

Figure S1 The photos of the tested materials. JHCA, Jiahecong'ai; GC13, Guangchang13; GLA4, Guangluai 4; XJC1, Xingjiacong 1

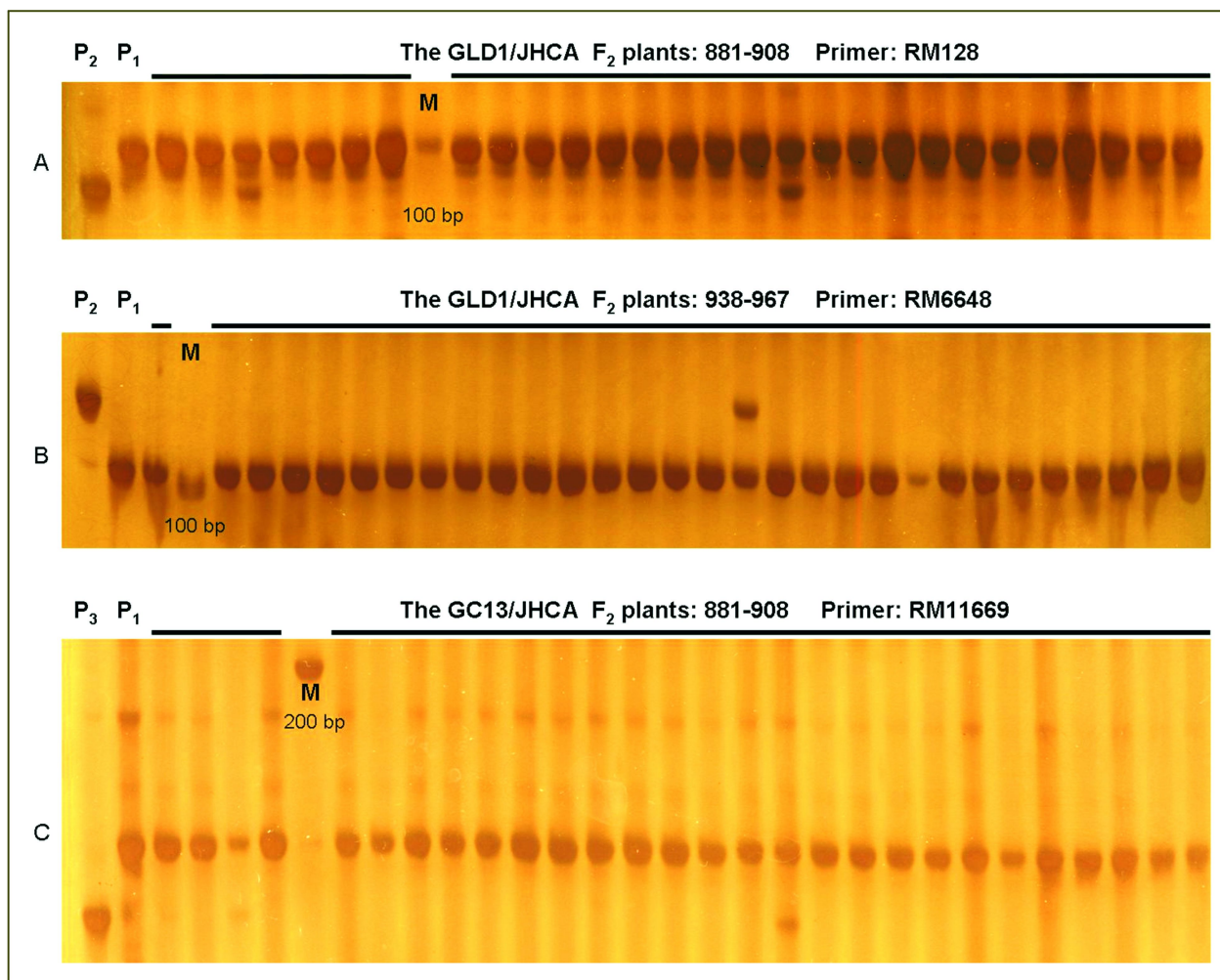


Figure S2 Representative images of SSR polymorphisms in the GLD1/JHCA and GC13/JHCA F<sub>2</sub> populations. P<sub>1</sub>: JHCA; P<sub>2</sub>: GLD1; P<sub>3</sub>: GC13; M:DNA marker.

