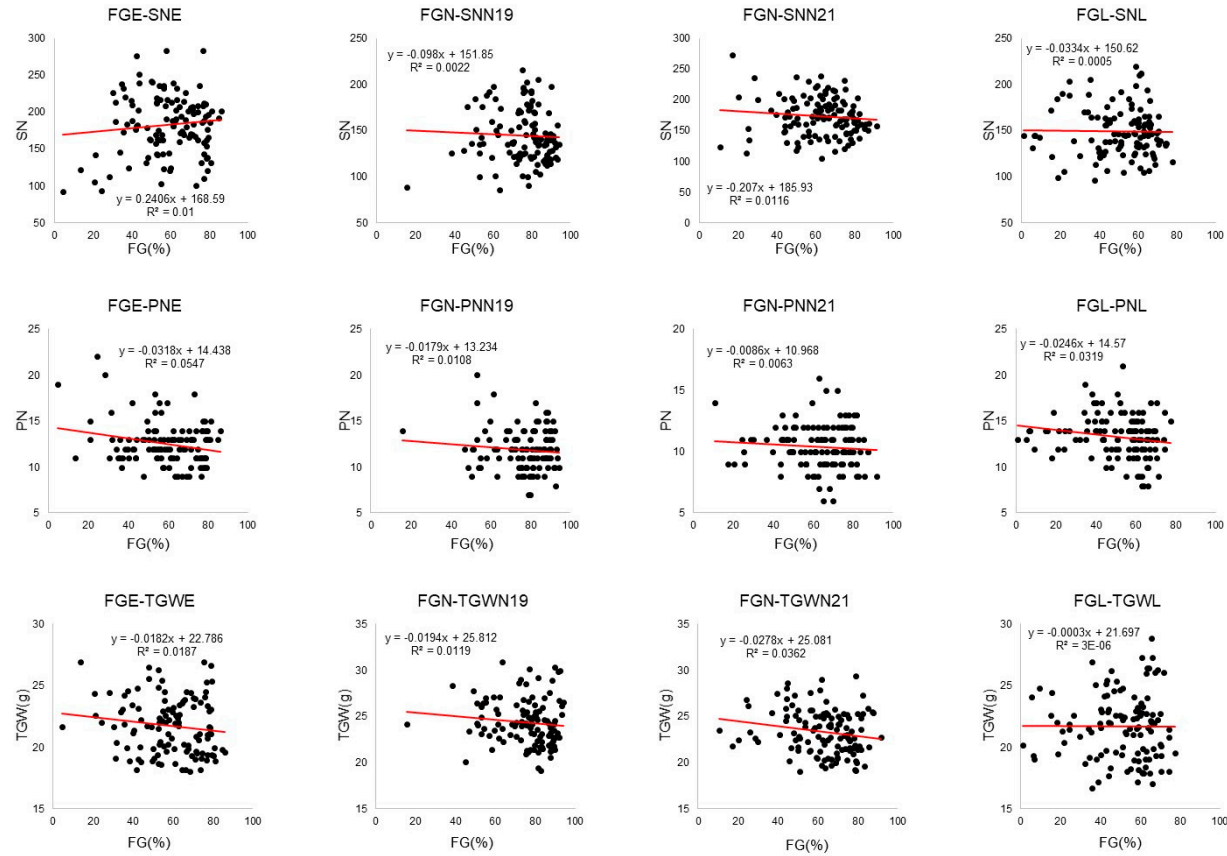


Figure S1. Example of allele discrimination plot of polymorphic SNP marker (KJ11_13, Table S6).



FGE, SNE, PNE, TGWE: early cultivation season
 FGN19, SNN19, PNN19, TGWN19: normal cultivation season (2019)
 FGN21, SNN21, PNN21, TGWN21: normal cultivation season (2021)
 FGL, SNL, PNL, TGWL: late cultivation season

Figure S2. Correlation between grain properties and yield component with normal fertilization level (y: FG, x: SN or PN or TGW, SN: spikelet number per panicle, PN: panicle number per plant, TGW: thousand-grain weight (g), FG: percentage of filled grain (%), E: early season, N: normal season, L: late season, R^2 : coefficient of determination).

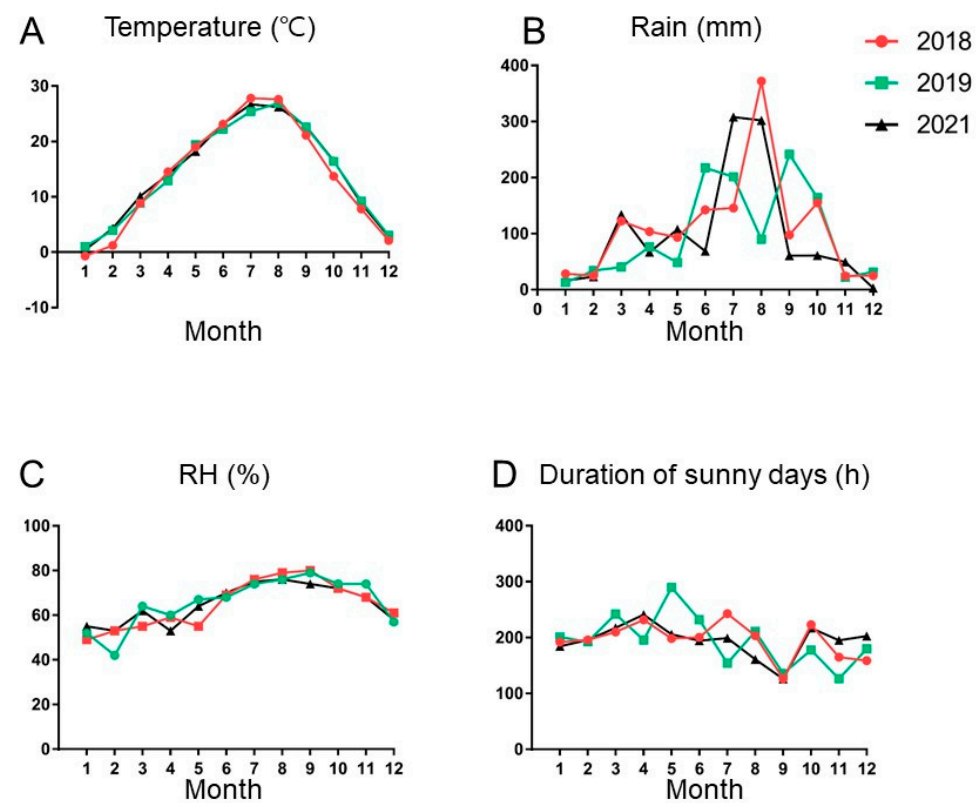


Figure S3. Weather conditions prevailing during 2018, 2019, and 2021 cultivation seasons.

