## **Supporting Information**

## Zheng et al. 10.1073/pnas.1318460111

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**Fig. S1.** (A) Schematic representation of the T-DNA insertions in *cdkg*1–1 and *cycL*1–1, positions of primers used in the study, and RT-PCR confirmation of the insertion sites. Primer sequences are provided in Table S2. (B) Phenotypic consequences of *cdkg*1–1 and *cycL*1–1 on fertility.



Fig. S2. Effect of cdkg1-1 on bivalent formation. The bars illustrate the ratio of univalent and bivalents in individual cells at metaphase I (red bars represents cdkg1-1, n = 93; the blue bar represents WT cells, n = 37) from plants grown under greenhouse conditions.



**Fig. S3.** Percentage of meiocytes at different meiotic stages in (A) WT and cdkg1-1 grown at 12 and 23 °C as judged by  $\alpha$ -Asy1 and  $\alpha$ -Zyp staining (*n* cells > 39); (B) WT and cdkg1-1cycL1-1 (*n* > 49) grown at 12 °C.



**Fig. S4.** Three-dimensional reconstruction of bivalents from WT pachytene (A–G) and mutant pachytene-like (H–N) meiocytes. Gray represents ZYP1 loading, while red represents ASY1. (*O*) Schematic representation of ZYP1 loading (red bars) and chromosome length in cdkg1–1 meiocytes. Data for 50 bivalents in pachytene-like was taken from 3D reconstructions with the least synapsed to the *Left* and the most to the *Right*. Bivalents from the same nucleus are clustered together (i.e., 1–5, 6–10, etc).



**Fig. S5.** *CDKG1* genetically interacts with *CYCLINL*. (*A*) Fertility in WT and the double-mutant *cdkg*1–1*cycL*1–1, grown at 12 °C (*B*) Immunolocalization of the SC proteins ASY1 (green) and ZYP1 (red) in nuclei at different stages of meiosis as indicated. DAPI-stained chromatin is shown in blue. (Scale bar, 2  $\mu$ m.) (*C*) Pollen viability in WT, *cdkg*1–1 single mutant, and *cdkg*1–1/*cycL*1–1 double-mutant grown under greenhouse conditions.

Table S1.	Pollen viability	as judged by	Alexander stain
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	WT, 23 °C			<i>cdkg1–1</i> , 23 °C		
	Live pollen	Dead pollen	Live pollen (%)	Live pollen	Dead pollen	Live pollen (%)
	213	2	99.07	7	29	19.44
	132	1	99.25	6	23	20.69
	225	1	99.56	4	35	10.26
Average			99.29			16.80*
SD			0.25			5.70

\*Significantly different from the WT for P < 0.001.

DNA C

## Table S2. Primer sequences

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Name	Sequence (5'-3')	
LBa1	TGGTTCACGTAGTGGGCCATCG-3'	genotyping SALK_075762
190-RP	TTCCCTCAATGATGTCAAAGG-3'	genotyping SALK_075762
190-LP	TTGATGTTTCCAGAAGTTCCG-3'	genotyping SALK_075762
CDKG1 promoter attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTAGGA CTGTGTAACAAATGCAA-3'	cloning
CDKG1 promoter attB2	GGGGACCACTTTGTACA AGAAAGCTGGGTCGTATTCTTCTCAATGAGAAA-3'	cloning
Flg CDKG1 attB2	GGGG ACCACTTTGTACAAGAAAGCTGGGTAAAATCGAACATGTTCACCCA-3'	cloning
CDKG1-F	GAGGGAAAAACGATAATGATG-3'	RT-PCR
CDKG1-R	ATCTTCCACT GTTAGACGTTTC-3'	RT-PCR
G2 80- LP	GTTCAGAAGTGAGGTTGTGGC	genotyping
G2 80- RP	AGGCTCAAGGGGATGTAGATG	genotyping
CyclinL Fw1	CGATGATTTACACTGCTATCGAC	RT-PCR
CyclinL Rv1	CCACAACCTCACTTCTGAACC	RT-PCR
Actin forward	TGGGATGGGGCAAAAGGATGCT	genotyping
Actin reverse	AGCACAATACCGGTAGTACGAC	genotyping