Material	Sequences of <i>D10</i>	Base No.
NIP	ATGTCTCCGCTATGCTGCAGGCGTCGTCGCTGTGCGTATCCGGCGGCTGTCAAGCGCC	60
JHCA	ATGTCTCCGCTATGCTGCAGGCGTCGTCGCTGTGCGTATCCGGCGGCTGTCAAGCGCC	
AJNT	ATGTCTCCGCTATGCTGCAGGCGTCGTCGCTGTGCGTATCCGGCGGCTGTCAAGCGCC	
GC13	ATGTCTCCGCTATGCTGCAGGCGTCGTCGCTGTGCGTATCCGGCGGCTGTCAAGCGCC	
.....		
NIP	TTCAAGAATGCGAATCTTTTCTGTATTGATTCAAAGGTTCCAGTACTCCATATC.	540
JHCA	TTCAAGAATGCGAATCTTTTCTGTATTGATTCAAAGGTTCCAGTACTCCATATC.	
AJNT	TTCAAGAATGCGAATCTTTTCTGTATTGATTCAAAGGTTCCAGTACTCCATATCC	
GC13	TTCAAGAATGCGAATCTTTTCTGTATTGATTCAAAGGTTCCAGTACTCCATATCC	
NIP	..... GCTTCTTGAGATCATCTATAAACTAAAGATCCTTTGAACATCTT	600
JHCA	..... GCTTCTTGAGATCATCTATAAACTAAAGATCCTTTGAACATCTT	
AJNT	ACATATAATACGGTGCTTCTTGAGATCATCTATAAACTAAAGATCCTTTGAACATCTT	
GC13	ACATATAATACGGTGCTTCTTGAGATCATCTATAAACTAAAGATCCTTTGAACATCTT	
.....		
NIP	ACCACATCACTGTGCAACAAATCCTTTATAATTAACCTAACCATTTTCATCTGTAGCAT	720
JHCA	ACCACATCACTGTGCAACAAATCCTTTATAATTAACCTAACCATTTTCATCTGTAGCAT	
AJNT	ACCACATCACTGTGCAACAAATCCTTTATAATTAACCTAACCATTTTCATCTGTAGCAT	
GC13	ACCACATCACTGTGCAACAAATCCTTTATAATTAACCTAACCATTTTCATCTGTAGCAT	
.....		
NIP	TAACACGCCAGGGTATATTACTTGCCGACTGTCAATTTAATTTCCACTGTGCCAGCAGT	900
JHCA	TAACACGCCAGGGTATATTACTTGCCGACTGTCAATTTAATTTCCACTGTGCCAGCAGT	
AJNT	TAACACGCCAGGGTATATTACTTGCCGACTGTATTTTAAATTTCCACTGTGCCAGCAGT	
GC13	TAACACGCCAGGGTATATTACTTGCCGACTGTATTTTAAATTTCCACTGTGCCAGCAGT	
.....		
NIP	GGAACACAACATATATACCCAGATTCTCTGCTCACCCCTAGCTTCGATCGGCGACAACAA	1080
JHCA	GGAACACAACATATATACCCAGATTCTCTGCTCACCCCTAGCTTCGATCGGCGACAACAA	
AJNT	GGAACACAACATATATACCCAGATTCTCTGCTCACCCCTCGCTTCGATCGGCGACAACAA	
GC13	GGAACACAACATATATACCCAGATTCTCTGCTCACCCCTCGCTTCGATCGGCGACAACAA	
.....		
NIP	TCAAAAOCTTGGTCTCCCTAACTCCAAGTGATCTTATCACTGTTCTTGCCAATTTGA	1200
JHCA	TCAAAAOCTTGGTCTCCCTAACTCCAAGTGATCTTATCACTGTTCTTGCCAATTTGA	
AJNT	TCAAAAOCTTGGTCTCCCTAACTCCAAGTGATCTTATCACTGTTCTTGCCAATTTGA	
GC13	TCAAAAOCTTGGTCTCCCTAACTCCAAGTGATCTTATCACTGTTCTTGCCAATTTGA	
NIP	TAGTGACTTGATTTGAGGAATTAATACAGGTGTACATGTAGTATAAATTTGTTAACTT	1260
JHCA	TAGTGACTTGATTTGAGGAATTAATACAGGTGTACATGTAGTATAAATTTGTTAACTT	
AJNT	TAGTGACTTGATTTGAGGAATTAATACAGGTGTACATGTAGTATAAATTTGTTAACTT	
GC13	TAGTGACTTGATTTGAGGAATTAATACAGGTGTACATGTAGTATAAATTTGTTAACTT	
.....		
NIP	AOGGCTACGCGAGCTGGTGGCGTCTCGTTCCGCGGCGCGCGCGTGGGCGCGCAAC	1560
JHCA	AOGGCTACGCGAGCTGGTGGCGTCTCGTTCCGCGGCGCGCGCGTGGGCGCGC...	
AJNT	AOGGCTACGCGAGCTGGTGGCGTCTCGTTCCGCGGCGCGCGCGTGGGCGCGCAAC	
GC13	AOGGCTACGCGAGCTGGTGGCGTCTCGTTCCGCGGCGCGCGCGTGGGCGCGCAAC	
NIP	GGCAGATCGAGTCGGAGGCGTACAAGCGCGCGCGCGCACGGCAAGGTGTGCTACCGG	1620
JHCA	..... GCACGGCAAGGTGTGCTACCGG	
AJNT	GGCAGATCGAGTCGGAGGCGTACAAGCGCGCGCGCGCACGGCAAGGTGTGCTACCGG	
GC13	GGCAGATCGAGTCGGAGGCGTACAAGCGCGCGCGCGCACGGCAAGGTGTGCTACCGG	
.....		
NIP	CGCTGTACAAGTTCGAGTGGCACCTCGAGTCCGGCAGTACATGCACGTCATGTGCAAGG	2160
JHCA	CGCTGTACAAGTTCGAGTGGCACCTCGAGTCCGGCAGTACATGCACGTCATGTGCAAGG	
AJNT	CACTGTACAAGTTCGAGTGGCACCTCGAGTCCGGCAGTACATGCACGTCATGTGCAAGG	
GC13	CACTGTACAAGTTCGAGTGGCACCTCGAGTCCGGCAGTACATGCACGTCATGTGCAAGG	
.....		
NIP	CCCGTACGGGCTGCCCTACGGCTTGCACTGCTGCTGGTGCOCAGGAAAGGAACAGCAA	3120
JHCA	CCCGTACGGGCTGCCCTACGGCTTGCACTGCTGCTGGTGCOCAGGAAAGGAACAGCAA	
AJNT	CCCGTACGGGCTGCCCTACGGCTTGCACTGCTGCTGGTGCOCAGGAAAGGAACAGCAA	
GC13	CCCGTACGGGCTGCCCTACGGCTTGCACTGCTGCTGGTGCOCAGGAAAGGAACAGCAA	
.....		

