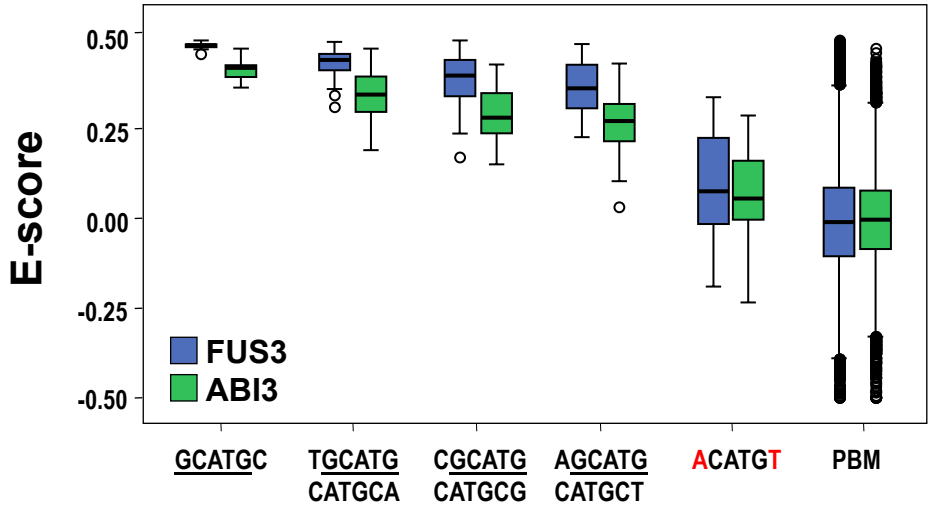


Fig S1 A :E-score distributions of top 4, 6mer cis-elements recognized by FUS3 and ABI3
The elements are shown in descending order in relation to their E-score. The motif *ACATGC* corresponds to a "mutant" version of the top-scoring *GCATGC* motif, reflecting a decrease in E-score. All the top scoring elements recognized by both proteins share the sequence CATGC, which could be considered as an RY-core. Note that the "canonical" RY 6mer previously described (*CATGCA*) appears in the second position for both proteins, with a clear decrease in affinity in relation to the top scoring 6mer (*GCATGC*). In general, both proteins recognize the same elements, although DNA-binding affinity was slightly lower for ABI3