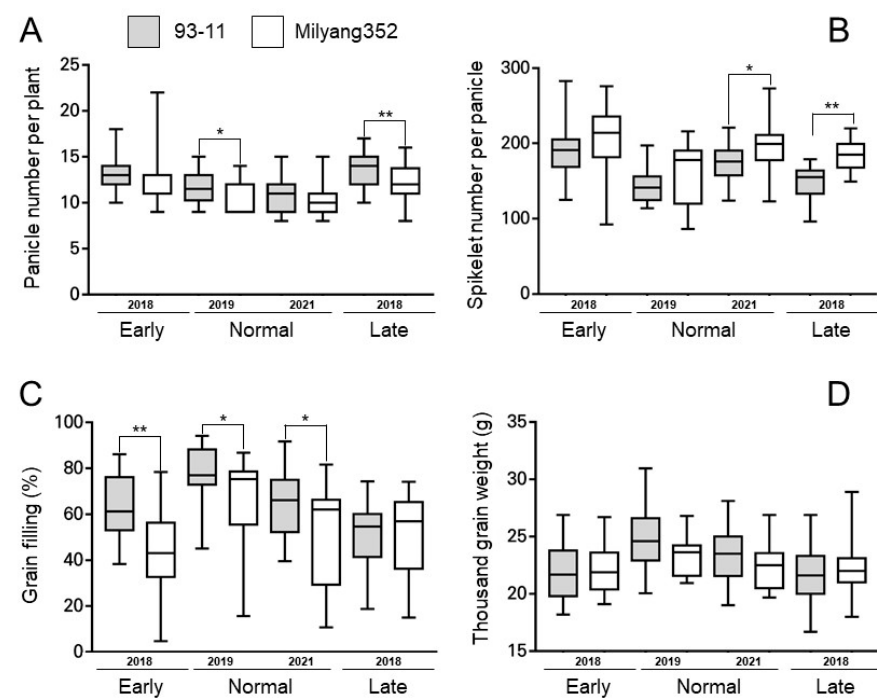


Figure S4. The distribution of grain properties of the two groups differed by the genotype of *qFG3* in different fertilization levels and cropping seasons.

Table S1. cM of each chromosome.

Chr.	Number of Markers	Number of Deviated Markers	Length (cM)	Average Gap of Markers (cM)
1	29	4	310.8	10.7
2	16	7	323.6	20.2
3	19	11	233.5	12.3
4	18	6	192.9	10.7
5	15	11	150.9	10.1
6	11	0	60.5	5.5
7	26	8	231.7	8.9
8	16	7	109.5	6.8
9	18	2	109.3	6.1
10	13	4	130.9	10.1
11	16	0	131.9	8.2
12	12	9	131.1	10.9
Total	209	69	2116.6	10.1

Table S2. List of SNP markers

Chr.	Position (bp)	Marker name	Source	Allele specific primer 1	Allele specific primer 2	Common reverse primer
1	422,620	id1000223	[30]	GACATTTGCAAGCAACTT ATACTGACA	ACATTTGCAAGCAACTT ATACTGACC	TGCTTCAGAGATGGC CTCGAA
1	728,809	KJ01_001	[29]	CAGCCTCACCTCATATCC ACCAT	AGCCTCACCTCATATCC ACCAC	CCTGATCAGTTGGAC GAGGTAAACAA
1	2,103,204	KJ01_005	[29]	AAGAGAATAAGTTCCTAC TCCGTTCAT	GAGAATAAGTTCCTACT CCGTTCAG	TGACAAGTTTGACAC CGGGGAGAAA
1	14,573,814	id1009557	[30]	GTGCTCATCTTTAGATTG ATTTGTCCAT	GTGCTCATCTTTAGATT GATTTGTCCAG	GATGGCACTTCACATT GGCCT
1	19,264,312	id1010652	[30]	TCTCAATTTAACAACAGC ATCTGAAGC	GATCTCAATTTAACAAC AGCATCTGAAGA	CCGTTGCTTTGTTGGT CGGA
1	19,985,793	KJ01_065	[29]	GAAGAAAGAGAGCTCTA CCGCTC	AGAAGAAAGAGAGCTC TACCGCTT	GCACCCAAAAGGTCA TCTTCTTCCTT
1	22,048,209	KJ01_073	[29]	ATCTTGTTAAATCAAAGA TGTTGTAGCA	ATCTTGTTAAATCAAAG ATGTTGTAGCC	CCCATTTGTATGTGGT TAGCCTTCTATTT
1	22,138,518	ah01001478	[30]	CGATGCCAATACTAGCCA ATGTCA	GATGCCAATACTAGCCA ATGTCTG	TGGACATATAACCGA TTGCTCAAAACCT
1	23,434,283	KJ01_075	[29]	AGGGGCTTTGTTGGTGGT CAAAT	GGGGCTTTGTTGGTGGT CAAAC	GCAGGGATTCGAGCA TAATATAATCAGAT
1	24,007,114	SaF-CT	[30]	CGGTGTCCAGGTAACCG G	CGGTGTCCAGGTAACCG A	GGTCACAATCAGCCG TGCC
1	24,199,706	id1012784	[30]	AATAGCATCTAAAAACAT GTTTTACACCGAA	AGCATCTAAAAACATGT TTTACACCGAG	CGGAGGGATGAAAAT TTAATTTTCTCTCCA A
1	24,366,725	KJ01_079	[29]	TGTCATTTCGATGTACGGA TTGATAAA	GTCATTTCGATGTACGGA TTGATAAC	GCTATGTATCAACTAA CCAGTGTTCTGTTT
1	24,958,106	KJ01_081	[29]	TAGTAGAAAAACAATGAT AATCGAATGC	CTTAGTAGAAAAACAAT GATAATCGAATGG	CCGGTTTAAATAGAG AGTTACGTCGATA
1	26,813,843	ah01001843	[30]	TTGATGCTAAAAACGCCA GTGAC	GTTGATGCTAAAAACGC CAGTGAT	TGTGGGTAGGCATCA TAAAAAGGAACT
1	27,013,911	Rd-GA	[30]	TCCACGGTGGGCTTGAC	TTCCACGGTGGGCTTGA T	ACGCCCATGGACTTC GAGT