Figure S3 The sequence comparison of the D10 among four used research materials.

NIP: Nipponbare, the sequence was downloaded from Gramene website. Base No.: the base number in D10. ‘.’ in the sequences: the deletion base, each ‘.’ shows one base deletion. ‘.....’ in the blank between two group sequences: the abbreviated base sequences, which show no difference between those four research materials.

Table S1. Measurement of Tiller number, panicle length and internode length in tested materials

Materials	TN	PL	IL1	IL2	IL3	IL4	IL5	IL6
		cm						
JHCA	107±16	10.8±2.5	16.3±3.2	7.8±1.6	3.4±1.0	1.8±0.7	0.8±0.5	0.4±0.2
AJNT	15±2	19.5±2.3	29.0±4.1	15.1±3.4	11.9±3.0	5.6±3.0	1.4±0.9	0.3±0.1
GLA4	18±5	22±1.8	29.2±3.8	18.6±4.1	9.2±4.1	2.7±1.7	1.0±0.5	0.3±0.0
GC13	20±8	29.2±2.6	34.6±3.2	27.1±3.3	22.6±2.9	16.2±4.4	6.1±3.1	0.6±0.4
GLD1	8±2	28.8±1.7	40.3±5.8	28.9±3.0	27.5±2.8	23±4.4	6.5±4.0	0.9±1.5
XJC1	87±28	14.2±3.1	19.9±4.5	15.0±2.7	11.7±3.3	11.1±2.8	4.3±2.5	1.4±0.8
XJC2	92±31	12.5±3.9	15.7±4.0	13.2±2.3	11.2±1.6	10.4±1.7	4.0±1.7	1.1±0.9