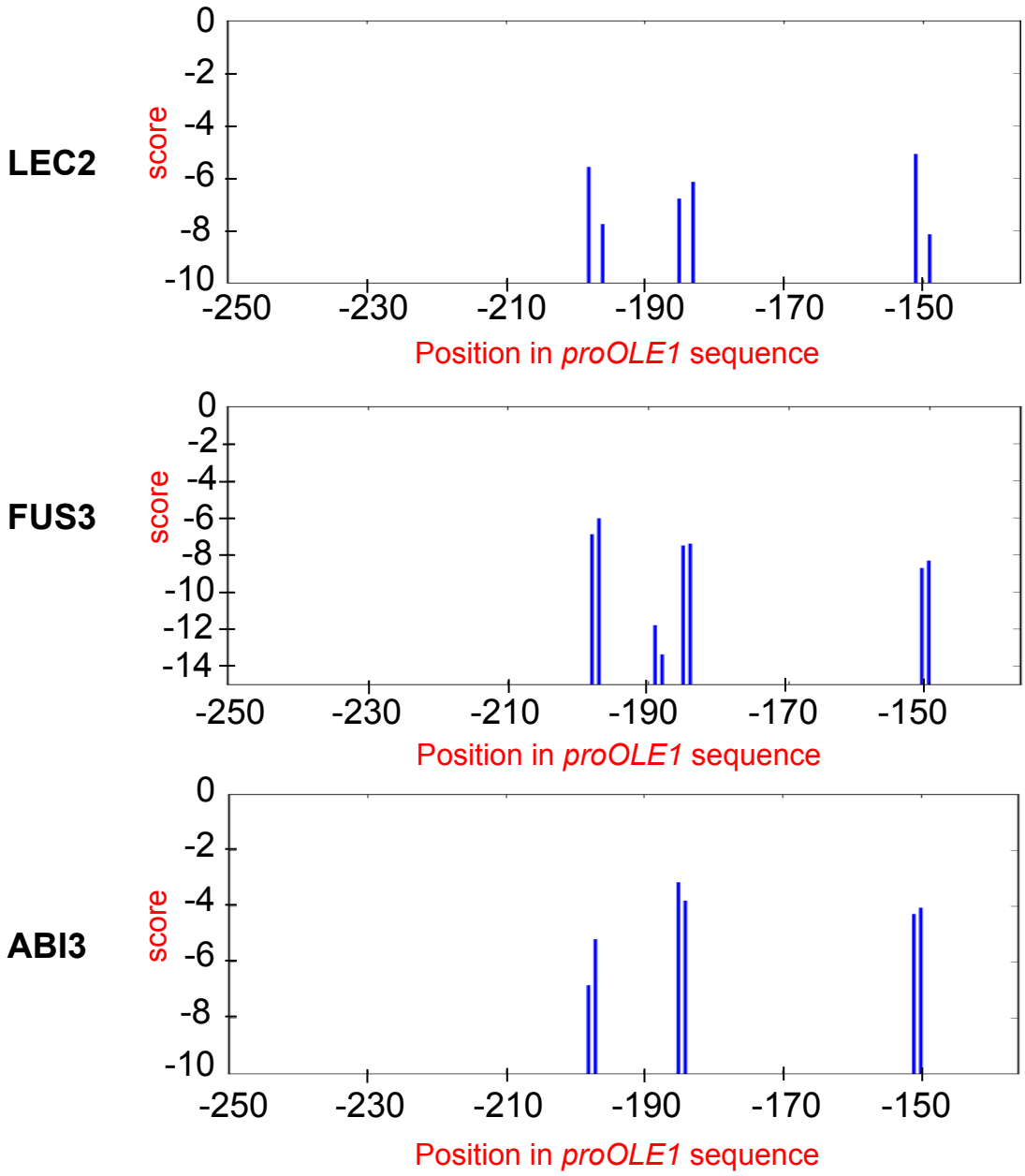


Figure S1B: Score plot of the *ProOLE1* sequence using matrix obtained for LEC2, FUS3 and ABI3. *ProOLE1* sequence was scanned using LEC2, FUS3 and ABI3 PWM. As these matrices are pseudo-palindromic, each binding site is systematically identified on both DNA strands with slightly different scores, explaining the presence of double bars in the plots. Numbers on the X axis indicate nucleotide number from translation start.