1	29,381,536	id1015984	[30]	CAGGCTGGACATTTTGAC TGAC	TCAGGCTGGACATTTTG ACTGAT	GTCAAGAATCTCTGTA AGAAATAGACAATAT GTCAGTA
1	32,551,664	KJ01_093	[29]	GTAACATGCTAGTAGCAT CACCATGA	AACATGCTAGTAGCATC ACCATGG	GAGAGATGGGTGTCTG GCGGAT
1	33,063,515	id1018870	[30]	CGCTAGTGTAGAGCACG AACATG	CGCTAGTGTAGAGCAC GAACATC	GGACCACGGTGAGCC AGA
1	33,340,511	KJ01_097	[29]	CAAACGGTTTCTCCACCA GTGG	ACAAACGGTTTCTCCAC CAGTGA	CGTCTTTGATCCGCGC AAAACCTCTA
1	34,978,783	ad01015967	[30]	AGGTGCTTCTGATGTTAG CTACG	CAGGTGCTTCTGATGTT AGCTACT	CCAGGCTGTTTAGGA GTTGGC
1	37,298,045	id1022407	[30]	AGGGACAGATGCTGCTTT GTTAA	GGGACAGATGCTGCTTT GTTAG	CCGCAACAGTAACCA GCACAA
1	38,191,474	qSH1-TG	[30]	GCATTTGGTGGTACGTGT ATCATGA	CATTTGGTGGTACGTGT ATCATGC	AGGGTTCGGCGATGA TGGT
1	40,437,865	KJ01_119	[29]	ATTGGAACCATACTATCA TCGTCAT	ATTGGAACCATACTATC ATCGTCAC	GAGAAGAAAAGAAAA GGGTCTTGACAGAA
1	40,892,591	id1024836	[30]	GCTTCAGGATTTTCAGTAG GATCCAC	GCTTCAGGATTTTCAGTA GGATCCAG	CCCGCTGAAGAACGT GCTG
1	41,138,835	KJ01_121	[29]	AAGGAAGGCCCGGCCCA TC	GAAAGGAAGGCCCGGC CCATT	TTAGTCCCTGCCGTTT TGAGGCAA
1	41,979,600	KJ01_125	[29]	GAGTACTACTTTGGCCGA GTTCAA	AGTACTACTTTGGCCGA GTTCAG	CACCATGTGTAGAAA AGTTTTGATGTGATA
1	42,482,913	KJ01_127	[29]	TCTCTCCTTCGCTCGCTCT	CTTCTCTCCTTCGCTCGC TCC	TCGTTTCGTTGTTAGTA GGGTTTAGAGTTT
1	42,494,829	P1193	[30]	GCATTTTCGAGACCAGAC CAGG	GCATTTTCGAGACCAGA CCAGT	GCCTAGGGGGCCTGA AAGTA
1	42,946,801	KJ01_129	[29]	AGTAGCAGCAGCAGCTTA GGTC	AAGTAGCAGCAGCAGC TTAGGTT	CTCTTGATCGCACCA TCCATATGAT
1	43,613,762	ad01020824	[30]	GGGCCAAGGAGTACACC A	GGGCCAAGGAGTACAC CT	TCTGCTCGGCAGGCA CT
1	44,672,306	id1028304	[30]	GTTGATGGTCCTTGCTAA AAGTGG	AGTTGATGGTCCTTGCT AAAAGTGA	ATCATCACCTTCAGAT TTCAAACAAAAAGAC A
2	9,619	id2000007	[30]	AGCAATCCTGAGGGCCAT AAC	AGCAATCCTGAGGGCC ATAAT	CGTCTCATGGCAAAG GCTGA

2	2,406,169	ad02000512	[30]	GCTTAGCTAGTACTACAG CTAATTTGACAT	GCTTAGCTAGTACTACA GCTAATTTGACAC	TTTGTATTATTAGTTTT TTATTTTGTGAGGAA TGAATGA CTAGAATCATCGTAAT TACTACTCATATATGT CACCATTT CAATGCCCGTGTATTAT TTCACGCCAA GGACTATTAAATAGC CCTCCGAAATCTTA CTCTTTGCCTTCGTGC AACGTCAA CTGAACTGCTCCAGCT CGGAGAT CCAACGTGCAATTTAA CAAACCAAATGCAA CGCTGGTCGCTGCCG
2	4,361,466	id2002293	[30]	CTGGTGCTGGTTTAAGCA GTAA	CTGGTGCTGGTTTAAGC AGTAG	
2	5,523,756	KJ02_009	[29]	CACATCGTTCCAATTTCA ACCAAACATTT	CATCGTTCCAATTTCAA CCAAACATTC	
2	22,684,234	KJ02_039	[29]	ATCGGTAATCTAAGTTTA ATACTCCTAAAC	TATCGGTAATCTAAGTT TAATACTCCTAAAT	
2	23,850,625	KJ02_043	[29]	GGAGGTAATCCCGTGGC GGA	GGAGGTAATCCCGTGG CGGT	
2	24,278,925	KJ02_045	[29]	CCCATGGCCAGACGGAG TCA	CCATGGCCAGACGGAG TCG	
2	24,582,137	KJ02_047	[29]	GCCTTTTAGGAAGAAATT ATAGCTAGTG	AGCCTTTTAGGAAGAAA TTATAGCTAGTA	
2	24,835,540	id2009889	[30]	GATCGATCACCTCGCTGC T	ATCGATCACCTCGCTGC C	
2	26,176,180	KJ02_053	[29]	GAAGGGGATATGATTGC ATTCGTCT	AAGGGGATATGATTGC ATTCGTCC	
2	26,691,450	KJ02_057	[29]	TTCTTGTGTGCTCTTTTC TTCCTTC	GTTTTCTTGTGTGCTCT TTTCTTCCTTT	
2	26,817,689	ad02011845	[30]	GGCTTAGCTACTTCATCG TTTCTAGT	GCTTAGCTACTTCATCG TTTCTAGC	
2	29,130,590	id2012773	[30]	CAGACAATCTTCAGGCAA AGCTC	CAGACAATCTTCAGGCA AAGCTT	
2	30,450,152	KJ02_067	[29]	AAGTTGCTAAAAAATCAT ATTAATCTATTTTAA	AAGTTGCTAAAAAATCA TATTAATCTATTTTTT	
2	30,861,574	ae02004877	[30]	GAGTGCTGTCATAATATT GCACTGG	GAGTGCTGTCATAATAT TGCCTGC	
2	32,719,981	cmb0232.7	[30]	CTTGACCGCAAAACCGGA TAT	CTTGACCGCAAAACCGG ATAC	
2	33,610,265	id2014575	[30]	AGTAGAAAATGTATTAC AGTTCCAGCT	AGTAGAAAATGTATTCA CAGTTCCAGCA	
2	36,626,894	cmb0236.6	[30]	GTTACAGCATAAAGGAA AGGAAAACCC	GTTACAGCATAAAGGA AAGGAAAACCT	

