Supplementary Materials:

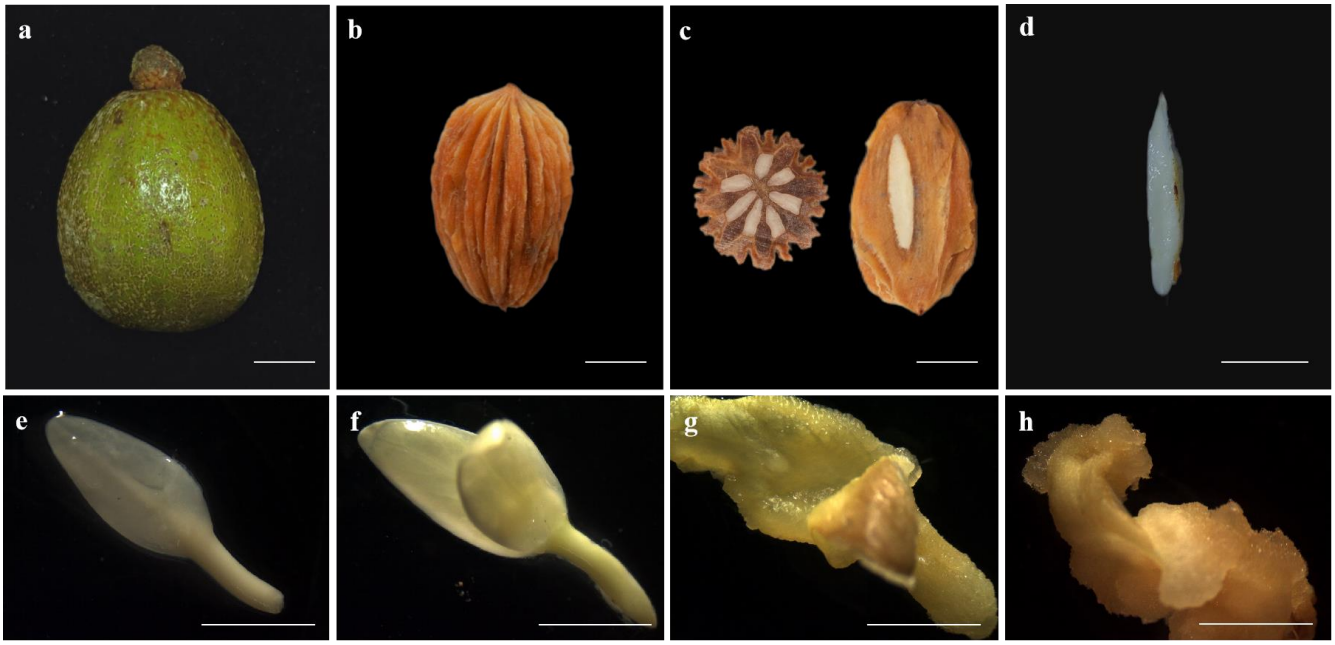

Figure S1: Seed structure and callus induction of *D. involucrata*: (a) Immature *D. involucrata* seeds. (b) Lignified seeds without exocarp and mesocarp. (c) Cross and vertical cutting of seeds. (d) Immature zygotic embryo surrounded by endosperm. (e~h) immature zygotic embryo 0 d, 5 d, 10 d, 15 d. Bar: 1 cm;

