. 21% O_2 (van Dongen et al., 2009)[1]	66	0.92	0.08	0.0027	0.63	0.76	0.0689	0.11	0.23	6.56E-05
ate1/2 and *prt6* vs. Col-0 (Gibbs et al., 2011)[2]	79	0.89	0.57	0.0006	0.79	0.59	0.0001	0.25	0.78	6.42E-04

[1] 10-day-old roots, 12h light cycle, grown on 0.5xMS, 1% Suc, SLR > 1

[2] 7-day-old whole seedlings, 16h light cycle, grown on 0.5xMS, 1% Suc, SLR > 1, Padj < 0.05

SUPPLEMENTAL DATASETS

Supplemental Data Set 1: Overview over homologous genes of the 49 core hypoxia-response genes in 25 species from the PLAZA 2.5 database

Supplemental Data Set 2: Overview over Position-specific scoring matrices (PSSMs) identified in this paper. **(A)** PSSMs for all cluster motifs. **(B)** List of all sequence motif pattern matches.

Supplemental Data Set 3: Occurrence of the nine motifs in the 49 core hypoxia-response genes, together with published microarray data.

Supplemental Data Set 4: Occurrence and overlap of the HRPE and the GT-rich region of At ARE (Hoeren et al. 1998) in the 49 core hypoxia-response genes, and in Zm *LBD41* and Zm *Adh1*.

Supplemental Data Set 5: (A) List of constructs used in this paper. **(B)** List of primers used in this paper. **(C)** List of AGI codes used in the paper.

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