3	25,505	ad03000001	[30]	TCCACACATGTCTTGTTA AAACCC	GTCCACACATGTCTTGT TAAAAACCA	CCTCCTTTTTCTTTCTA TCTGTGAGCATCT
3	1,729,434	KJ03_007	[29]	ACCTTCCAACCCTAGCAT GCG	CACCTTCCAACCCTAGC ATGCA	GAAACACACCCTTC AATTACTGTGCTTT
3	3,524,497	ah03000403	[30]	TTGATCAAAGCACACAGA AAGCG	CTTGATCAAAGCACACA GAAAGCA	TGTGGCGTCGATACTT TACAGTTGA
3	5,676,626	KJ03_017	[29]	TTTTTTTCTAAAAGAATA ATACAACTCGTGT	CTTTTTTTTCTAAAAGAA TAATACAACTCGTGA	CAATAAGTAAACACA CAAATTTGTAGGATA
3	5,920,066	id3003462	[30]	TGCCTTTAATGGAGCATC ATGGA	GCCTTTAATGGAGCATC ATGGG	GGATTGCATGACCAT CAAGGCA
3	10,023,081	id3005168	[30]	GTTGTTTGACTGTACCCA AATGTACT	GTTGTTTGACTGTACCC AAATGTACC	AGCAACATCTATAGTT GTCCAGGGATTTT
3	11,972,407	KJ03_027	[29]	ATATCTGTCGGATTTTAA AAAGCCCTA	ATATCTGTCGGATTTTT AAAAGCCCTC	GGATAATATCCACTCC ATATTTGTCCGAA
3	12,321,614	ah03001094	[30]	GCTCTGCTCTCTGTCTC GA	CTCTGCTCTCTGTCTC GG	GGGACACGGACAGAA AGGAAAAAA
3	12,785,160	KJ03_031	[29]	CCTGACCAGGGGCGGTCT A	CTGACCAGGGGCGGTC TG	ACCACCGTTGTGAGG CCGGTTA
3	13,122,748	KJ03_033	[29]	GAAGAAGAGAATTGACC CAGTTTATAAGA	AGAAGAGAATTGACCC AGTTTATAAGG	GATGTATGGTTTTCG GGTCCGGTTA
3	15,548,178	id3007541	[30]	GATCCGGGTGGTGTCAGT T	GATCCGGGTGGTGTC GTC	CAGAGTAATGGGAAG GCATGCA
3	24,305,190	id3010700	[30]	GAAGAAGATGCCAAGTTT GCTGTT	AAGAAGATGCCAAGTTT GCTGTC	AGGGAAGCTTCAGCC ATCGT
3	25,848,924	ad03013905	[30]	GGAAGGCTCTGTGCTTAC GTTTA	GAAGGCTCTGTGCTTAC GTTTC	CCACAAGCCTGAATA CAAGGCA
3	27,135,408	ad03014175	[30]	GATGGCGAGTTTGACACA GATCTA	TGGCGAGTTTGACACAG ATCTG	TGGGAGGTCGTCGTC GC
3	32,355,773	KJ03_069	[29]	TTTTAACTGTAAACGG TATGTTTTTTGT	CTTTTTAACTGTAAAA CGGTATGTTTTTGC	GCAGCGATTAGCGGT TGATTAATTAAGTA
3	32,410,973	Hd6-AT	[30]	TGTGGAGGTCCAAACATT GTGT	TGTGGAGGTCCAAACAT TGTGA	CTAGGAGTCTTAGAA TGTTGATCTCTGACA
3	32,981,871	id3015453	[30]	TTGCCACTGTGTGCAACA TTT	TTGCCACTGTGTGCAAC ATTC	CATCGGCAACGAGAC GAAACA
3	35,132,848	ah03002520	[30]	CTTACAACACTCTCTCA TGCTCT	TTACAACACTCTCTCA TGCTCC	GCCATGCAAAAGATT TTTATATAGATTGTGG C

3	36,572,765	cmb0336.5	[30]	TCTGAAGATCACGAGAG GAAGGT	CTGAAGATCACGAGAG GAAGGC	G TTCACATGGGCCTCC GC
3	37,181,952	id3018439	[30]	TCAATCTGCACATACGGG ATAAATGT	CAATCTGCACATACGGG ATAAATGC	GGCGATATATTCTCTT CATT CATGCTAAAGTG ACTAGCTAGAAAGAA ATCTCTGACTTTTTGT GT
4	2,456,955	id4001096	[30]	AGTTAAACAAGTAGTTAC TCTAACCGTTGAA	AGTTAAACAAGTAGTTA CTCTAACCGTTGAT	CGGCGATTTCGGTAG GACTGAAATT
4	4,526,234	KJ04_021	[29]	GAAATGTGCCGAAAATCA CGAAATTTCA	AAATGTGCCGAAAATCA CGAAATTTTCG	GGCCAAATAAGATTG ACCCAAGGCAA
4	6,384,872	KJ04_029	[29]	GTATCTGGACAAGTTCTA TAATCGAAAG	AAGTATCTGGACAAGTT CTATAATCGAAAA	GATGCTTGAAGAATT TGTTTGTCGGGATT
4	9,051,840	KJ04_039	[29]	TTGCATTAGCTTATCTAA GCGATAAAGA	GCATTAGCTTATCTAAG CGATAAAGC	TAGGGATACACAAGA CAATTGGGGATAA
4	10,695,483	KJ04_043	[29]	GAAGATGTCGATGTTGA GCACAG	ACGAAGATGTCGATGTT GAGCACAA	CTAGGGAAAAACCTA CACCGGTGAA
4	11,832,332	KJ04_047	[29]	CAACCGCTGCCCCCTATGC C	GCAACCGCTGCCCCCTAT GCT	GAGATCTCGTTGATCC CCATCGATT
4	12,548,965	KJ04_049	[29]	AGAAGTAGACGAAACTG ACGATTCC	AAAGAAGTAGACGAAA CTGACGATTCT	ACCGAGTTCAAGACA TTGAAGTTCTAGTA
4	17,250,626	KJ04_053	[29]	TCTTCAATGTCCTCACTAA TTGTCAG	TTCTTCAATGTCCTCACT AATTGTCAA	CACAAACGATCTCAA ACTGTTAAGTTCTTT
4	18,114,091	KJ04_057	[29]	GAACTATTATAACATGGT TAATTAAGTGTTA	GAACTATTATAACATGG TTAATTAAGTGTTT	ACCATTTGACAGTTTG AAAAGGATGGTAATA AAAA
4	18,813,976	cmb0418.8	[30]	AGGTGGTGTTCTTTTTTA ATTAAGACAGATTC	AGGTGGTGTTCTTTTTT AATTAAGACAGATTT	GTAAAAGCTCAACTG GATGACAGAGAAAA GGACGCTTTATGTAC ACGTTAAGGAAAT
4	19,541,114	KJ04_059	[29]	CGGGACATTTTAAGGGAC TCCTG	CGGGACATTTTAAGGG ACTCCTC	TTCGCTGTAGGGGTG CGACGAA
4	20,356,970	KJ04_061	[29]	CCGTCTGTGGACTCCGTG ATA	CCGTCTGTGGACTCCGT GATG	GGAGGTCAGTCAAAT TTCTATAATCTTTAGA AGCA
4	20,703,190	KJ04_063	[29]	GATTGCATTGTGTCATCA TTGCCAAG	AGATTGCATTGTGTCAT CATTGCCAAA	GCAAGTCACCTCTTG TTGTTTTAACGA
4	20,730,844	cmb0420.7	[30]	TGGAGTTGAAAGTTGAA ACTCATCAAC	GTGGAGTTGAAAGTTG AAACTCATCAAT	
4	22,750,935	cmb0422.7	[30]	TCAGTGTGGCTGGAAGA AGTC	CATCAGTGTGGCTGGAA GAAGTA	