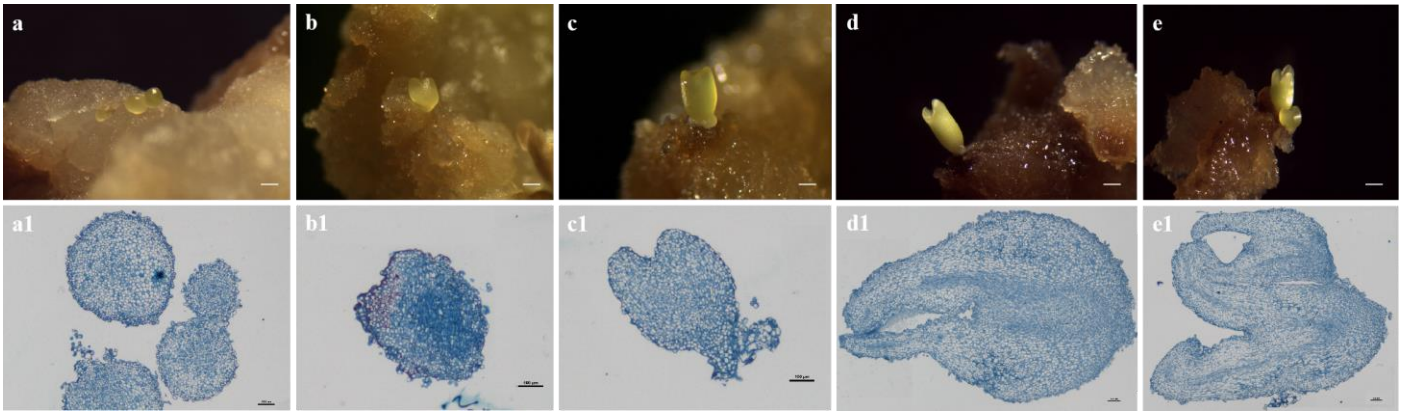

Figure S2: Different developmental stages and histology of somatic embryos from *D. involucrata*. (a,a1) Globular stage somatic embryo. (b,b1) Heart-shaped stage somatic embryo. (c,c1) Torpedo-shaped stage somatic embryo. (d,d1) Cotyledonary stage somatic embryo. (e,e1) Mature somatic embryo. (a~e) Bar: 1 mm. (a1~e1) Bar: 100 μm;

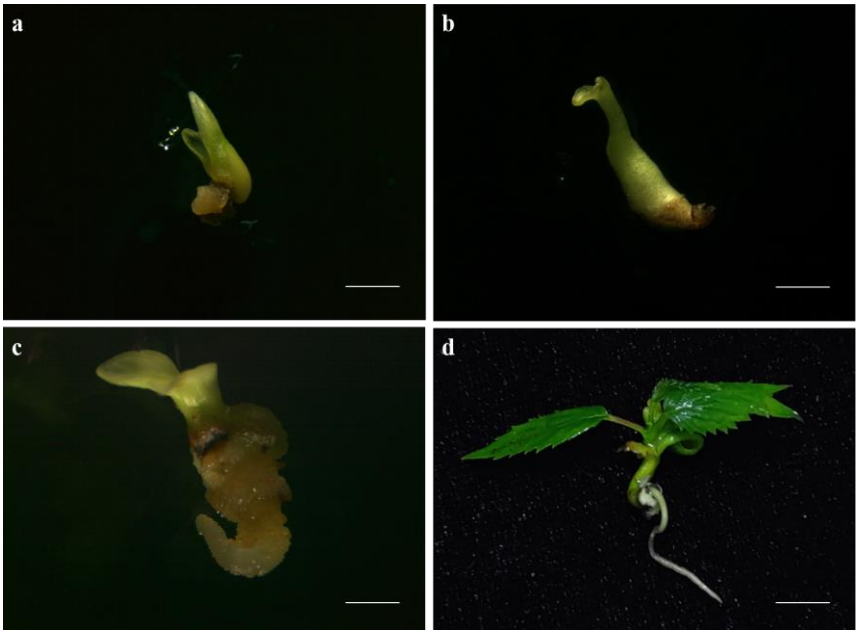

Figure S3: Somatic embryo germination and conversion of *D. involucrata*. (a) Anomalously germinated somatic embryo with cotyledons only. (b) Anomalously germinated somatic embryo with root only. (c) Normally germinated somatic embryo with both shoot and root. (d) Conversion plantlets. (a~c) Bar: 1 mm. (d) Bar: 1cm;