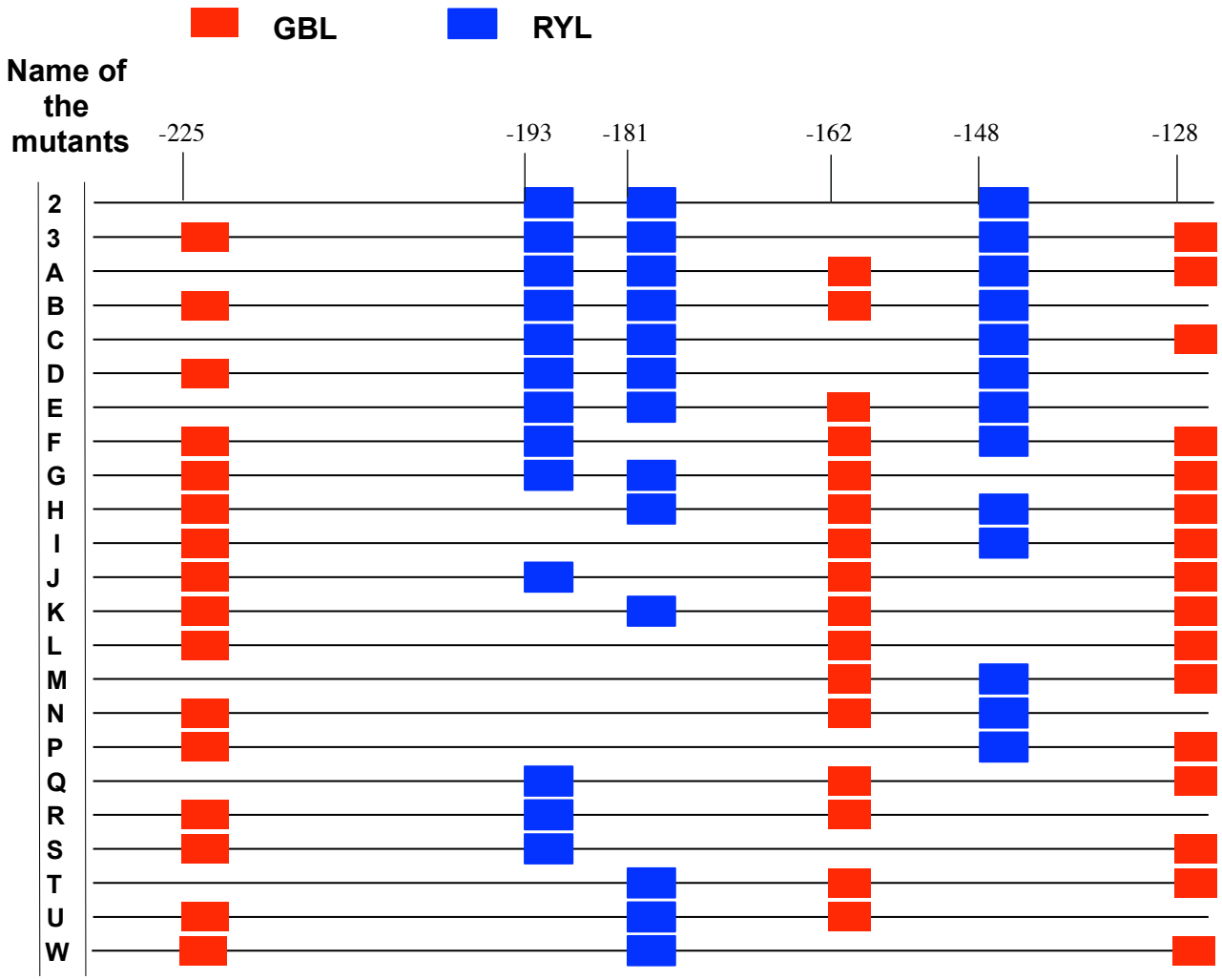
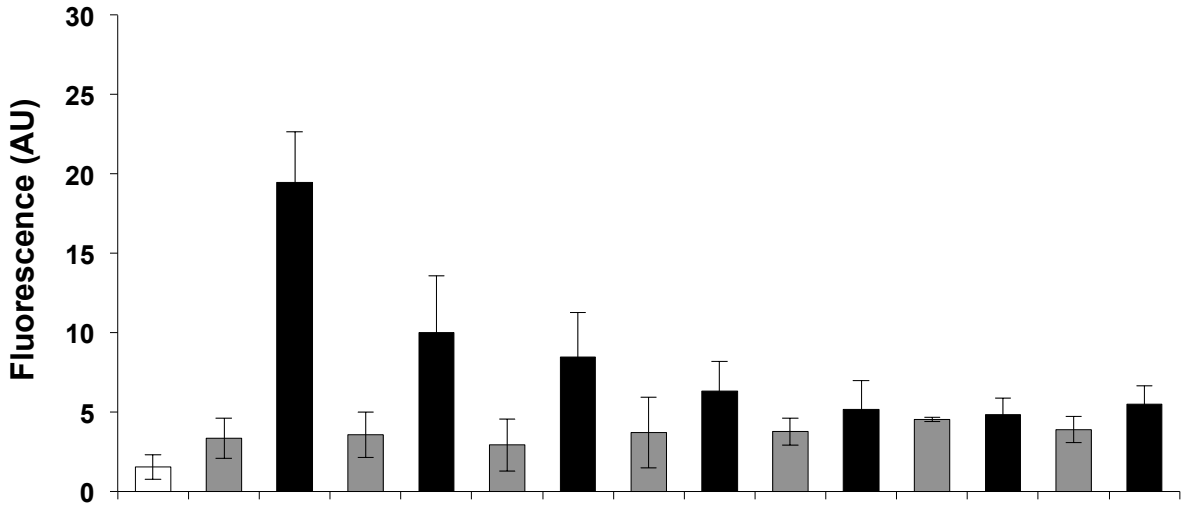
