Supplementary figures:

Figure S1A. E-score distribution of top four 6mers recognized by FUS3 and ABI3.

The elements are shown in descending order in relation to their E-score. All top scoring elements recognized by both proteins share the sequence GCATG (underlined), which could be considered as a RY-core. The motif ACATGT corresponds to a “mutant” version of RY-core in which the nucleotide G at the 5' end has been replaced by an A, reflecting a decrease in E-score. Both proteins recognize similar elements, although DNA-binding affinity was slightly lower for ABI3 compared to FUS3.

Figure S1B. Score plots of the *proOLE1* sequence scanned with DNA-binding matrices described for LEC2, FUS3 and ABI3.

Since matrices correspond to pseudo-palindromic sequences, each binding site is systematically identified on both DNA strands with slightly different scores. This explains the presence of double bars in the plots.

Figure S2. Schematic representation of the mutagenized versions of the *OLE1* promoter used in this study.

Regulatory elements (RYL and GBL domains) present in the minimal *OLE1* promoter were mutagenized using site-directed mutagenesis. Mutagenized RYL (blue box) and GBL (red box) are represented. Figures indicate the position of these elements relative to the translational start site of *OLE1*.

Figure S3. Activation of the native or mutated *OLE1* promoter versions by LEC2 in moss protoplasts. Means of at least 3 replicates +/- SD

Figure S4. Complementary analyses related to activation studies in moss protoplasts.

Transient activation of the *OLE1* promoter by LEC2 (A) or ABI3 (B) fused to a strong activator domain (VP16) were assayed in moss protoplasts. Means of at least 3 replicates +/- SD are presented.

Figure S5. Test of synergistic effect of LEC2, LEC1, and ABI3 on the activation of several oleosin promoters in moss protoplasts.

(A) Transient expression assays were carried out in moss protoplasts. GFP activity was measured in protoplasts transfected with *ProOLE1:GFP, ProOLE2:GFP*, or *ProOLE3:GFP* reporter and constructs allowing the expression of L-AFLs (LEC2, ABI3 or LEC1), alone or in combination. Means of at least 3 replicates +/- SD are presented. AU, arbitrary units.

(B) Schematic representation of *proOLE1* (At4g25140), *proOLE2* (AT5G40420), and *proOLE3* (At5g51210) genomic regions. The RYL and GBL elements are highlighted in blue and red, respectively.

Figure S6. *In vitro* binding of the L-AFLs to the *OLE1* promoter.

Electrophoretic mobility shift assays (EMSA) with LEC1, LEC2, and ABI3 alone or in combination were carried out using a labelled 100-bp long probe corresponding region -228 to –121 (relative to the translational start site) of the *OLE1* promoter. Competition experiments were performed by adding non-labelled competitor DNA added in 25-fold molar excess. Shifted bands are indicated with stars, arrows indicate supershifts.

Figure S7. Complementary results to pull-down experiments (Figure 6).

(A-B) NF-YC2 interacts with LEC1 or its mutated version (LEC1m, D55K).

The HA- or Myc-tagged proteins have been co-expressed in *Arabidopsis* protoplasts. INPUT, 2 % of the full protein extract; IP, immunoprecipitated sample; *, heavy and light chains of the antibody used for the immunoprecipitation.

(C-D) LEC1 and NF-YC2 interact with each other but do not interact with LEC2

The HA- or Myc-tagged proteins have been co-expressed in *Arabidopsis* protoplasts. INPUT, 2 % of the full protein extract; IP, immunoprecipitated sample; *, heavy and light chains of the antibody used for the immunoprecipitation.

Figure S8. Study of protein-protein interactions in yeast.

(A) Summary of interaction studies carried out using a yeast two-hybrid system in strain AH109. Reciprocal interactions between LEC1, LEC2, ABI3, and FUS3 were assayed.

AD, fusion to activation domain; BD, fusion to DNA-binding domain; W, tryptophan; L, leucine; H, histidine; A, alanine.

(B) Study of homodimer formation between native or mutant LEC1 proteins. Yeast two hybrid experiments were performed using native (LEC1) or mutant (LEC1m D55K) proteins. W, tryptophan; L, leucine; H, Histidine; A, alanine; 3-AT, 3-amino -1,2,4-triazole.

