

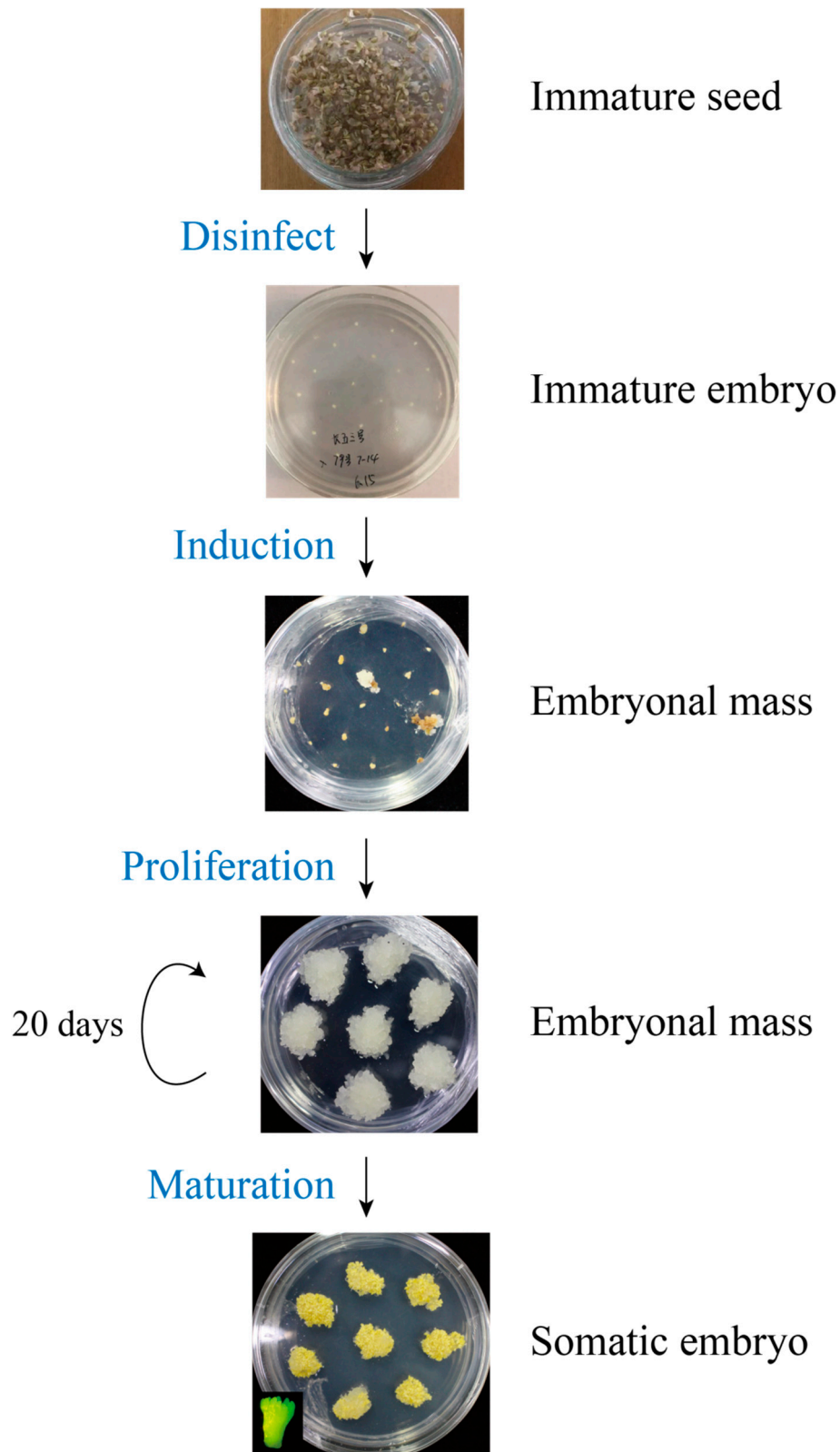
**Table S1.** The mediums used in *L. keampferi* somatic embryogenesis