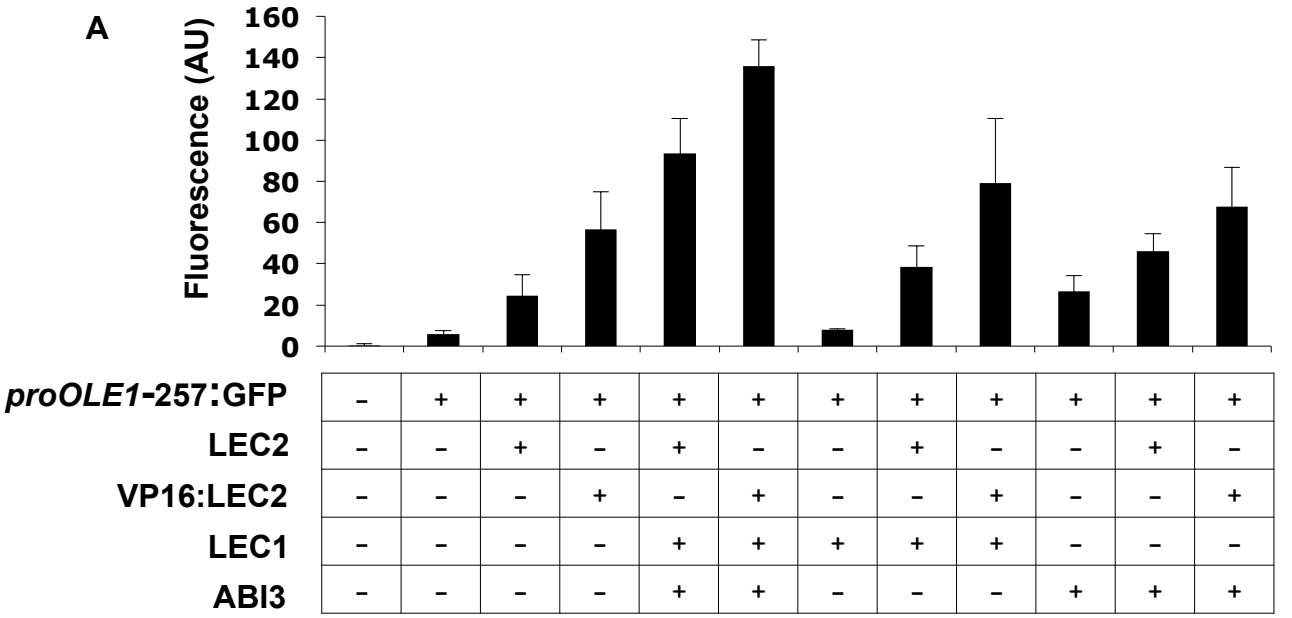