Supplementary table 1. Primers and genes used in this study.

Primer name	5'→3' sequence	Gene	AGI
oSB110R	TATGCTCGAGCTAGTAGAAGTCATCGA	FUS3	At3g26790
oETH1132	GGCCATGGTTGATGAAAATGTGGAA	FUS3	At3g26790
oSB109F	TGCCATATGGCAGAGACTCAGTTACCT	ABI3	At3g24650
oSB109R	TGCGGCCGCTTGTCCGCTCGGTTGTCT	ABI3	At3g24650
73 mer selex	TGGAGAAGAGGAGAGATCTAGC$(N)_{30}$CTTGTTCTTCTTCGATTCCGG	selex	
Selex F	TGGAGAAGAGGAGAG ATCTAG	selex	
Selex R	CCGG AATCGAAGAAGAACAA	selex	
LEC2 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGATGGATAACTTCTTACC	LEC2	At1g28300
LEC2 R GW	GGGGACCACTTTGTACAAGAAAGCTGGGTTCACCACCACTCAAAG	LEC2	At1g28300
ABI3 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGATGAAAAGCTTGCATGTGGCGG	ABI3	At3g24650
ABI3 R GW	GGGGACCACTTTGTAAAGAAAGCTGGGT GGAAATGGTGTTTGTGTTATAT	ABI3	At3g24650
FUS3 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGATGATGGTTGATGAAAATGTGG	FUS3	At3g26790
FUS3 R GW	GGGGACCACTTTGTAAAGAAAGCTGGGTCTAGTAGAAGTCATCGAGAG	FUS3	At3g26790
LEC1 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCG ATGGAACGTGGAGCTCCCTTC	LEC1	At1g21970
LEC1 R GW	GGGGACCACTTTGTAAAGAAAGCTGGGTTCACTTATACTGACCATAATGG	LEC1	At1g21970
NF-YC2 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGAGCAGTCAGAAGAGGGTC	NF-YC2	AT1G56170
NF-YC2 R GW	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAGACTCATCAGGGTGTTG	NF-YC2	AT1G56170
LEC2-stop R GW	GGGGACCACTTTGTAAAGAAAGCTGGGT CCCACTCAAAGTCGTTAAA	LEC2	At1g28300
LEC1-stop R GW	GGGGACCACTTTGTAAAGAAAGCTGGGTCCTTATACTGACCATAATGG	LEC1	At1g21970
ABI3-stop R GW	GGGGACCACTTTGTAAAGAAAGCTGGGTCAATGGTGTTTGTGTTATAT	ABI3	At3g24650
NF-YB 7 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGACTGAGGAGAGCCCAGAAGAAG	NF-YB7	At2g13570

NF-YB 7 R GW	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCACCAGTGAATTGAATCAATGTTATTATC	NF-YB7	At2g13570
L1L F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGAACGTGGAGGCTTCCATGGC	L1L	At5g47670
L1L R GW	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAGTACTTATGTTGTTGAGTCGG	L1L	At5g47670
pOleo R GW	GGGGACCACTTTGTAAAGAAAGCTGGGTCTTTTTTGTTCTTGTTTACTAG	pOleo	At4g25140
pOleo Δ526 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGGAAGAGAGACGACG	pOleo	At4g25140
pOleo Δ257 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCAACGCCACATTCTGAG	pOleo	At4g25140
pOleo Δ220 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTTTGAATAGACTCCTCTCGTTAAC	pOleo	At4g25140
pOleo Δ187 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTGCGGCTGCATGGTGACGCC	pOleo	At4g25140
pOleo Δ140 F GW	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTCTCCATTGACACGTGACTTC	pOleo	At4g25140

Supplementary table 2. List of primers used for site-directed mutagenesis of *ProOLE1*.