4	24,379,789	id4007882	[30]	CATGCGTTGGTCATTGCC TAC	CATGCGTTGGTCATTGC CTAA	AGTATGGCAAACCGG GAGCA
4	26,443,283	ad04009559	[30]	GCTGGATCTATAGCCCC C	TGCTGGATCTATAGCCC CCT	AAATCCAACACGCCG GAAGC
4	28,788,134	ah04001252	[30]	AAAGCCACCAGCAATTGT CATTT	AAGCCACCAGCAATTGT CATTC	ACGTCGGACAACAAA TTGAATGAAAATATG AT
4	30,014,981	id4009823	[30]	GCTTGCTGGTTTGTCAAG TGC	GCTTGCTGGTTTGTCAA GTGT	AGTTTCTTTATCTTCG CATCGGATGGA
4	32,268,324	cmb0432.2	[30]	TCTGTATCTCACTGTAGT CCTGGT	TCTGTATCTCACTGTAG TCCTGGG	GGATCTCACAGTAGC CTATCAAATGGA
4	34,108,743	cmb0434.1	[30]	CAAAACGGCGGCAGAAT TGT	AAACGGCGGCAGAATT GC	GACAAAGCTAGGATT ATTAGATATGATCACC AAGT
4	34,535,832	KJ04_093	[29]	CATCTTGGAATTTGCAGG ATGTGGAA	ATCTTGGAATTTGCAGG ATGTGGAG	CCACCATCCATCCATT CATTCTGGAA
4	35,843,455	id4012434	[30]	TTCAGGTACTGATGCCAA GTACC	GATTCAGGTACTGATGC CAAGTACT	TGTGGACTAGCCCTA CGTACTCT
5	2,831,817	KJ05_011	[29]	AAATAGTTTAACTTTAAC TAAAGTTAAATCGTT	AAATAGTTTAACTTTAA CTAAAGTTAAATCGTC	GTCCTTCTGGGGCTG GTAAGAATTA
5	4,734,427	id5002497	[30]	TTCCTTTTCACTGCATTAC AAATCAGAC	CTTCCTTTTCACTGCATT ACAAATCAGAT	GGAATATCATCATATT ATAGGTTGACTAGCT ACTCC
5	4,783,888	KJ05_013	[29]	CAAGCCACGGATGGCTG GCAA	AGCCACGGATGGCTGG CAG	AGAAAGAAGGGATGA GAGATGCTTTTCAT
5	5,984,919	KJ05_017	[29]	CGTCACCATCTCCGCAGG CA	GTCACCATCTCCGCAGG CG	GGAGGACGGGGACG GCGAT
5	6,562,635	KJ05_019	[29]	AGCTAATACTTAATTAAT CACACACTAATG	CTAGCTAATACTTAATT AATCACACACTAATA	CAGTGAGCACGGAAA ATAGAGCGAT
5	7,392,294	KJ05_023	[29]	GCCGAAGCACTCAACCCT CTAT	GCCGAAGCACTCAACCC TCTAA	ACCGTATTCAATGGTT TGGGGTGTAATAAT
5	8,028,641	id5004086	[30]	ACCAAATATTGTTGTAT AGGAGTAAGAGC	CACCAAATATTGTTGT ATAGGAGTAAGAGT	CGGCCAGGGTTCTGT CAAA
5	11,127,260	cmb0511.1	[30]	CGTGCAAGACCATTTGAA GCTC	CGTGCAAGACCATTTGA AGCTA	GGGCGCCAACACCAA AACC
5	12,691,869	KJ05_029	[29]	AATACACATACATTCTAG TTATATGATTAACC	AATACACATACATTCTA GTTATATGATTAACT	CAGGAAGGCATCGGA TAGAGGATAT

