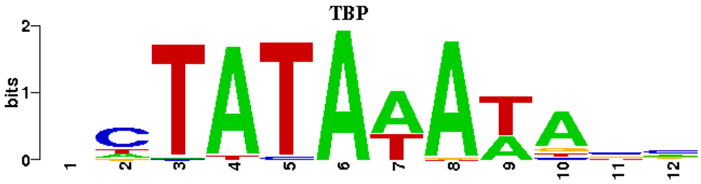
Supplemental Table S1. Predicted transcription factor binding sites for TATA binding protein (TBP).

TBP sites, mapped in the -500 upstream region of *EC1* genes. Predictions are according to AthMap (http://www.athamap.de/index.php). The sequence logo of TBP DNA binding motif (Franco-Zorilla et al., 2014) is shown below.

Gene	Factor	Family	Position	Relative orientation	Relative distance	Max. Score	Threshold Score	Score
At1g76750.1	TBP	- other	28815898	+	-36	10.98	5.16	7.6
At2g21740.1	TBP	- other	9289511	+	-68	10.98	5.16	7.11
At2g21740.1	TBP	- other	9289664	+	-221	10.98	5.16	5.16
At2g21750.1	TBP	- other	9290888	+	-64	10.98	5.16	8.09
At4g39340.1	TBP	- other	18293561	+	-55	10.98	5.16	10.44
At5g64720.1	TBP	- other	25890092	+	-53	10.98	5.16	6.88

Name: **TBP**

Logo:



Matrix:

```
A |  48  27   5 162   0 171 106 166  65 125  22  51
C |  46 108   2   0   7   0   0   0   2  14  72  72
G |  29   9   0   0   0   0   0   3   0  17  48  27
T |  48  27 164   9 164   0  65   2 104  15  31  19
```

Max. score: 10.98

Threshold: 5.16

Supplemental Table S2. List of proteins able to bind the *EC1.1* promoter in yeast.

The proteins listed have been found more than once as *pEC1.1* interactors.

Accession	**Description**
At1g0782/ At1g07820/At3g53730	Histone 4
At2g46980	ASY3, a coiled-coil domain protein
At1g07820	Histone superfamily protein
At1g69690	AtTCP15
At1g01960	Embryo sac Development Arrest 10 (EDA10)
At1g30970	SUF4
At5g62470	Myb 96
At3g27670	RESURRECTION1, RST1
At5g22880	Histone H2B

Supplemental Table S3. SUF4 affects activity of *EC1.1* and *EC1.2* promoters.

GUS analyses performed with mature ovules of F1, obtained by crossing homozygous *suf4-1* mutants with homozygous *pEC1.1(-457)::GUS* or *pEC1.2(-893)::GUS* lines (*suf4-1 suf4-1xpEC1.1(-457)::GUS pEC1.1(-457)::GUS* and *suf4-1 suf4-1xpEC1.2(-893)::GUS)*. Note that the χ^2 statistics indicate that SUF4 regulates expression of *pEC1.1(-457)::GUS*, as well as *pEC1.2(-893)::GUS*.

Genotypes	Ovules						
	observed GUS+	observed GUS-	total	expected GUS+	expected GUS-	χ^2 value*	p-value
SUF suf4-1 EC1.1::GUS +/-	356 25,6%	1,036 74,4%	1,392	348 25%	1,044 75%	0.24	0.5<P<0.75
SUF suf4-1 EC1.2::GUS +/-	301 24,6%	924 75,4%	1,225	306.3 25%	918.7 75%	0.12	0.5<P<0.75

GUS+, GUS positive ovules; GUS-, GUS negative ovules

Supplemental Table S4. List of genes co-expressed with *SUF4*.