Name of the construct	Mutations (*)	Construct used as a DNA template	Primers	5'-->3' Sequence
mutA	RY3,2,1/G*,2,1	ProS3-257 (wild type) in pDONR207	mutA-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mutA-R	TTCAAAGACACAATTGTTTTTTGCCT
mutB	RY3,2,1/G3,2,*	ProS3-257 (wild type) in pDONR207	mutB-F	CATGATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutB-R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATCATG
mutC	RY3,2,1/G*,*,1	mut3 (RY3,2,1/G3,*,1)	mutC-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mutC-R	TTCAAAGACACAATTGTTTTTTGCCT
mutD	RY3,2,1/G3,*,*	mut3 (RY3,2,1/G3,*,1)	mutD-F	CATGATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutD-R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATCATG
mutE	RY3,2,1/G*,2,*	mutA (RY3,2,1/G*,2,1)	mutE-F	CATGATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutE-R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATCATG
mutF	RY3,*,1/G3,2,1	ProS3-257 (wild type) in pDONR207	mutF-F	CGTTAACACATGCAGCGGCTACAACGTGACGCCATTAACACGTG
			mutF-R	CACGTGTTAATGGCGTCACGTTGTAGCCGCTGCATGTGTTAACG
mutG	RY3,2,*/G3,2,1	ProS3-257 (wild type) in pDONR207	mutG-F	GGCCTACAATTACAACATGTCTCCATTG
			mutG-R	CAATGGAGACATGTTGTAATTGTAGGCC
mutH	RY*,2,1/G3,2,1	ProS3-257 (wild type) in pDONR207	mutH-F	AGACTCCTCTCGTTAACAGTTGTAGCGGCTGCATGGTGACG
			mutH-R	CGTCACCATGCAGCCGCTACAACTGTTAACGAGAGGAGTCT
mutI	RY*,*,1/G3,2,1	mutH (RY*,2,1/G3,2,1)	mutI-F	CGTTAACAGTTGTAGCGGCTACAACGTGACGCCATTAACACGTG
			mutI-R	CACGTGTTAATGGCGTCACGTTGTAGCCGCTACAACTGTTAACG
mutJ	RY3,*,*/G3,2,1	mutG (RY3,2,*/G3,2,1)	mutJ-F	CGTTAACACATGCAGCGGCTACAACGTGACGCCATTAACACGTG
			mutJ-R	CACGTGTTAATGGCGTCACGTTGTAGCCGCTGCATGTGTTAACG
mutK	RY*,2,*/G3,2,1	mutH (RY*,2,1/G3,2,1)	mutK-F	GGCCTACAATTACAACATGTCTCCATTG
			mutK-R	CAATGGAGACATGTTGTAATTGTAGGCC
mutL	RY*,*,*/G3,2,1	mutK (RY*,2,*/G3,2,1)	mutL-F	CGTTAACAGTTGTAGCGGCTACAACGTGACGCCATTAACACGTG
			mutL-R	CACGTGTTAATGGCGTCACGTTGTAGCCGCTACAACTGTTAACG
mutM	RY*,*,1/G*,2,1	mutI (RY*,*,1/G3,2,1)	mutM-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mutM-R	TTCAAAGACACAATTGTTTTTTGCCT
mutN	RY*,*,1/G3,2,*	mutI (RY*,*,1/G3,2,1)	mutN -F	CATGATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutN -R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATCATG
mutP	RY*,*,1/G3,*,1	mutI (RY*,*,1/G3,2,1)	mutP-F	CGTGACGCCATTAACAGTTGGCCTACAATTGCATG
			mutP-R	CATGCAATTGTAGGCCAACTGTTAATGGCGTCACG
mutQ	RY3,*,*/G*,2,1	mutJ (RY3,*,*/G3,2,1)	mutQ-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mutQ-R	TTCAAAGACACAATTGTTTTTTGCCT
mutR	RY3,*,*/G3,2,*	mutJ (RY3,*,*/G3,2,1)	mutR-F	CAACATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutR-R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATGTTG
mutS	RY3,*,*/G3,*,1	mutJ (RY3,*,*/G3,2,1)	mutS-F	CGTGACGCCATTAACAGTTGGCCTACAATTACAAC
			mutS-R	GTTGTAATTGTAGGCCAACTGTTAATGGCGTCACG
mutT	RY*,2,*/G*,2,1	mutK (RY*,2,*/G3,2,1)	mutT-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mutT-R	TTCAAAGACACAATTGTTTTTTGCCT
mutU	RY*,2,*/G3,2,*	mutK (RY*,2,*/G3,2,1)	mutU-F	CAACATGTCTCCATTGACAGTTGACTTCTCGTCTCCTTTC
			mutU-R	GAAAGGAGACGAGAAGTCAACTGTCAATGGAGACATGTTG
mutW	RY*,2,*/G3,*,1	mutK (RY*,2,*/G3,2,1)	mutW-F	GGTGACGCCATTAACAGTTGGCCTACAATTACAAC