5	14,387,882	id5005882	[30]	GCCTGAAAATGCTTGTTT CTCTGT	GCCTGAAAATGCTTGTT TCTCTGA	TGTTCATTAACCGATC GGATTCCGAAT GTACAGCAAACCTCTTC
5	22,039,255	ad05008445	[30]	CAGCCGTCCAAACGGTTC	CAGCCGTCCAAACGGTT T	TATATATGATCTGTTC GT
5	24,121,914	id5010886	[30]	GAACTGTCCCTTTCTTGG TCATC	GGAACGTGCCCTTTCTT GGTCATT	GACGCGTGCTTGACA GCAT
5	25,852,536	KJ05_063	[29]	AAGGAGTCCATAGGCTG CTGCT	GGAGTCCATAGGCTGCT GCC	AAAATGGTATCAAAG TGAACAGGCCCTT
5	26,029,645	KJ05_065	[29]	CCTCTAGCTAATTTATCCT CTCGC	GCCTCTAGCTAATTTAT CCTCTCGT	TCACCACCGGTCGCC AGACAAA
5	26,356,605	cmb0526.3	[30]	TGTACGTTGTCCAAATAC ATCTCTAGAAA	ATGTACGTTGTCCAAAT ACATCTCTAGAAT	GCATGTCCTGAAGTA CTACTCCTGT
5	27,795,820	KJ05_071	[29]	GCCGATGTAATTTAAGCA ACAAGATCTAT	CCGATGTAATTTAAGCA ACAAGATCTAC	CTGGTTTGGGGCAA GTGTTTACTTTATT
5	28,700,370	id5014265	[30]	GCCAACTTTGTCAGAAA CAGGTT	GCCAACTTTGTCAGAA ACAGGTC	GCATGATACTTCTATC ATGTACACTCCTGA
5	29,798,006	cmb0529.7	[30]	GGGAGGGAAAGGACTCC C	AGGGAGGGAAAGGACT CCA	AGTATTAACAAACA GAAGAAAGGATAATG ATACTCTGT
6	243,274	id6000073	[30]	GCAAGCCGATTGTTACGA ACTT	GCAAGCCGATTGTTACG AACTC	GCTTTGCTATGTGGTT GGTGATACA
6	1,038,324	KJ06_005	[29]	GCGTGATTAATTAACAT TAGCTAATTTTTTTA	GCGTGATTAATTAACAT TTAGCTAATTTTTTTT	CGGTTAAACGGTGCA TTTTTACAAAAAGTT
6	2,936,067	KJ06_009	[29]	TACAACTTAAAAATAGA TATGTTTCTTTTTA	ACAACTTAAAAATAGA TATGTTTCTTTTTT	TCGATCAAACCTGTTAT AAACAACACGCTTT
6	3,365,147	KJ06_011	[29]	TTTCTTTGATAACCATTTA AGTTGCAACTAAA	CTTTGATAACCATTTAA GTTGCAACTAAC	GTAGAATATTGGAGT CAGTATCCCTTCAA
6	5,593,526	cmb0605.5	[30]	CCGAATTAGGCATAAATT TGGCACG	CCGAATTAGGCATAAAT TTGGCACC	TGCTGCACAGATTGC ACGAC
6	5,760,512	S5-TC	[30]	TGAGGAATAATCGACGAT CAGCAAA	TGAGGAATAATCGACG ATCAGCAAG	CCAGGGGAAACAATT CGGCTT
6	7,077,663	cmb0607.0	[30]	CTGATACTAAGGGAAACA AAATGCATGAA	TGATACTAAGGGAAAC AAAATGCATGAC	CTCCTGGGCATTGGC ATGAA
6	7,708,089	KJ06_027	[29]	CACATTTCATATTGATATT AATGAGTCTAAATAC	CACATTTCATATTGATAT TAATGAGTCTAAATAG	GTTTAACCTTAATCTT GTCTAAAACGTCAA

6	7,841,654	cmb0607.8	[30]	TGAAGCATGGCCTTGAAG ACT	GAAGCATGGCCTTGAA GACC	ACAGTGTGTGGAGAT CAAGGACAT
6	7,837,648	KJ06_029	[29]	CCCTCTTTTCGTAAATATA AGTATTTAAAGC	CTCCCTCTTTTCGTAAATA TAAGTATTTAAAGT	TGGGAGGTGAAATGG GAAGAAATTTGTTA
6	8,481,127	KJ06_031	[29]	ACTATGATGTCAATATTT AGTATTAGGTAAAT	ACTATGATGTCAATATT TAGTATTAGGTAAAG	TATTTGGACTTGCTCC ATCCGTTCTTAAA
6	8,725,792	id6005608	[30]	CGTAATAATGATATAATA ACCGCGCTGAATTAC	CGTAATAATGATATAAT AACCGCGCTGAATTAA	GCTGTTGTGATGCGT GGGAT
6	13,653,907	id6008118	[30]	AAAAAACCTACCTGATCA GATCCACT	AAAAACCTACCTGATCA GATCCACA	GAGATGATATTTTATA GTGTAGTCTTACCATC
6	18,066,599	id6009699	[30]	ACAATCCATGGTCGGTTG ATGAA	ACAATCCATGGTCGGTT GATGAT	GCCTGCATGACCATC GGC
6	18,278,072	cmb0618.2	[30]	TCCACACGGACACGGTTT C	TCCACACGGACACGGTT TT	ACAAAACAATAATGG AATGGATCTGAAAAG
7	122,298	cmb0700.1	[30]	ACCTGTACTCCTGTAGGT TTAGGTT	TACCTGTACTCCTGTAG GTTTAGGTA	CGTCTTGCCAAGCAA GCCA
7	2,277,644	KJ07_011	[29]	CATTGAAGATTACCAACA AGAATTAAGTAAG	GCATTGAAGATTACCAA CAAGAATTAAGTAAA	CATATATTACGACGAC TCTCCTTTTCCTT
7	2,563,993	ud7000187	[30]	CAAAATCCCTTATATTATT GCTATTAAACCTTTGAT	CAAAATCCCTTATATTA TTGCTATTAAACCTTTG AC	AATTACATTACTGTAT ATTTTATATTCTATG TTGTCAAA
7	2,749,068	KJ07_013	[29]	GTGTATCAACAGATAGAA CTTACTCTCTT	GTATCAACAGATAGAAC TTACTCTCTC	AAGGATCAAATTCCTT TCTAGGTAAAGTTT
7	3,292,230	cmb0703.2	[30]	GATTCATTTAGCTCAGCT TAGCTGTG	GATTCATTTAGCTCAGC TTAGCTGTC	CCCACACTAGCTGACT GTCCT
7	4,239,741	KJ07_019	[29]	TTAATACTTTACATGTGTC CAAACATTTCAAT	AATACTTTACATGTGTC CAAACATTTCAAC	ATCGATTTAGGCCAT GTTTCAGTTCTCAAA
7	4,265,929	ad07001853	[30]	CCCCAACTATTACAGTT GCTCG	ACCCCAACTATTACAG TTGCTCA	GGGTGTTAAATATCT AGTATTTGAGTTTAAAG GAGGTA
7	4,644,793	KJ07_021	[29]	AAAGATCCAACGCACCAA AATTTGACT	AGATCCAACGCACCAAA ATTTGACC	CAGCTTTGCTAAAATT ATGTCGGCATCTT
7	7,019,781	id7001155	[30]	GCCACACATACACATCAG CATACA	CCACACATACACATCAG CATACG	AAAAATTCAAATAGA AATATATATATCCTGT GAGCAAACA

