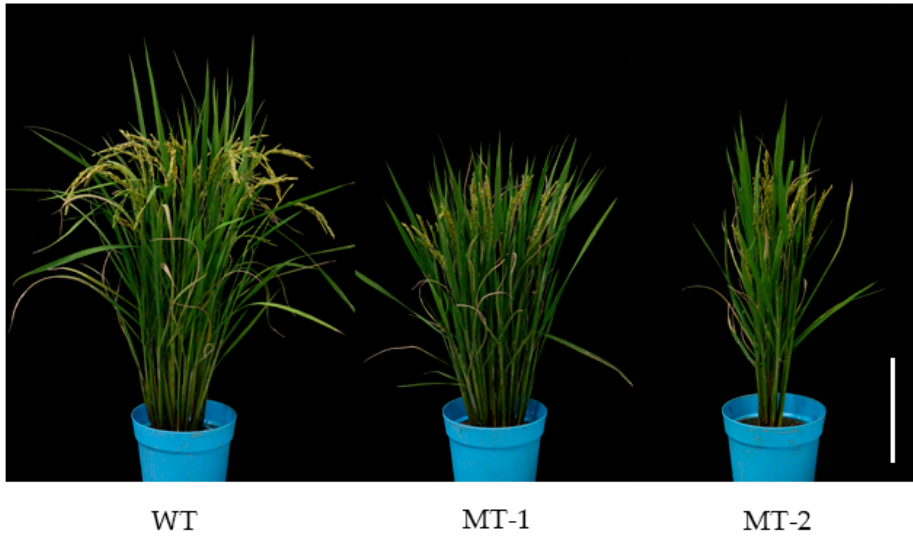


**Supplementary Figure S1** Comparison between the NIL-*qLL9*<sup>CJ16</sup> and NIL-*qLL9*<sup>C84</sup> for the 2nd leaf length (d), the 2nd leaf width(e), the 2nd leaf area (f), the 3rd leaf length (d), the 3rd leaf width(e), and the 3rd leaf area (f). Data are represented as mean ± SD (n=15). Asterisks represent significant difference determined by Student's *t*-test at p-value<0.01(\*\*), p-value<0.05 (\*).



**Supplementary Figure S2. Phenotypes of the CRISPR/Cas9 transgenic and wild-type plants.** WT, Nipponbare; MT-1, Mutant 1; MT-2, Mutant 2. Bar=18 cm.

**Supplementary Table S1.** Primers for qRT-PCR of eight cell cycle related genes

<b>Primer</b>	<b>Forward (5'-3')</b>	<b>Reverse (5'-3')</b>
Actin	ATCCATCTTGGCATCTCTCAGC	CACAATGGATGGGCCAGACT
CAK1	GACGGTCAGATTAGACGCAAGA	TCCAAAGGATGTCCACA
CDKA1	GGTTTGGACCTTCTCTCTAAAATGC	AGAGCCTGTCTAGCTGTGATCCTT
CAK1A	GACCGACAAGGGTTTCAGCAT	CCAGCATGTTCAGGAAGATACAAT
MCM5	AAGGAGAACTGCCTGTCCATGA	AGTGGCCTTAGCTTTCACCCCTC
CYCT1	GCATTTGTTGCAGCTCAAG	TCACCACTTCGCTGACTTATTG
CYCA2.2	AGGTTGTCAAGATGGAGAGCGA	CGCTTTTGTCTTCCTGGCA
CYCA2.3	GTTTCGGTTGACGAGACGATGT	CGCTGCAAGGAACCTAGAACTG
CYCB2.2	CTCAAGGCTGCACAATCTGACA	GCATTGACGGCTGGAATTTG