			mutW-R	GTTGTAATTGTAGGCCAACTGTTAATGGCGTCACC
mut2	RY3,2,1/G*,*,*	mutD (RY3,2,1/G3,*,*)	mut2-F	AGGCAAAAAACAATTGTGTCTTTGAA
			mut2-R	TTCAAAGACACAATTGTTTTTTGCCT
mut3	RY3,2,1/G3,*,1	ProS3-257 (wild type) in pDONR207	mut3-F	GGTGACGCCATTAACAGTTGGCCTACAATTGCATG
			mut3-R	CATGCAATTGTAGGCCAACTGTTAATGGCGTCACC

A	proOLE1:GFP	proOLE1:GFP + LEC1	proOLE1:GFP + LEC2	proOLE1:GFP + ABI3	proOLE1:GFP + FUS3	proOLE1:GFP + LEC1 + LEC2	proOLE1:GFP + ABI3 + LEC1	proOLE1:GFP + FUS3 + LEC1	proOLE1:GFP + ABI3 + LEC2	proOLE1:GFP + FUS3 + ABI3	proOLE1:GFP + LEC2 + ABI3 + LEC1
proOLE1:GFP + LEC1	0.2406										
proOLE1:GFP + LEC2	5.2e-13	1.9e-07									
proOLE1:GFP + ABI3	6.6e-12	4.2e-07	1.33e-4								
proOLE1:GFP + FUS3	4.8e-07	6.4e-05	3.819e-4	4.741e-08							
proOLE1:GFP + LEC1 + LEC2	3.21-11	1.2e-06	4.066e-3	0.6098	NR						
proOLE1:GFP + ABI3 + LEC1	6.6e-12	4.2e-07	1.515e-09	8.839e-06	NR	8.83e-05					
proOLE1:GFP + FU3 + LEC1	3.06e-08	1.0e-05	7.082e-05	3.647e-09	0.2636	5.41e-07	1.802e-07				
proOLE1:GFP + ABI3 + LEC2	1.3e-11	5.3e-07	8.532e-08	6.117e-3	NR	NR	0.0151	NR			
proOLE1:GFP + ABI3 + LEC1 + LEC2	8.2e-15	6.0e-08	2.299e-11	1.643e-07	NR	6.331e-07	0.02368	NR	6.243e-05		
proOLE1:GFP + FUS3 +ABI3	8.742e-07	5.017e-05	5.891^{e}-3	0.472	2.955e-4	NR	0.00783	NR	0.1375	NR	
proOLE1:GFP + FUS3 + ABI3 + LEC1	2.997e-06	9.486e-05	8.544e-05	6.115e-3	6e-4426	NR	0.9628	6.426e-4	NR	0.09447	8.03e-3

