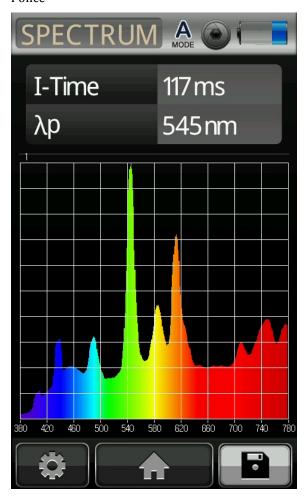
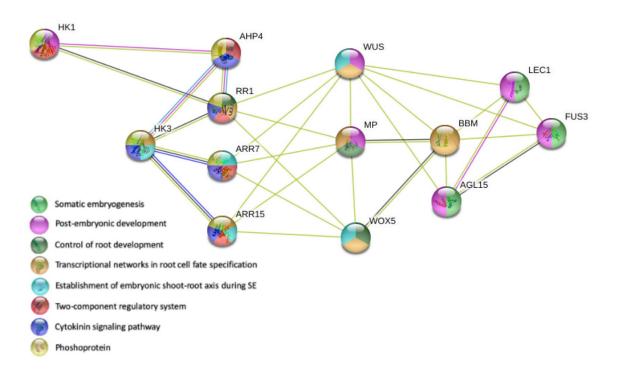
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Supplementary Figure 1. Light spectrum used for SEs maturation and conversión to plantlet of C. arabica var. Typica.

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Supplementary Figure 2. Gene network using STRING database with high confidence (0.700) of two component and cytokinin signaling genes, AHK1, AHK3, AHP4, ARR1, ARR7, ARR15, Auxin signaling; ARF5 (Monopteros), homedomains and master regulators of SE.

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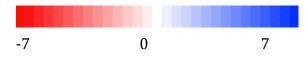
Supplementary Table 1. Sequence primer qPCR and protein function of genes analyzed during SEs in *C. arabica* var. Typica.

Gene	ID AT (A. thaliana)	ID XP (C. arabica)	Protein function	% ID At/Ca	Primer
АНК1	AT2G17820.1	XP_027075540	Histidine kinase 1; Functions as an osmosensor histidine kinase that detects water stress and transmits the stress signal to a downstream MAPK cascade.	64.07	5' CTTAGCAGCGGGAAGTGTTC 3' 3' CCATGCAAGCGAGTAGTTGA 5'
АНК3	AT1G27320.1	XP_027097259	Histidine kinase 3; Cytokinins (CK) receptor related to bacterial two-component regulators.	67.12	5′ TGGAAGATGGAGAGATTGG 3′ 3′ ATTCCCACGATCTTCCTGTG 5′
AHP4	AT3G16360	XP_027125278	Arabidopsis thaliana histidine phosphotransfer proteins (AHPs). Encodes AHP4, a histidine-containing phospho-transmitter involved in Histidine (His)-to-Aspartate (Asp) phosphorelay signal transduction. AHP4 is one of the six	70.34	5'TCAACTGCGACGAAAACTTG 3' 3'GGTTCTTCTCCAGTGCTTGC 5'
ARR1	AT3G16857.2	XP_027115945	Two-component response regulator ARR1; Transcriptional activator that response regulator involved in His-to-Asp phosphorelay signal transduction system.	52.11	5' TTGCCCGGTAATAGTTTTGC 3' 3' CATTTTGCATACCCCAATCC 5'
ARR7	AT1G19050.1	XP_027098055.1	Arabidopsis response regulator (ARR) family, most closely related to ARR15. A two-component response regulator protein containing a phosphate accepting domain in the receiver domain but lacking a DNA binding domain in the output domain.	63.35	5′AGGGTTTGGCAAGAGAAAATTG 3′ 3′AGTTTGTGTTGGTGAGGAG 5′
ARR15	AT1G74890.1	XP_027065231.1	Two-component response regulator ARR15; Functions as response regulator involved in His-to-Asp phosphorelay signal transduction system. Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote the transcription of target genes.	50.85	5' GTGGGTTGTGGATTTTGGTG 3' 3'GTATGAGCTGAGGTGAGATGAG 5'
WUS	AT2G17950.1	XP_027100463.1	Homeodomain-like superfamily protein; Transcription factor that plays a central role during early embryogenesis, oogenesis and flowering. Required to specify stem cell identity in meristems, such as shoot apical meristem (SAM).	40.4	5' CCGGTCCCAGAATTAGAAACTC 3' 3'GAATAACCCACGTTGCCATTG 5'
WOX5	AT3G11260.1	XP_027109768.1	WUSCHEL related homeobox 5; Transcription factor, which may be involved in the specification and maintenance of the stem cells (QC cells) in the root apical meristem (RAM)	58.54	5'TCGCAGAGTTTCGATTGATG 3' 3'GCTGCTTCTCTGCCTCTGAT 5'
ARF5	AT1G19850.1	XP_027090708.1	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related; Auxin response factors (ARFs) are transcriptional factors that bind specifically to the DNA sequence.	58.01	5'CAATTGAGCGGATGTTTGGAC 3' 3'TCCACATACACCAGTTTCCAG 5'
LEC1	AT1G21970.1	XP_027085797	Nuclear transcription factor Y subunit B-9; Transcriptional activator of genes required for both embryo maturation and cellular differentiation. Sequence is similar to HAP3.	76.47	5' CCAGGAATGTGTATCGGAGTAC 3' 3'GAAAGCGGTGGAGATATAGGG 5'
BBM	AT5G17430	XP_027062561	AP2-like ethylene-responsive transcription factor BBM; Transcription factor that promotes cell proliferation, differentiation and morphogenesis, especially during embryogenesis	41.53	5′ TTCAACCCCAACGAGATCAG 3′ 3′GTTGTAGTTCTCCTTCCAGTCC 5′
FUS3	AT3g26790.1	XP_027102113.1	Transcriptional factor with high similarity to the B3 region of the VP1/ABI3-like proteins. Present in many seed-specific promoters. AGL15 (AGAMOUS-Like 15) is a	44.92	5'GGCTTACGACATGGAGACTAC 3' 3'GCATTTATCTCCGACTCAGGG 5'
AGL15	AT5G13790.1	XP_027113896.1	AGL15 (AGAMOUS-Like 15) is a member of the MADS domain family of regulatory factors. Is preferentially expressed during embryogenesis, may play a role during post-germinative development.	55.77	5' TGGGAGGAAGAATTCTGGTG 3' 3'CTAACAGGCAAACACGCTGA 5'

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Supplementary Table 2. Genes involved in SEs maturation of *C. arabica* identified from differentially expressed genes (DEGs).

Non-osmotic stress M3	osmotic stress M9	GENE ID	Annotation in the <i>Coffea arabica</i> genome
0.25	2.29	AHK1	XP_027075540
1.12	-0.27	АНК3	XP_027097259
-1.47	1.94	AHP4	XP_027125278
-3.84	4.22	ARR1	XP_027115945
1.32	-3.13	ARR7	XP_027098055.1
0.68	-2.69	ARR15	XP_027065231.1
-2	1.89	ARF5	XP_027090708.1
-5.06	3.53	WUS	XP_027100463.1
-0.79	5.06	WOX5	XP_027109768.1
-6.64	5.81	LEC1	XP_027085797
-5.64	4.27	FUS3	XP_027102113.1
-5.06	4.36	BBM	XP_027062561
0.95	2.15	AGL15	XP_027113896.1



*SE-M3: Embryogenic medium with 3 g/L gelrite; SE.M9: Embryogenic medium with 9 g/L gelrite. See text and Table S1 for the identification of genes.