Figure S2: schematic representation of the mutations of the regulatory elements (mutated version of RYL and mutated version of GBL) found in *proOLE1*. Numbers on the top indicate nucleotide number from translation start.



LEC2	–	–	+	–	+	–	+	–	+	–	+	–	+	–	+
***proOLE1*-257:GFP**	–	+	+	–	–	–	–	–	–	–	–	–	–	–	–
***proOLE1*-257 mut G:GFP**	–	–	–	+	+	–	–	–	–	–	–	–	–	–	–
***proOLE1*-257 mut H:GFP**	–	–	–	–	–	+	+	–	–	–	–	–	–	–	–
***proOLE1*-257 mut I:GFP**	–	–	–	–	–	–	–	+	+	–	–	–	–	–	–
***proOLE1*-257 mut F:GFP**	–	–	–	–	–	–	–	–	–	+	+	–	–	–	–
***proOLE1*-257 mut J:GFP**	–	–	–	–	–	–	–	–	–	–	–	+	+	–	–
***proOLE1*-257 mut K:GFP**	–	–	–	–	–	–	–	–	–	–	–	–	–	+	+

Figure S3: activation of the native or mutated *OLE1* promoter by LEC2 in moss protoplasts



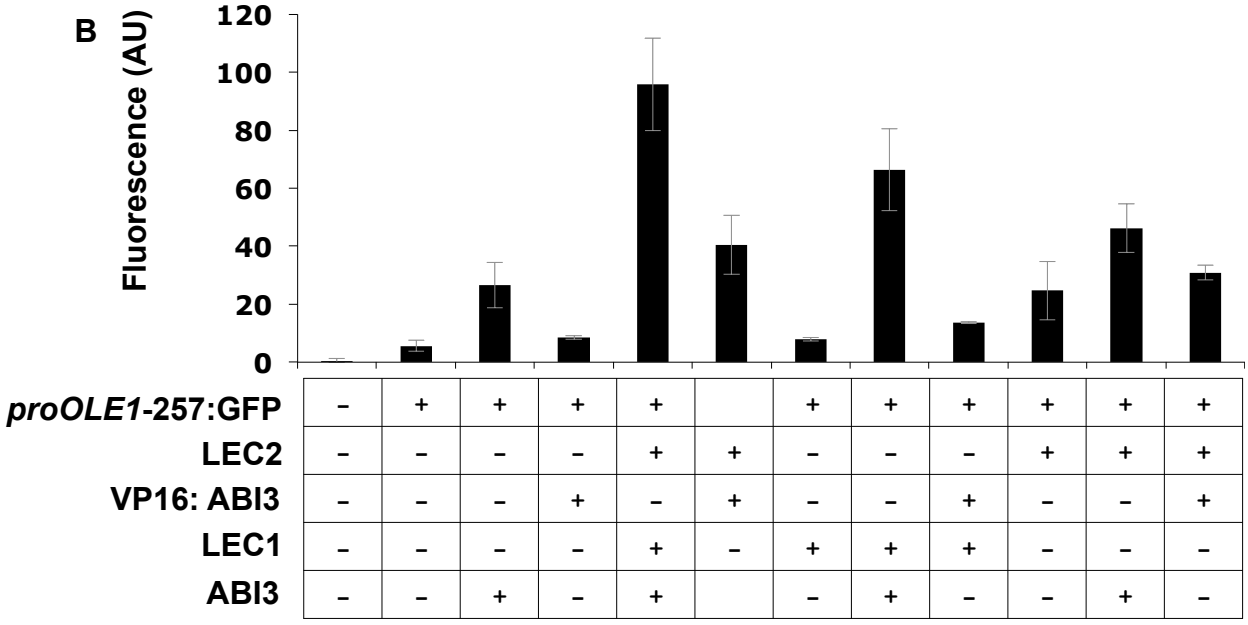


Figure S4 : activation of *OLE1* promoter by LEC2 (A) or ABI3 (B) fused to a strong transcriptional activator (VP16) in moss protoplasts

