

Figure S1. Schematic representation of BiFC constructs. The seven interactor candidates were fused at their respective C-terminus to the N-terminal part of Venus (pVYNE vector), while the regulatory subunit PP2A-B'ζ was fused at its C-terminus to the C-terminal part of Venus (pVYCE vector). All fusion proteins were expressed from the CaMV 35S promoter. N173: amino acids 1-173 of Venus. C155: Venus amino acids 155-238.

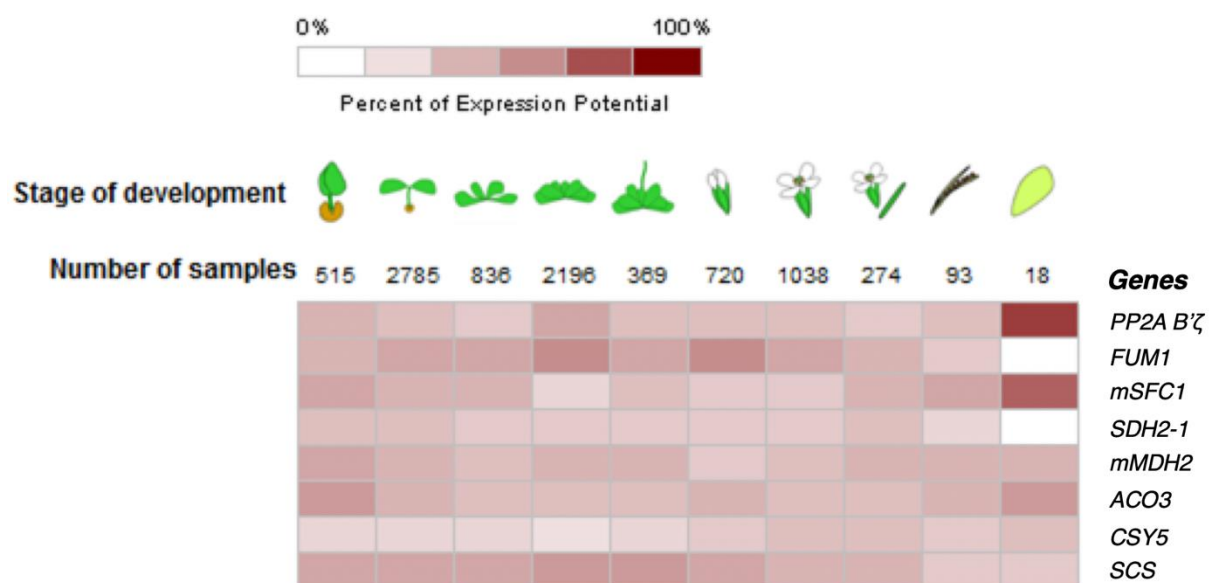


Figure S2. GeneVestigator expression study of genes coding for proteins involved in energy metabolism. All genes are expressed throughout development, and *PP2A-B'ζ*, *mSFC1* and *ACO3* are upregulated in senescent leaves.

Table S1. Oligonucleotide sequences for genotyping and cloning.

Name	Template	Sequence	Usage
Z1_150586_LP	AT3G21650	TTTTCAC TTCAGAGTCAGCCG	Genotyping
Z1_150586_RP	AT3G21650	ATGGTGCATCGACCTTACATC	
Z2_107944_LP	AT3G21650	CACTCGTCGAAAAGAACTTGG	
Z2_107944_RP	AT3G21650	CCGAATCTCTTTATCGGGAAG	
Z_F	AT3G21650	ATAGTCGACATGATCAAACAGATATTTGG	Cloning (BiFC Venus)
Z_R	AT3G21650	ATGGTACCCGACCCTGTGGACTCAGA	
FUM1_F	AT2G47510	ATACTAGTATGTTCGATTTACGTCGCGTCG	
FUM1_R	AT2G47510	ATATCTCGAGATCGGAGGGACCAATCAT	
mSFC1_F	AT5G01340	ATACTAGTATGGCGACGAGAACGGAA	
mSFC1_R	AT5G01340	ATATCTCGAGTAAAGGAGCATTCGGAAG	
SDH2-1_F	AT3G27380	ATACTAGTATGGCGTCTGGTTTGATCG	
SDH2-1_R	AT3G27380	ATATCTCGAGACGCTGAAGTTGCTTGAT	
mMDH2_F	AT3G15020	ATACTAGTATGTTCCGATCAATGATTGTTC	
mMDH2_R	AT3G15020	ATATCTCGAGTTGGTTGGCAAATTTGAT	
ACO3_F	AT2G05710	ATACTAGTATGTATTTAACCGCTTCATCTTCC	
ACO3_R	AT2G05710	ATATCTCGAGTTGCTTGCTCAAGTTTCT	
CSY5_F	AT3G60100	ATACTAGTATGGTGTTTTTTCGCAGCGTAT	
CSY5_R	AT3G60100	ATATCTCGAGGCGGTTCAAGCGCGTGAAGTT	
SCS_F	AT5G08300	ATACTAGTATGTCTAGACAAGTGGCAAGGC	
SCS_R	AT5G08300	ATATCTCGAGCTGCTTCAAAAGACCTCT	