Accession	Description	Pearson coefficient (Log)
At1g30970	Zinc finger (C2H2 type) family protein, contains Pfam domain	1
At1g78930	Mitochondrial transcription termination factor-related /	0,6780
At5g63200	Tetratricopeptide repeat (TPR)- protein	0,6676
At1g50910	Unknown protein	0,6624
At5g47400	Unknown protein	0,6601
At1g08060	**MOM1**	**0,6555**
At3g44530	Transducin family protein	0,6551
At4g18600	Unknown protein	0,6484
At5g06100	Myb transcription factor (MYB33)	0,6471
At2g35540	DNAJ heat shock	0,6455
At2g47820	Expressed protein	0,6441
At5g20200	Nucleoporin-related protein	0,6407
At5g18770	F-box protein	0,6381
At1g77410	Putative beta-galactosidase	0,6378
At2g43980	Inositol 1,3,4-trisphosphate 5/6-kinase	0,6353
At4g35930	F-box family protein	0,6345
At5g05350	Unknown protein	0,6295
At5g05130	SNF2 domain-containing protein /	0,6268
At4g25540	DNA mismatch repair protein (MSH3)	0,6254
At1g52620	Pentatricopeptide (PPR) repeat-containing protein	0,6248
At5g13470	Unknown protein	0,6222
At2g40950	bZIP transcription factor	0,6206
At2g28330	Unknown protein	0,6200

Supplemental Table S5. Primers used in this work.

Name	Sequence
Promoter analysis	
EC1.2p(-869)_fw(PstI)	TGATTACGCCCTGCAGCGTTTATACAAGGACAGAG
EC1.2p (-750)_fw(PstI)	TGATTACGCCCTGCAGAGGTAACTTGTCCAAGAAG
EC1.2p(-631)_fw(PstI)	TGATTACGCCCTGCAGTATATTTGTATTCGAGATTGTG
EC1.2p(-502)fw(PstI)	TGATTACGCCCTGCAGCACATCGACAACACTATAGC
EC1.2p(-374)_fw(PstI)	TGATTACGCCCTGCAGCATAAAGTTCAATGAGTAGT
EC1.2p (-252)_fw(PstI)	TGATTACGCCCTGCAGCGCTACTGATTCAACATG
EC1.2p(-222)_fw(PstI)	TGATTACGCCCTGCAGCTAAATACGTTTCTACAGTCAAA
EC1.2p(-212)_fw(PstI)	TGATTACGCCCTGCAGTTCTACAGTCAAATGCTTTAAC
EC1.2p(-192)_fw(PstI)	TGATTACGCCCTGCAGACGTTTCATGATTAAGTGACTAT
EC1.2p(-183)_fw(PstI)	TGATTACGCCCTGCAGATTAAGTGACTATTTACCGTC
EC1.2p(-172)_fw(PstI)	TGATTACGCCCTGCAGTATTTACCGTCAATCCTTTCC
EC1.2p(-152)_fw(PstI)	TGATTACGCCCTGCAGCCATTCCTCCCACTAATCCA
EC1.2p(-132)_fw(PstI)	TGATTACGCCCTGCAGACTTTTTAATTACTCTTAAATCAC
EC1.2p(-112)_fw(PstI)	TGATTACGCCCTGCAGTCACCACTAAGCTTCGAATC
EC1.2p_rev(BamHI)	TGCTCACCATGGATCCACTTGTGTTAGAAGCCATTA
EC1.1p(-463)_fw	caccTGCCTTATGATTTCTTCGGTTT
EC1.1p(-326)_fw	TTCTATTGAACTAAATCAAACGAGTTT
EC1.1p(-192)_fw	CTAATTATCTCACAATCTAATGAGCTTC
EC1.1p_rev	TTCTCAACAGATTGATAAGGTCGA
EC1.2p(-894)_fw	caccAAGCATTTGCGTTTGGTTTATCATTGCG
EC1.2p_rev	TATTCTTTCTTTTTGGGGTTTTTGTTT
EC1.3p(-293)_fw	caCCACTCTTGTTATACAATCTTCAAAGTTTCTATA
EC1.3p(-133)_fw	caccACTAAAAACCATCTTTAATCATAATTAAA
EC1.3p_rev	TGTGTTTTCTTTTGAAGATTTTGTG
EC1.4p(-263)_fw	caccGTTGCTCTTGCTGCATCAAATACATA
EC1.4p(-163)_fw	caccACTAATCATTTACTTTCACTTATCCCT
EC1.4p_rev	TGGTGTGGTTTTTGTTTGGAATTTTA
EC1.5p(-251)_fw	caccGGGTTTCCATAAAGCCCAATTTAGTT
EC1.5p(-146)_fw	caacTAATTAAATTAACCACGATCACTGTGATAATTAC
EC1.5p_rev	TGCTTCTTTTTGTGTTATGGATTTTTTGT