B

	pS3$_{-257}$:GFP	pS3$_{-257}$:GFP + LEC2	pS3$_{-257}$:GFP + LEC2 + LEC1	pS3$_{-257}$:GFP + ABI3	pS3$_{-257}$:GFP + ABI3 + LEC1	pS3$_{-257}$:GFP + ABI3 + LEC2	pS3$_{-257}$:GFP + LEC2 + LEC1 + ABI3	pS3$_{-257}$: GFP +LEC2 +ABI3 +NFYB7
pS3$_{-257}$:GFP + LEC2	5.222e-13							
pS3$_{-257}$:GFP + LEC2 + LEC1	3.214e-11	4.066e-3						
pS3$_{-257}$:GFP +LEC2 +NFYB7	4.209e-3	0.195	0.3667					
pS3 $_{-257}$:GFP +LEC2 +LEC1mut	0.004209	0.1003	0.01807					
pS3$_{-257}$:GFP + ABI3	6.654e-12	1.332e-4	0.6098					
pS3$_{-257}$:GFP + ABI3 + LEC1	6.654e-12	1.515e-09	8.83e-05	8.839e-06				
pS3$_{-257}$:GFP +ABI3 +NFYB7	4.209e-3	NR	NR	0.4407	0.02917			
pS3$_{-257}$:GFP +ABI3 +LEC1mut	0.004209	NR	NR	0.04274	5.092e-3			
pS3$_{-257}$:GFP + ABI3 + LEC2	1.336e-11	8.532e-08	NR	0.006117	0.01515			
pS3$_{-257}$:GFP + LEC2 + LEC1 + ABI3	8.232e-15	2.299e-11	6.331e-07	1.643e-07	0.02368	6.243e-05		
pS3$_{-257}$:GFP +LEC2 +ABI3 +NFYB7	1.821e-4	NR	NR	NR	NR	0.2421	8.974e-3	
pS3$_{-257}$:GFP +ABI3 +LEC2 +LEC1mut	4.209e-3	NR	NR	NR	NR	0.1337	0.01367	0.8607

C-1

		pWt +LEC2	pWt +ABI3	pWt +LEC1 LEC2 ABI3	pmutA +LEC2	pmutA +ABI3	pmutA +LEC1 LEC2 ABI3	pmut3 +LEC2	pmut3 +ABI3	pmut3 +LEC1 LEC2 ABI3	pmutB +LEC2	pmutB +ABI3	pmutB +LEC1 LEC2 ABI3	pmut2 +LEC2	pmut2 +ABI3	pmut2 +LEC1 LEC2 ABI3	pmutH +LEC2	pmutH +ABI3	pmutH +LEC1 LEC2 ABI3
pmut A	gain LEC2	0.12																	
pmut A	gain ABI3		0.28																
pmut A	gainLEC2 LEC1 ABI3			0.014	0.005	0.002													
pmut 3	gain LEC2	0.25			0.15														
pmut 3	gain ABI3		0.11			0.25													
pmut 3	gainLEC2 LEC1 ABI3			0.001			0.008	0.97	0.012										
pmutB	gain LEC2	0.84			0.40			0.34											
pmutB	gain ABI3		0.16			0.09			0.039										
pmutB	gainLEC2 LEC1 ABI3			0.057			0.52			0.019	0.007	0.016							
pmut2	gain LEC2	0.003			0.004			0.05			0.079								
pmut2	gain ABI3		0.001			0.008			0.13			0.023							
pmut2	gainLEC2 LEC1 ABI3			0.002			0.004			0.014			0.010	0.010	0.007				
pmutH	gain LEC2	0.009			0.003			0.051			0.072			0.34					
pmutH	gain ABI3		0.13			0.26			0.89			0.037			0.21				
pmutH	gainLEC2 LEC1 ABI3			0.02			0.20			0.42			0.13			0.086	0.047	0.056	
pmutF	gain LEC2	0.007			0.002			0.052			0.077			0.55			0.35		
pmutF	gain ABI3		0.18			0.37			0.88			0.047			0.14			0.79	
pmutF	gainLEC2 LEC1 ABI3			0.002			0.024			0.16			0.040			0.002			0.81
pmutG	gain LEC2	0.013			0.006			0.06			0.11			0.26			0.004		
pmutG	gain ABI3		0.75			0.45			0.18			0.31			0.06			0.17	
pmutG	gainLEC2 LEC1 ABI3			0.040			0.76			0.07			0.45			0.026			0.31
pmutI	gain LEC2	0.006			0.0014			0.049			0.070			0.30			0.82		
pmutI	gain ABI3		0.011			0.03			0.34			0.026			0.27			0.47	
pmutI	gainLEC2 LEC1 ABI3			0.005			0.014			0.13			0.022			0.010			0.20
pmutJ	gain LEC2	0.009			0.005			0.049			0.070			0.26			0.41		
pmutJ	gain ABI3		0.018			0.044			0.42			0.026			0.23			0.55	
pmutJ	gainLEC2 LEC1 ABI3			0.003			0.006			0.017			0.012			0.42			0.081
pmut K	gain LEC2	0.009			0.004			0.050			0.071			0.28			0.57		
pmut K	gain ABI3		0.08			0.29			0.70			0.052			0.035			0.63	
pmut K	gainLEC2 LEC1 ABI3			0.006			0.08			0.31			0.057			0.042			0.93
pmutL	gain LEC2	0.009			0.005			0.045			0.062			0.13			0.03		
pmutL	gain ABI3		0.002			0.022			0.32			0.033			0.16			0.45	
pmutL	gainLEC2 LEC1 ABI3			0.001			0.007			0.30			0.008			0.12			0.21