7	11,030,430	KJ07_033	[29]	CCTCAGCGCCTGCAGCCA	CCTCAGCGCCTGCAGCC G	CCCTCTCTCGACGGTG CCATA
7	11,588,122	id7001998	[30]	GGTTGGTTTGGCGATCTC ATCT	GTTGGTTTGGCGATCTC ATCA	AGGTGCTCCAGTGCT GTAAGG
7	15,667,894	id7002392	[30]	ACTGATGTGAAGAACAGT CTAGAGC	CACTGATGTGAAGAACA GTCTAGAGT	TGCTTCATGCCATCGA TCAGGA
7	17,762,865	KJ07_049	[29]	GTGACCTCTCCAAGGAGA TTA	CTGTGACCTCTCCAAGG AGATTG	ACAACTGGCGTCGGG CCTTCTT
7	18,017,078	cmb0718.0	[30]	AATTAATGTTTGTCTCA CCTATTTTCGTTTAG	AATTAATGTTTGTCTC ACCTATTTTCGTTAA	TTTACGTGGTTTTC AAAGAAAATAATAAT AATGAAGGA
7	18,168,615	KJ07_051	[29]	TTATAATAATTCGCGTTT ATATACATGCATGT	ATAATAATTCGCGTTTA TATACATGCATGC	CGCCGCAGGTTAGGT ATATTTTCGTA
7	20,321,276	id7003072	[30]	CGGAATCTCATTTTCTTA AGCTGCATA	CGGAATCTCATTTTCTT AAGCTGCATT	GTAAGAAAATATATT GGTCTATTAGCCTATA CAATCCTGT
7	22,377,948	KJ07_067	[29]	GGTATCAGTTGGTACCGA TTGATCT	GTATCAGTTGGTACCGA TTGATCG	GCCAGATCTGGTACTT GTTAGTACCAA
7	23,014,905	cmb0723.0	[30]	TGCTCTTTCTTCTGCTTG ACTTTG	GTGCTCTTTCTTCTGCTT TGACTTTT	GCGAATGGACACGGC AGC
7	23,471,376	KJ07_069	[29]	CGGAGGCGTTGTTTCACC ACA	CGGAGGCGTTGTTTCAC CACG	GTTTGCCATCGAGCA CCTGGCAT
7	24,146,716	KJ07_071	[29]	GTAGACGATGTTCCCGTT TTCTTC	CGTAGACGATGTTCCCG TTTTCTTT	GTTGCCACTCGACTCA TGGGCTA
7	25,326,292	SLG7-GC	[30]	CAAAGCCTTCTCAAGGGA AGAAC	CAAAGCCTTCTCAAGGG AAGAAG	GCTTCTTGGACTCTTC GAGACCT
7	25,682,560	id7004645	[30]	ACGTGGCTCAAGCTCACT G	AACGTGGCTCAAGCTCA CTA	TGCGCAAATCGCAGT GTGAC
7	27,003,411	cmb0727.0	[30]	ACTGACAAATACCTGCCA CACA	CTGACAAATACCTGCCA CACG	TCAAACCTCAAACTTTT ATTTTGAACACTGCT
7	28,576,878	cmb0728.5	[30]	CAGATAACAGGGACATA GTGGACATA	AGATAACAGGGACATA GTGGACATG	GAGCCGCCTAAGATT TTCCTTTTCG
7	29,529,536	KJ07_085	[29]	CCTCCTGCTGGAGTCTAC AGAT	CCTCCTGCTGGAGTCTA CAGAA	CCTGTGTACAATTTGG CATGACAATGAAA
7	29,931,834	id7006027	[30]	CATAAATCAGAATTACAG GTTGCAGCT	CATAAATCAGAATTACA GGTTCAGCA	AAACCTTGAGGAAT GTCATCGTCT

7	30,325,349	cmb0730.3	[30]	GCAGTGGGATGGCAGC	TGCAGTGGGATGGCAG T	CGGCGCTTTGCTGCA GG
8	2,855,479	cmb0802.8	[30]	ATCTCTAGTAAAAGGGTG CCATACG	GATCTCTAGTAAAAGGG TGCCATACA	AGCCTATAGCCATAAT GATGTCATTGTGA
8	4,097,511	KJ08_017	[29]	TCACAAAATCCCCAAATA CATCAAGC	CTTTCACAAAATCCCCA AATACATCAAGT	GGTTAGAGTGAATGG GATTTGGAGAAAAT
8	5,648,540	cmb0805.6	[30]	CCACAAAGACACTGACAC CAATT	CCACAAAGACACTGACA CCAATC	CTGCCCCCGGCCAAT G
8	5,786,550	KJ08_023	[29]	AAATACTACTGTAACGTT AGTACGGAC	CTAAATACTACTGTAAC GTTAGTACGGAT	CGTACTAGCCAAGTT ATTGTACTAGTGTA
8	6,204,862	KJ08_025	[29]	TATTATCTTGGATGGAAA TAAAATATACAGCT	ATCTTGGATGGAAATAA AATATACAGCC	GTCAATATTTGCAACG AGATAATTCCAGAA
8	8,332,647	KJ08_035	[29]	CGCGTGTGTTGCATGGAG ACG	CGCGTGTGTTGCATGGA GACA	GCAGAGATCGTATAG GTGTCCTGAT
8	8,424,668	wd8001250	[30]	CCAACGGGTCGCTGGTG	CCAACGGGTCGCTGGTA	ACAGGAGTTCATCAT AGATTTGCCTGT
8	10,499,283	KJ08_045	[29]	ATTCTCTAACAACCATAT ACAATGAGTTGT	CTCTAACAACCATATAC AATGAGTTGC	ATGGTTCGACTGATA CTCTCCATCATAAA
8	11,622,925	KJ08_049	[29]	AGCCGTTGATGTAGTTGA GGGATTA	CCGTTGATGTAGTTGAG GGATTC	TCGGCCAGAGGTCGT TGTCTTA
8	11,798,820	id8003584	[30]	TCAAGGTGGTCCTCGACA CTA	CAAGGTGGTCCTCGACA CTC	GTATTGCGCTATGCCA CGGT
8	12,459,153	KJ08_053	[29]	ACTCGTTTTCTTCCGCGT GATTAG	ACTCGTTTTCTTCCGCGT GATTAC	CACAATGGCATAACGT TGTAAGAAGCAA
8	13,990,791	KJ08_059	[29]	GGCGACAACCTAGAGTAG TGACG	CGGCGACAACCTAGAGT AGTGACA	CACCATCGCCGCGCC GTCAT
8	20,253,954	KJ08_085	[29]	GCATTGGACTTGCGAGAT TTGTCA	GCATTGGACTTGCGAGA TTTGTCT	AGCGGTCGTCGGGTC GGGT
8	21,503,195	ae08007378	[30]	TCTTCCACCAAACCTTGCA TGAATTC	TCTTCCACCAAACCTTGC ATGAATTT	AGAAAATACCATCCTC AAGGAGCACA
8	23,740,826	id8006751	[30]	CTCATTGGTGATAATGCA CTTGTATGAAT	TCATTGGTGATAATGCA CTTGTATGAAC	GCATTCTCACAAAGT GTATATAATGCCAGA TC
8	24,799,130	cmb0824.7	[30]	CTCAAGGCCGTACATCCA TATGTA	TCAAGGCCGTACATCCA TATGTG	CCTTCTCTAATATTCA CGTCTTTTAGATTAC GCT