Medium	Basal medium	Glutamine (mg/L)	Inositol (mg/L)	2,4-D (mg/L)	BA (mg/L)	Casein hydrolysate (mg/L)	PEG4000 (mg/L)	ABA (mg/L)
Induction medium	S	450	1000	2.2	0.8	500		
Proliferation medium	S+B	450	1000	0.11	0.04	500		
Maturation medium	S+B	450	100			500	110	42

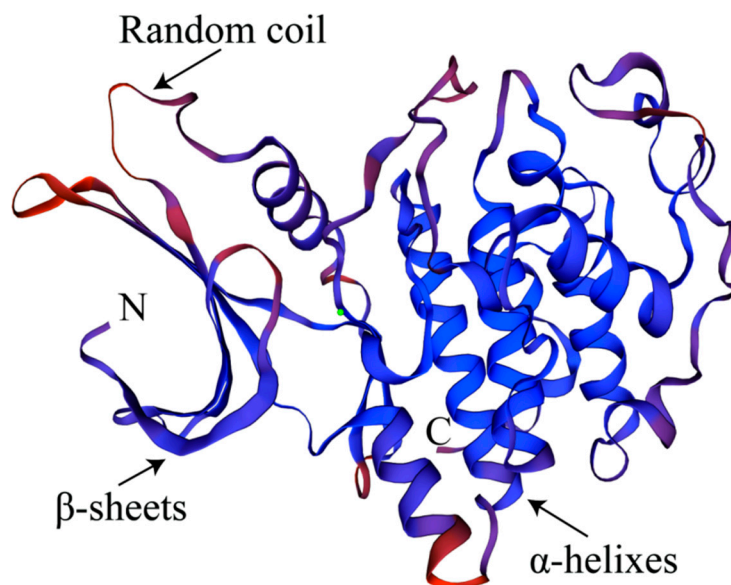
Note: S: S basal medium (Ewald et al., 1995); S + B: S + B basal medium (Ewald et al., 1997)

**Table S2** Promoter elements of *LaCDKB1;2*

Name	Organism	Position	Sequence	Function
ABRE	<i>Arabidopsis thaliana</i>	1167	ACGTG	cis-acting element involved in responsiveness to abscisic acid
CAT-box		975	GCCACT	cis-acting regulatory element related to meristem expression
GT1-motif		873	GGTTAA	light-responsive element
MYB recognition site		1141	CCGTTG	
TGA-element	<i>Brassica oleracea</i>	882	AACGAC	auxin-responsive element
MSA-like	<i>Catharanthus roseus</i>	1517	(T/C)C(T/C)AAC GG(T/C)(T/C)A	cis-acting element involved in cell-cycle regulation
CCAAT-box	<i>Hordeum vulgare</i>	1141	CAACGG	MYBHv1 binding site
TGACG-motif		565	TGACG	cis-acting regulatory element involved in MeJA-responsiveness
CAAT-box	<i>Nicotiana glutinosa</i>	29	CAAT-box	common cis-acting element found in promoter and enhancer regions
TC-rich repeats		1290	GTTTTCTTAC	cis-acting element involved in defense and stress responsiveness
Sp1	<i>Oryza sativa</i>	721	GGGCGG	light-responsive element
TATC-box		756	TATCCCA	cis-acting element involved in responsiveness to gibberellin
Box-II	<i>Petroselinum crispum</i>	1410	CCACGTGGC	part of a light-responsive element
A-box		1065	CCGTCC	cis-acting regulatory element
TCCC-motif	<i>Spinacia oleracea</i>	1400	TCTCCCT	part of a light-responsive element
G-box	<i>Zea mays</i>	1166	CACGTC	cis-acting regulatory element involved in light responsiveness
O2-site		1115	GATGATGTGG	cis-acting regulatory element involved in regulating zein metabolism