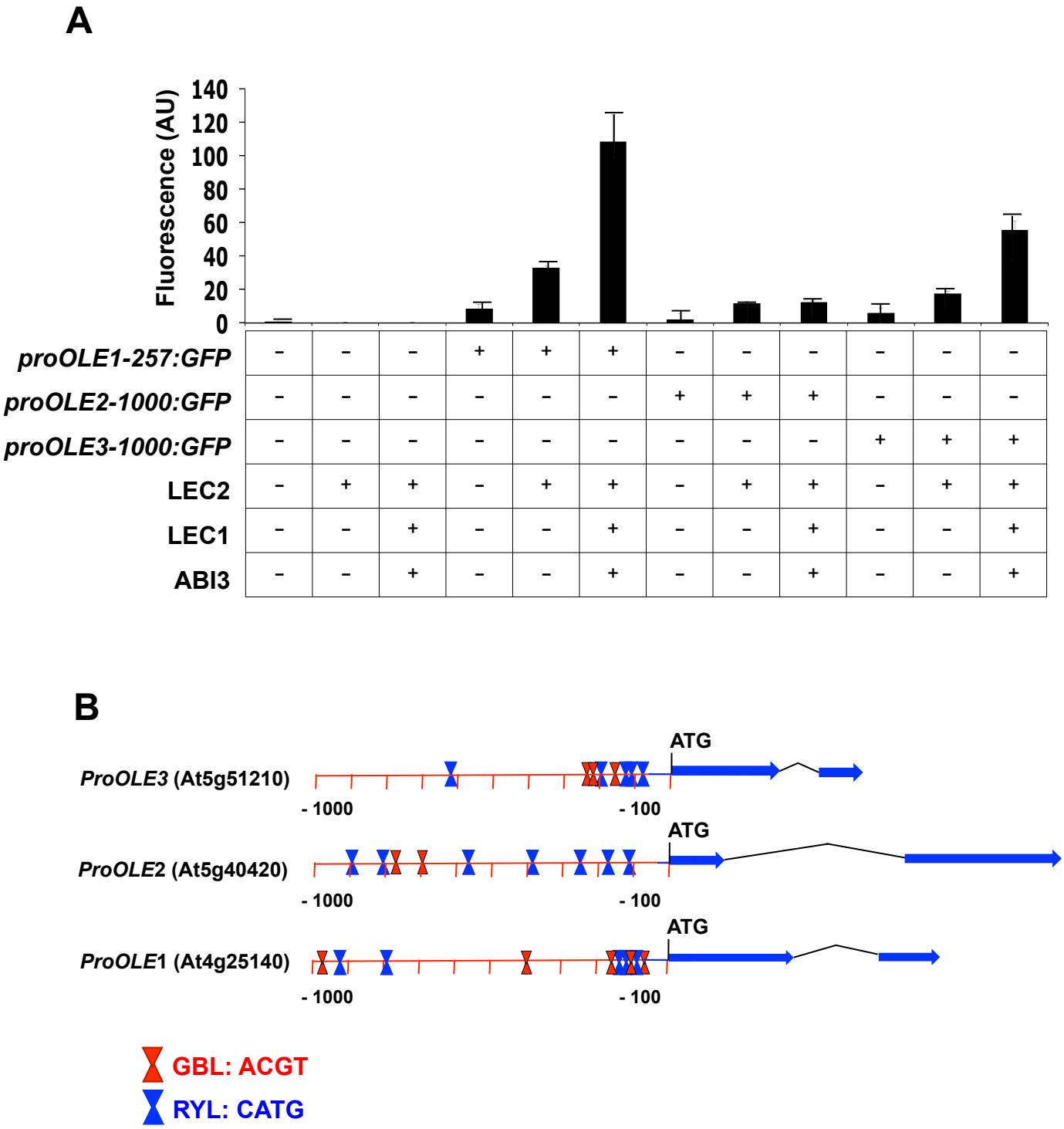


Figure S5: Effect of LEC2 and AFL complex on other oleosin promoters

A- activation of promoter *OLE1*, *OLE2*, and *OLE3* by the LEC1, LEC2, ABI3 complex in moss protoplasts.
B- schematic representation of *proOLE1*(At4g25140), proOLE2 (AT5G40420) and *proOLE3* (At5g51210) genomic regions. The RYL and the GBL core regions are highlighted in blue and red respectively.