Housekeeping and control genes	
ACT3 (AT3G53750)_fw	GATTTGGCATCACACTTTCTACAATG
ACT3 (AT3G53750)_rev	GTTCCACCACTGAGCACAATG
ACT8 (AT1G49240)_fw	CTCAGGTATTGCAGACCGTATGAG
ACT8 (AT1G49240)_rev	CTGGACCTGCTTCATCATACTCTG
UBQ10 (AT4G05320)_fw	GGAAAAAGGTCTGACCGACA
UBQ10 (AT4G05320)_rev	CTGTTCACGGAACCCAATTC
IAA8 for ChIP experiment_fw	GAACGTAACTACTTGGGTCT
IAA8 for ChIP experiment_rev	GTCTTTAGAAGGTAGCAAC
IAA8 RTqPCR_fw	CAATGGCTTCTTCTACTTCG
IAA8 RTqPCR_rev	CCAATCACCGTCTTTATCT
Primers for quantitative PCR	
EC1.1_rev	AGTCATTGCCATCACAGTAACC
EC1.1_fw	CTTGTGTACAGGCTCAAGCTTG
EC1.2_fw	GGCTTCTAACACAAGTTTCCTC
EC1.2_rev	ATGACCTCGACGGCTTGACA
EC1.2_rev	CCGAGTTTGGTCTCACCGTT
EC1.2_fw	CTCTTCTCCTCGTTCTCAACG
EC1.4_fw	ATGGCTTCGAACACTACTTTCC
EC1.4_rev	CCATCAGTCCTCCACTTTGG
EC1.5_rev	CGGTTCACTCGTACCGGTTTGA
EC1.5_fw	GACCTTTCATGTCATCACTGTCG
Yeast constructs	
pAtEC1.11 plus EcoRI_fw	CGAATTCTGCCTTATGATTTCTTCGG
pAtEC1.11 plus XbaI_rev	CGTCTAGATAATTAGTGGGTCTGTTTAGG
pAtEC1.12 plus EcoRI_fw	CGAATTCCAGACCCACTAATTACG
pAtEC1.12 plus XbaI_rev	CGTCTAGACTCAACAGATTGATAAGG
Other primers	
GUS_rev	TCATTGTTTGCCTCCCTGCTG
SUF4-1_fw	GTATGGCAAATGCCACCTC
SUF4-1_rev	CTGAGATTCGTCTGTCTATCGC
TDNA pSKI015 derivative (Dinneny et al. 2004)	CATTTTATAATAACGCTGCGGACATCTAC
SUF4 alternative splicing_fw	GGGGCTCAGCAACCATCTCAT

SUF4 alternative splicing_rev	ATCCGCCCAGCAAGCCTACT
SUF4 CDS pENTR-D-TOPO_fw	CACCATGGGTAAGAAGAAGAAGAG
SUF4 CDS_rev	CTAAAACGCCATCCGCCC
MOM1.3_fw	AAGCAGTTGTCTTCTACCAG
MOM1.3_rev	TTGCCGCTTATTTTGCCTAG
T-DNA SALK LBb1 primer	GCGTGGACCGCTTGCTGCAACT
MOM1 promoter_fw gateway	GGGGACAAGTTTGTACAAAAAAGCAGGCTGATCGACTCTAAACATTATGGG
MOM1 promoter_rev gateway	GGGGACCACTTTGTACAAGAAAGCTGGGTCATATTCACTGAGAGCACGCAA

Supplemental table cited literature

Franco-Zorrilla JM, López-Vidriero I, Carrasco JL, Godoy M, Vera P, Solano R (2014) DNA-binding specificities of plant transcription factors and their potential to define target genes. Proc Natl Acad Sci USA 111: 2367-72