Note: JHCA, Jiahecong' ai.; GLD1, Gaoliangdao 1; C13, Guangchang13; AJNT, Aijiaonante; GLA4, Guangluai 4; XJC1, Xingjiacong 1; XJC2, Xingjiacong 2; TN, tiller number; PL, panicle length.; IL1 to IL6, the internode length with figure that counted down from the top (except panicle).

The same blow.

Table S2. Contributions of panicle length and internode length to plant height

Materials	IL6	IL5	IL4	IL3	IL2	IL1	PL
	%						
JHCA	1.0	1.9	4.4	8.3	18.8	39.3	26.2
AJNT	0.3	1.7	6.7	14.4	18.2	35.0	23.6
GLA4	0.4	1.2	3.2	11.0	22.3	35.1	26.8
GC13	0.4	4.5	11.9	16.6	19.9	25.3	21.4
GLD1	0.6	4.2	14.7	17.6	18.6	25.8	18.5
XJC1	1.8	5.6	14.4	15.1	19.5	25.3	18.3
XJC2	1.6	5.9	15.3	16.5	19.3	23.1	18.3

Table S3. Simple sequence repeat (SSR) markers used in linkage map construction.

Marker name §	Population No. †	Primer sequences (5' to 3')	
		Forward	Reverse
RM128	1, 2	AGCTTGGGTGATTTCTTGAAGCG	ACGACGAGGAGTCGCCGTGCAG
RM212	1, 2	AAGGTCAAGGAAACAGGGACTGG	AGCCACGAATTCCACTTTCAGC
RM237	1	CAAATCCCGACTGCTGTCC	TGGGAAGAGAGCACTACAGC
RM246	1, 2	CGAGCTCCATCAGCCATTCAGC	ACTTGAGAGCGAGATTGGGAATCG
RM265	1, 2	CGAGTTCGTCCAAGTGAGC	CATCCACCATTCCACCAATC
RM297	1	ACAGGGCTATGCAGACACAGTGC	AGCAAGCGAAGGGAAGTGACC
RM302	1	TGCAGGTAGAACTTGAAGC	AGTGGATGTTAGGTGTAACAGG
RM486	1, 2	GCTTGCATTATGCGATTGTACTCC	TGAGCTTTCTCAACAACGACTGC

Note: A total of 505 SSR markers were used to screen polymorphisms between the two parental lines of the two populations characterized in this work. Then the markers that showed polymorphisms between the two parental lines were used to detect polymorphisms between mutant DNA pool and WT DNA pool from the F<sub>2</sub> populations. Listed are the SSR markers that detected polymorphisms between the two DNA pools and were further used to genotype F<sub>2</sub> plants. The genotyping data were used to construct molecular linkage maps of the two F<sub>2</sub> populations.

§ SSR markers were selected from the GRAMENE database (<http://www.gramene.org/markers/>).

† Two F<sub>2</sub> populations were characterized in this work. Population 1: GLD1/JHCA; population 2: GC13/JHCA.

Table S4. The newly designed SSR primers with polymorphism between parents

Maker name	Primers sequence (5' to 3')	PCR product size (bp)
XMd-SSR4F <sup>§</sup>	GGCTTTGTGTTGGTTTCTCA	392
XMd-SSR4R <sup>†</sup>	TTCATTACTCTGTTCGTCCG	
XMd-SSR8F <sup>§</sup>	CCCTAACGCTCCAGGTTTA	348
XMd-SSR8R <sup>†</sup>	CCTCACGAACGCAAATGT	
XMd-SSR16F <sup>§</sup>	ATGGAGCCCTTGATGGTCT	320
XMd-SSR16R <sup>†</sup>	ACTATGGAACCTCGGCGACT	
XMd-SSR25F <sup>§</sup>	ACTAAAGCCACCGACACTCT	410
XMd-SSR25R <sup>†</sup>	ACCAAACCCATCCATTCC	