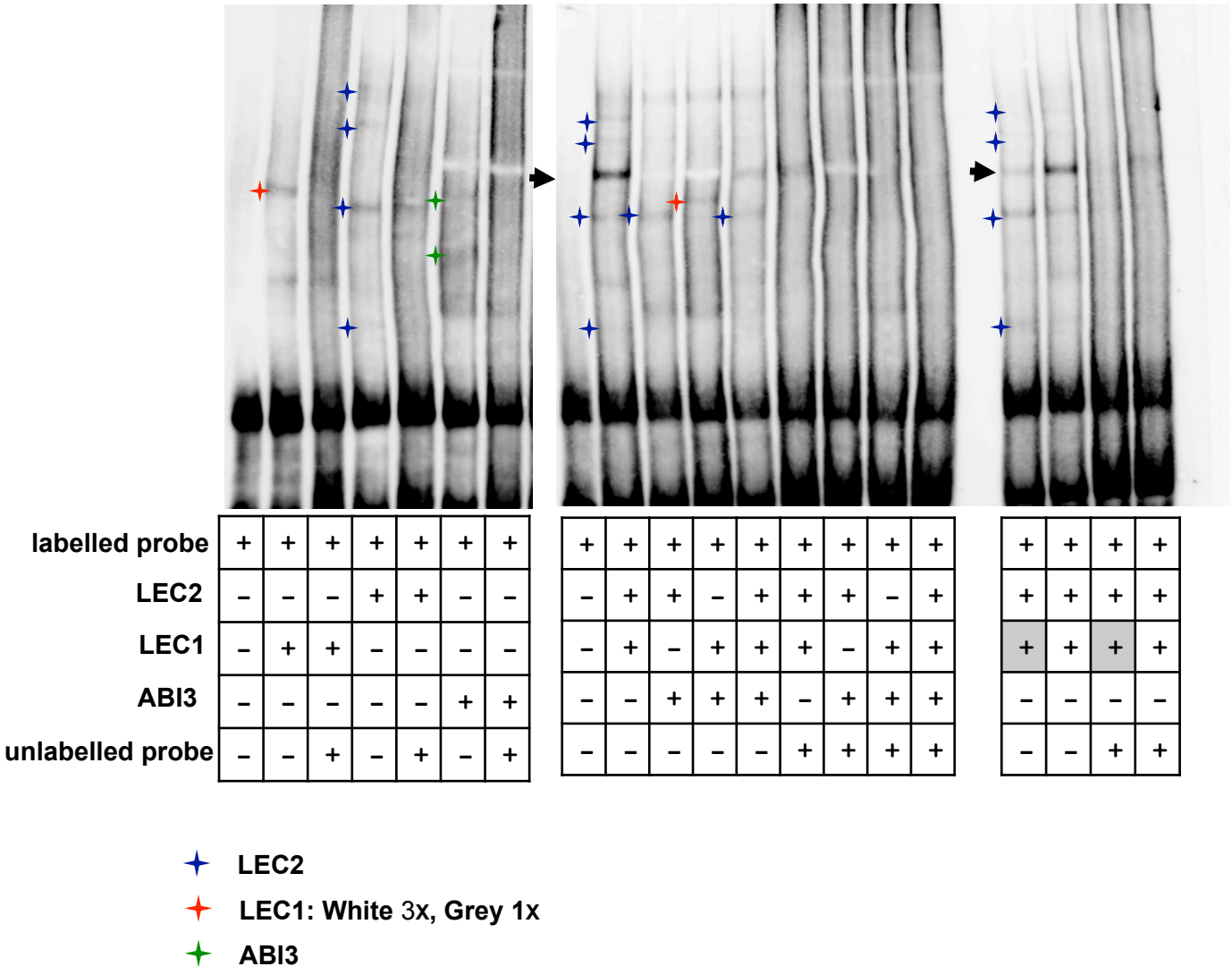


Fig S6: LEC1 and LEC2 bind to pro*OLE1*.
EMSA binding assay with LEC1, LEC2 and ABI3 alone or in combination with labelled 100bp wild-type pro*OLE1* probe. Competitions were performed with 25x more labelled probe. Three time more LEC1 were usually used for interaction studies, except on the right panel were less (1x) was used to check stoichiometry.