**Figure S1****Figure S1.** The flow diagram of *L. keampferi* somatic embryos

**Figure S2**



**Figure S2.** The tertiary structure of the LaCDKB1;2 protein. N: N-terminal region of the LaCDKB1;2 sequence; C: C-terminal region of the LaCDKB1;2 sequence

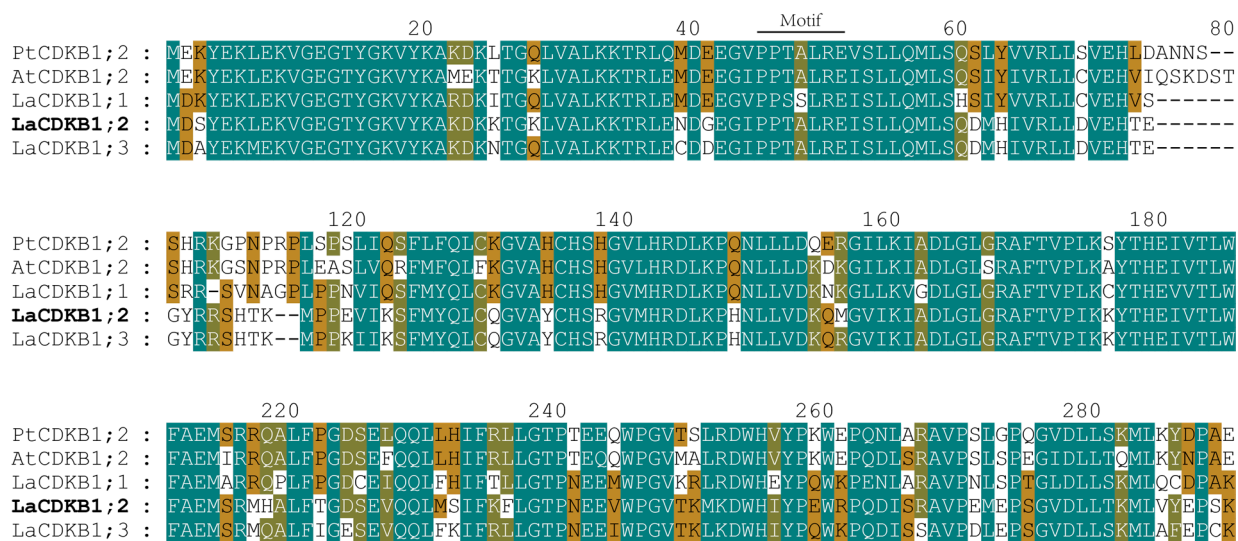
**Figure S3****Figure S3.** Sequence alignment of the amino-acid sequence deduced for *L. kaempferi* CDKs (*LaCDKB1;1*, MW132640; *LaCDKB1;2*, MW132641; *LaCDKB1;3*, MW132642) with *A. thaliana* CDKB1;2 (*AtCDKB1;2*, AJ297937), and *P. trichocarpa* CDKB1;2 (*PtCDKB*, U5FL09). line: PPTALRE motif