C-2

		pmutF +LEC2	pmutF +ABI3	pmutF +LEC1 LEC2 ABI3	pmutG +LEC2	pmutG +ABI3	pmutG +LEC1 LEC2 ABI3	pmutI +LEC2	pmutI +ABI3	pmutI +LEC1 LEC2 ABI3	pmutJ +LEC2	pmutJ +ABI3	pmutJ +LEC1 LEC2 ABI3	pmutK +LEC2	pmutK +ABI3	pmutK +LEC1 LEC2 ABI3	pmutK +LEC2	pmutK +ABI3
pmut A	gain LEC2																	
pmut A	gain ABI3																	
pmut A	gainLEC2 LEC1 ABI3																	
pmut 3	gain LEC2																	
pmut 3	gain ABI3																	
pmut 3	gainLEC2 LEC1 ABI3																	
pmutB	gain LEC2																	
pmutB	gain ABI3																	
pmutB	gainLEC2 LEC1 ABI3																	
pmut2	gain LEC2																	
pmut2	gain ABI3																	
pmut2	gainLEC2 LEC1 ABI3																	
pmutH	gain LEC2																	
pmutH	gain ABI3																	
pmutH	gainLEC2 LEC1 ABI3																	
pmutF	gain LEC2																	
pmutF	gain ABI3																	
pmutF	gainLEC2 LEC1 ABI3	0.002	0.009															
pmutG	gain LEC2	0.013																
pmutG	gain ABI3		0.22															
pmutG	gainLEC2 LEC1 ABI3			0.14	0.020	0.026												
pmutI	gain LEC2	0.34			0.09													
pmutI	gain ABI3		0.32			0.052												
pmutI	gainLEC2 LEC1 ABI3			0.027				0.0003	0.015									
pmutJ	gain LEC2	0.18			0.005			0.76										
pmutJ	gain ABI3		0.38			0.10			0.84									
pmutJ	gainLEC2 LEC1 ABI3			0.005			0.026			0.001	0.0014	0.19						
pmut K	gain LEC2	0.21			0.003			0.87			0.79							
pmut K	gain ABI3		0.86			0.23			0.13			0.18						
pmut K	gainLEC2 LEC1 ABI3			0.84			0.20			0.12			0.041	0.023	0.031			
pmutL	gain LEC2	0.048			0.007			0.11			0.021			0.036				
pmutL	gain ABI3		0.31			0.10			1			0.82			0.10			
pmutL	gainLEC2 LEC1 ABI3			0.08			0.033			0.92			0.11			0.12	0.034	0.052

(A) Statistical analyses corresponding to the results presented in Figure 3.
(B) Statistical analyses corresponding to the results presented in Figure 4
(C) Statistical analyses corresponding to the results presented in Figure 5 (C1, to be continued with C2)
Red: significant differences at 5%
NR: not relevant.
For A and B, the normality of the data was checked with a Shapiro-Wilk test. As the samples were not all following a Normal law, a Kolmogorov-Smirnov test was then performed on the relevant comparisons. All the tests are included in the R package

C: The normality of the data was checked with a Shapiro-Wilk test. Student t-test was performed on the relevant comparisons using the R stats Package (https://www.r-project.org/) version 3.2.