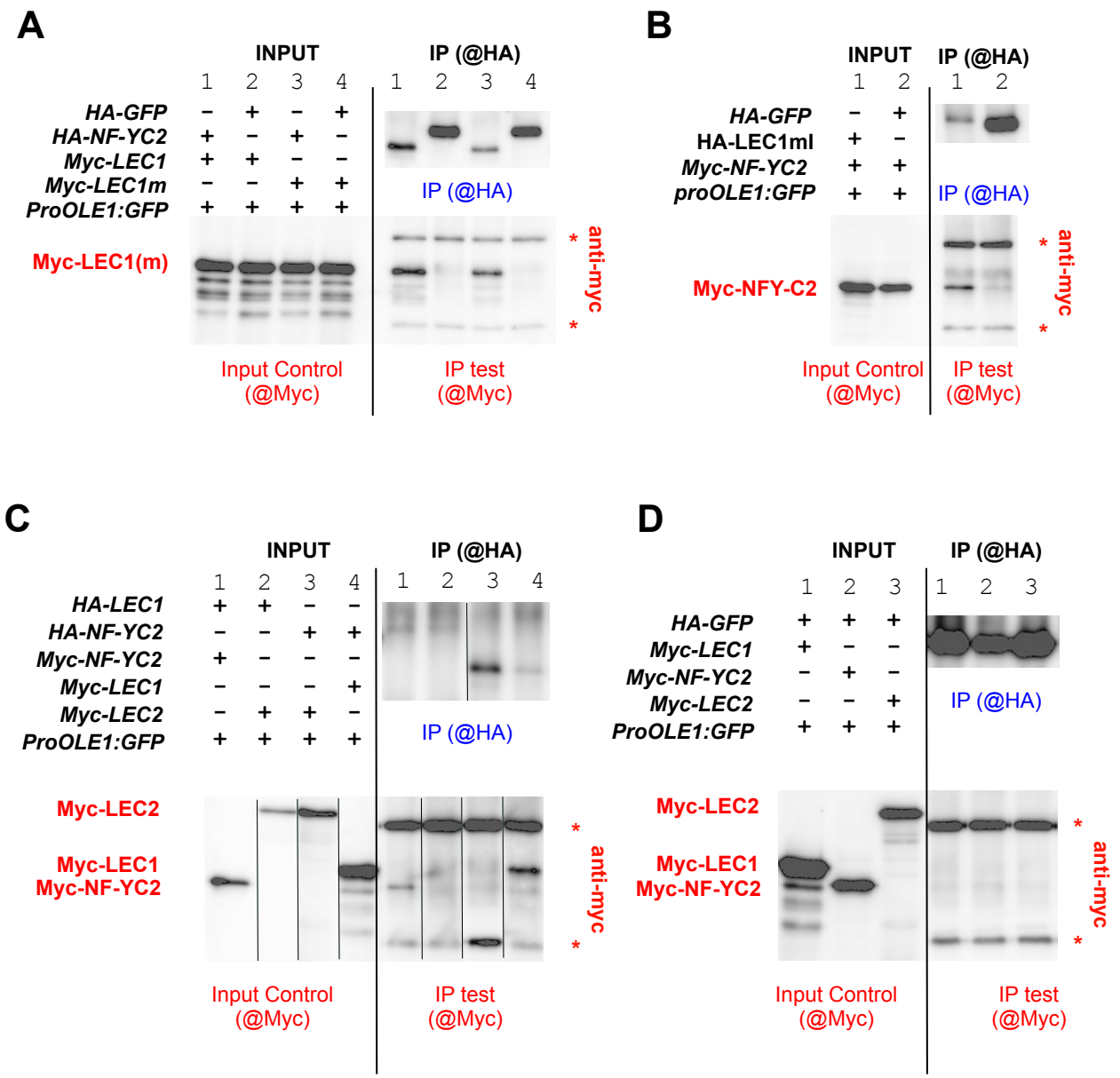


Fig S7 : Interaction controls.
in presence of *proOLE1*:GFP

A-B NF-YC2 interacts with the mutated LEC1 (Lec1mut).

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 protoplast. INPUT : 2 % of the full protein extract. IP : immunoprecipitated sample. (*) : heavy and light chains of the antibody used for the immunoprecipitation.

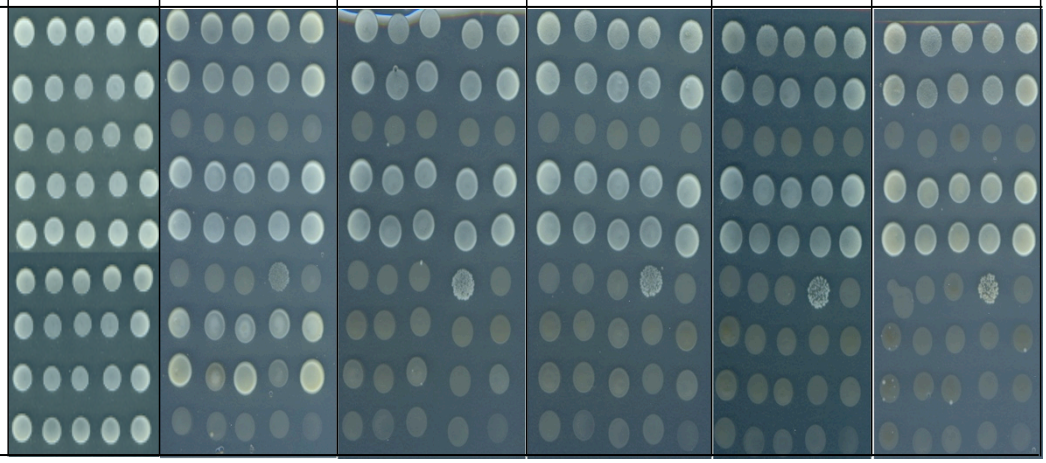
A

AD / BD	LEC1	LEC2	ABI3	FUS3	pDEST22
LEC1		+	+	+	+
LEC2	++		++	++	++
ABI3	++	++		++	++
FUS3	–	–	–		–
pDEST32	–	–	–	–	–

– grows on SD-WL only
\+ grows on SD-WLH
++ grows on SD-WLHA

B

AD	BD	-WL	-WLH 5mM 3 AT	-WLH 10mM 3 AT	-WLH 20mM 3 AT	-WLH	-WLHA
LEC1m	LEC1m						
LEC1m	LEC1						
LEC1m	pDEST32						
LEC1	LEC1						
LEC1	LEC1m						
LEC1	pDEST32						
pDEST22	LEC1m						
pDEST22	LEC1						
pDEST22	pDEST32						



FigS8: Interactions in Yeast