Figure S4

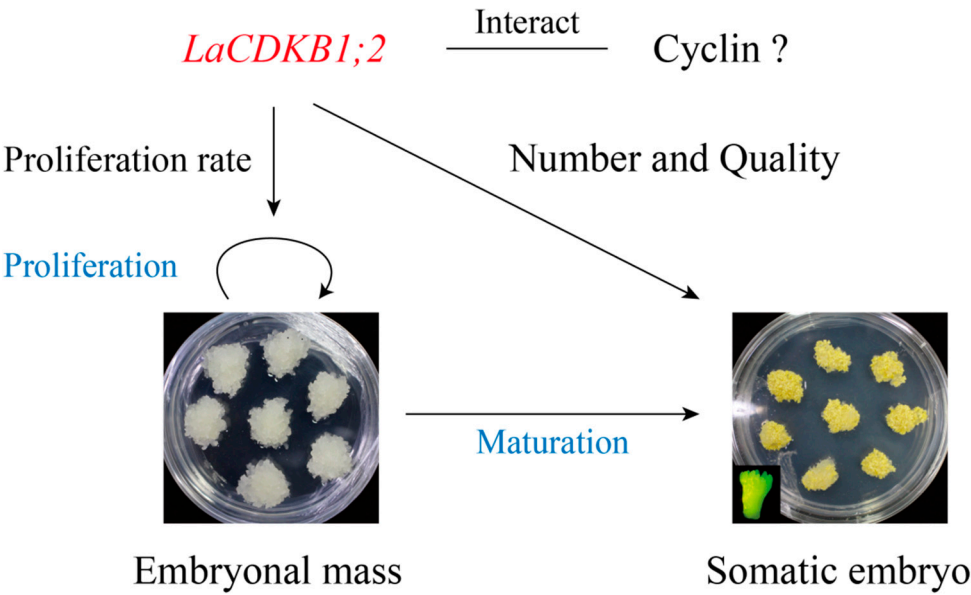


Figure S4. A working model for *LaCDKB1;2* in *L. kaempferi* somatic embryogenesis

## Data S1

The sequence of *LaCDKB1;2* (MW132641):

>*LaCDKB1;2*

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ATGGACTCATATGAGAACTGGAGAAGGTGGGAGAAGGAACCTATGGGAAGGTG-
TACAAAGGCCAAGGACAAGAAAACAGGGAACTGGTCGCCCTTAAAAAGACCAGGCTAGA-
GAACGATGGTGAGGGAATTCCTCCAACCTGCTCTCCGTGAGATTTCTCTCCTG-
CAGATGCTTTCTCAAGATATGCACATTGTAAGGCTGTTGGATGTGGAACACACTGAGAACAA-
GAAGGGGAAGACCTTCTGTACTTGGTTTTTGAATTCATGGACTCTGATCTCAAGAA-
GCACATCGACGGTTATCGCCGCAGCCACACAAAAATGCCTCCCGAGGTTATCAA-
GAGCTTCATGTACCAGTTGTGCCAGGGGGTTGCTTACTGCCACAG-
TCGCGGTGTGATGCACAGGGACTTGAAGCCTCACAACTGCTGGTGGACAA-
GCAATGGGTGTGATAAAAAATAGCAGATCTTGGCCTGGGAAGGGCTTTCACAGTTCC-
TATCAAGAAGTACACTCACGAGATTGTGACCCCTTGGTACAGGGCTCCTGAAGTGCTCTT-
GGGGGCTACTACTACTCCACACCTGTTGACATTTGGTCTGTTGGCTGTATATT-
GCTGAAATGTCCAGAATGCATGCTCTGTTCACTGGAGATTCTGAAGTACAACAACTCATGAG-
CATTTTCAAGTTTTTAGGAACTCCTAATGAAGAAGTATGGCCAGGAG-
TGACTAAAATGAAGGATTGGCATATCTATCCAGAGTGGAGGCCTCAAGATA-
TAAGTCGTGCTGTTCCAGAAATGGAACCAAGTGGTGTAGATCTGTT-
GACTAAAATGCTGGTTTATGAGCCATCGAAGAGAATCTCAGCTAAGAAGGCATT-
CGAAGATCCTTATTTGAGCCCTTGATAAAATCTCAATTCTGA*
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>*LaCDKB1;2*

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MDSYEKLEKVGEGTYGKVYKAKDKKTGKLVALKKTRLENDGEGIPPTALREISLLQMLSQDM-
HIVRLLDVEHTENKKGKTLLEYLVEFEFMDSDLKKHIDGYRRSHTKMPPEVIKS-
FMYQLCQGVAYCHSRGVMHRDLKPHNLLVDKQMGVIKIADLGLGRAFTVPIK-
KYTHEIVTLWYRAPEVLLGATHYSTPVDIWSVGCIFAEMSRMHALFT-
GDSEVQQLMSIFKFLGTPNEEVWPGVTKMKDWHIYPEWRPQDISRAVPE-
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