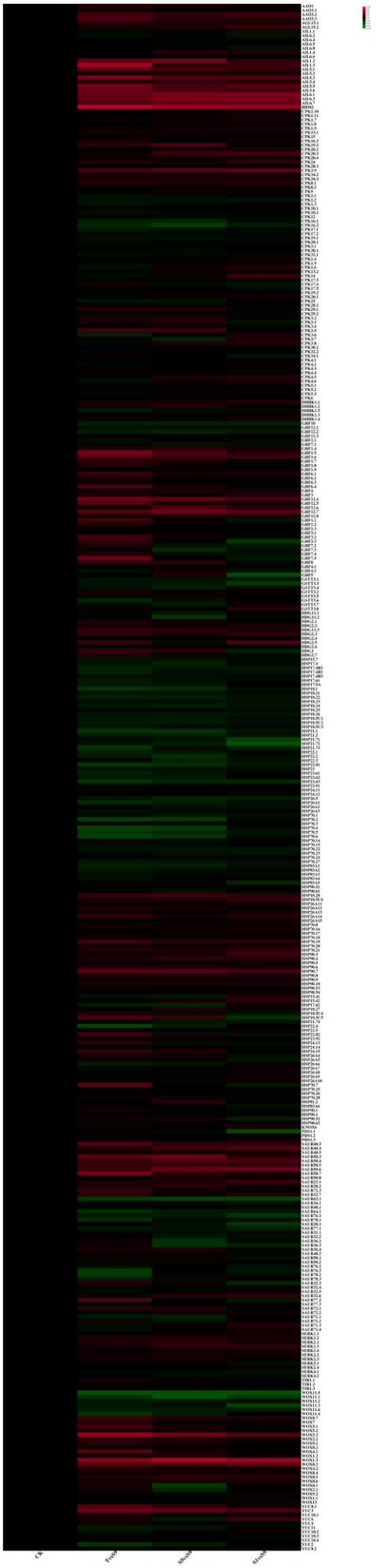

Figure S4: Genes associated with somatic embryogenesis from EC of *D. involucrata*;

Table S1: qRT-PCR primer design;

Gene	Forward primers	Reverse primers
DiPRU1	CAGGATTAGCCAAGAGGT	GGCGAAGGCAGCCATTAC
DiPHI1	TCAACGACATTCTCCACC	CACCCACTCCATTTCACA
DiHIP21	GTGTCTTGCCAAACTCCA	ACCTTCATTATCCCTACCA
DiASPA1	TCAGTGGCATCACCGTTT	ACCCGCAAGGTCCATCAT
DiGOLS1	GAGCCCTAAAGCACTCCACA	GGCGAATCCCACCCTACCT
DiIAA9	TGGTTGTCAGGTGGATAG	TTTGCGTAAAGTGAAGAGT
DiKWL1	CTTGAGGGGCATAAGGATAA	ATGGACTGTGATGGCTGTG
DiASPA2	CAGGCGGACTGCTATTGT	AAACTTGGGAGTGAAACC
DiEP1	TTTGTTGGCAGTGTTGGT	CCGTTTAGGCTTTGTTTC
DiFB60	GGGTTTGCTCACAGGGAT	GCCGTGGAAGTTGAAGGA
DiPGKH	CTTGCCACTAAGGTCTGC	GGATGGTTGGATGGGATT
DiRG1	GGTCACGAAGGGCTCTAT	GAAACTCGGTCTAAATGC
DiCSE	ACCTCCCCAAACACCAAATC	CCGCCAGCAAGGACAAGA
DiKALSE	GAGTCGTCGCTGGTGAGA	CGTGTCGGGTGTTTGTGA
DiACX3	TGAGGGTAGAACTTGTGAGC	ATGCCGTGAAGCCTGTGG
DiCAN2	TAAACAAGGACTCCCAAACA	AGAGGCAGACGCAATACA

Table S2: Reverse transcription reaction system;

Procedure	Reagents name	Volume
Removal of Genomic DNA Reaction	5×gDNA Emaser Buffer	2μl
	gDNA Emaser	1μl
	Total RNA	Calculated according to the concentration, not to exceed 1 μg
	RNase Free ddH_2O	Up to 10μl
Reverse transcription reaction	The product obtained in the previous step	10μl
	RNase Free ddH_2O	4μl
	5×PrimeScript Buffer 2	4μl
	RT Primer Mix	1μl
	PrimeScript RT Enzyme Mix I	1μl

Table S3: Reverse transcriptional response program;

Procedure	Temperature	Time
Removal of Genomic DNA Reaction	42 ℃	2 min
Reverse transcription reaction	42 ℃	15 min
	85 ℃	5 s

Table S4: qRT-PCR reaction system;

Reagents Name	Volume
2 × Q3 SYBR qRT-PCR Master Mix	10 μl
RNase Free ddH_2O	8 μl
Primer F	0.5 μl
Primer R	0.5 μl
cDNA	1 μl

Table S5: qRT-PCR procedure.

Procedure	Reaction temperature	Reaction time	Number of cycles
pre-denatured	95 ℃	60 s	1
	95 ℃	10 s	
cyclic reaction	57 ℃	10 s	40
	72 ℃	30 s	
	95 ℃	15 s	
melting curve	65 ℃	60 s	1
	95 ℃	15 s	
cool down	37 ℃	30 s	1