Table S2. Phosphopeptides retrieved from PhosPhAt4 and the literature. Sites are experimentally verified, except if denoted as ‘Predicted’ on column 5.

AGI	Annotation	Phosphopeptide	Hits
AT3G14940	PPC3	⁹ MASIDAQLR ¹⁷ (*)	34
AT4G37870	PCK1	⁶² SAPTTPINQNAAAAFAAVSEEER ⁸⁴ (*)	1
		⁶² SAPTTPINQNAAAAFAAVSEEER ⁸⁴	5
		⁶² SAPTTPINQNAAAAFAAVSEEER ⁸⁴	1
		⁶⁰ KRSAPTTPINQNAAAAFAAVSEEER ⁸⁴	1
		⁶⁰ KRSAPTTPINQNAAAAFAAVSEEER ⁸⁴	2
		⁶⁰ KRSAPTTPINQNAAAAFAAVSEEER ⁸⁴	7
		⁶⁰ KRSAPTTPINQNAAAAFAAVSEEER ⁸⁴	1
AT1G77360	PPR6	MKNVYRVLK	2
AT2G05710	ACO3	⁸⁰¹ DFNSYGSR ⁸⁰⁸	1
		⁸⁰¹ DFNSYGSRR ⁸⁰⁹	1
		⁸⁹ TFSSMASEHPFK ¹⁰⁰	2
		⁸⁹ TFSSMASEHPFK ¹⁰⁰	46
AT5G01340	mSFC1	⁹⁴ QTAFKDSEIGUVSNRGRFLSGFG ¹¹⁶ ²³⁵ KTRLMAQSRDSEGGIRY ²⁵¹	
AT2G47510	FUM1	¹⁹⁴ TLHSTLESKSFEFK ²⁰⁷	1
AT3G27380	SDH2-1	⁴⁰ SSGGGRGSNLKTFQIYR ⁵⁶	
		¹⁵⁶ NQYKSIEPWLKRKTTPASVPA ¹⁷⁵	
		²²⁰ LLHANRWISDSRDEYTKERLE ²⁴⁰	
AT3G15020	mMDH2	¹⁷⁴ VTTLDVVRARTFYAGKSD ¹⁹¹	
AT3G60100	CSY5	¹ MVFFRSVSAISRLRSRAVQQSSLNSVRWLHSSE ³⁴	
AT5G08300	SCS	⁴³ ASDPHPPAAVFVDK ⁵⁶	1
		¹⁸⁵ IGIMPGYIHKPGK ¹⁹⁷	1
		²⁹⁶ MGHAGAIVSGGK ⁴⁰⁷	4
		³⁰⁸ GTAQDKIK ³¹⁵	1
		³³¹ IGSAMYELFQER ³⁴²	5

(*) Identical to phosphopeptide detected in our phosphoproteomics analysis (Table S3).

Table S3. PP2A-B'Z interactors identified by phosphoproteomics.

AGI	Annotation	Detected phosphopeptide	Probability
AT3G14940	PPC3	⁹ MASID ^S AQLR ¹⁷	1
AT4G37870	PCK1	⁶² SAP ^T TPINQNAAAAFAAVSEEER ⁸⁴	0.967, 0.776
AT1G77360	PPR6	⁴⁶¹ ^T ^T QKACVLL EEMIGIRP ^S GVTFGR ⁴⁸⁶	1, 1, 0.786