8	26,590,280	GW8-AG	[30]	ATCTAAAGGCGAGCAAA GAGGT	CTAAAGGCGAGCAAAG AGGC	TCCTTTAGCTCGGCAA CTCGT
8	27,921,569	id8007764	[30]	TCGTTACAGCATGTCAGT AGCC	CTCGTTACAGCATGTCA GTAGCA	GTGCACTTCGTTCCAA GGCT
9	438,538	id9000045	[30]	CAAGGCAAGTACACTTTT CTCCAAT	CAAGGCAAGTACACTTT TCTCCAAC	GACCACATGTAATCTT AGTTTACATGATAAA ATCGG
9	4,288,667	id9000884	[30]	TGCTCCTCAATACATTTG ATAACAGCT	GCTCCTCAATACATTTG ATAACAGCC	GAACGCGAGTTGTCT GCCTT
9	7,214,648	cmb0907.2	[30]	TGAGCCCCGAGCTTGACAT AA	TGAGCCCCGAGCTTGACA TAC	GCTGAGGCTCAAAGC TAGGGT
9	8,073,443	KJ09_027	[29]	AAATTAAGAAAGGCT GATGGGAGTTTAA	AAAAGAAAGGCTGATG GGAGTTTAG	AGCCTTTAGCCACTAG TCTAGCTTTATAT
9	8,513,936	id9002419	[30]	TGCATTGCTCCGATTGAT AGGAG	GCATTGCTCCGATTGAT AGGAC	TCTATTCTGGACTACA GTCCGAACATATCA
9	8,744,926	KJ09_029	[29]	CTGACACCGGACTTGAAA GCC	CTCTGACACCGGACTTG AAAGCT	CGAAATCACCGACGC TTCTGCAAT
9	9,607,302	cmb0909.6	[30]	ATGGATCAACAAAATTGT GCTCCTATTT	GATGGATCAACAAAATT GTGCTCCTATTA	CAAAGTGAGCAAGGG TCAGCA
9	11,439,570	KJ09_039	[29]	TATAAAGTTGAAGTGTAT ACAGTTTGGC	CTTATAAAGTTGAAGTG TATACAGTTTGGT	CGAGTGTCTGTAGC AAATTTTGCCTAAA
9	11,776,387	KJ09_041	[29]	ATGTGCCCAACATTTTAG CCTACG	AATATGTGCCCAACATT TTAGCCTACA	CCTAACTCTTTTTTGG TTTCAGCCATCAT
9	12,505,826	id9003183	[30]	AAGATGGTGAAAGCCAC CTGA	AGATGGTGAAAGCCAC CTGG	AGGGCAACCAAAAGC ATTGGTC
9	14,468,502	cmb0914.4	[30]	GCCCAAGCACACTCACTA ATTTTTTA	GCCCAAGCACACTCACT AATTTTTT	TACTAGTATTAACCTA TAGGGGATTAGTGTA GATCATTTT
9	15,394,586	id9004072	[30]	ACCACATGACCTGATCTT TGCA	CCACATGACCTGATCTT TGCG	CAGCTAGAAGAATTT TTGATGCAACTCCA
9	17,509,141	ae09005437	[30]	CTACTCCTACGTGTTCTGT TCCAAT	ACTCCTACGTGTTCTGT TCCAAC	GCTCTCTGAAATAGTA TACGTGTAAAGCTTA GT
9	18,502,078	KJ09_067	[29]	CGAAACGACAGTCAAATA TAAATATCCATTT	CGAAACGACAGTCAAAT ATAAATATCCATTA	ATAGGGCGACTTCCC ATGCAATTTTATAT
9	19,337,813	KJ09_071	[29]	GATAGGAAGAAGAATCA TGGAGAGG	GATAGGAAGAAGAATC ATGGAGAGA	CATAGTACCTCGTCG GCAGTATACAA

9	20,044,954	id9006953	[30]	ATAGAAGTTCTGAATCTG CTAACACTGA	GAAGTTCTGAATCTGCT AACACTGC	TTGAAATCGCCGGTT ACCGC
9	20,091,056	KJ09_073	[29]	GATGGCACGTCAAGTTTT ACAAAAGTTT	ATGGCACGTCAAGTTTT ACAAAAGTTC	GAGAATCCTTCTTCGC GTTGAATTTCAAT
9	20,497,375	KJ09_075	[29]	CACGTACGAAGTATGTAT GTACATGATA	ACGTACGAAGTATGTAT GTACATGATC	CCCACGTCACCCGTAC GTGTA
9	21,615,845	TAC1-CT	[30]	AGAAATTCCCTTTACCTT TTGCG	AAGAAATTCCCTTTAC CTTTTGCA	AGCGTGAGGATGGAT CCAACA
9	22,166,657	KJ09_081	[29]	GACACTTGTAACCTTGTTG CACATGTATA	ACACTTGTAACCTTGTTG CACATGTATG	GGCGCTGAATAAACT CATTCACATGTAAA
9	22,403,093	KJ09_083	[29]	CTATTGCTATTTCCAAGA CCG	GGCTCTATTGCTATTTT CAAGACCA	TCTGAGAATGCTCGA CAGAAACAAAGTTT
9	23,484,844	id9007784	[30]	GAACAAGTCGCTGCATTT GGTATTA	ACAAGTCGCTGCATTTG GTATTG	GCGTCACCATTGGCC CT
10	973,578	KJ10_003	[29]	GAAAATCGGCTAAAAGG CTGAAGG	GGAAAATCGGCTAAAA GGCTGAAGA	GTAATTTTGCTGCCAG GGATAAGGATTTT
10	1,796,849	KJ10_005	[29]	GAGAAAGTACATTAAATA AGGGTGTGATTT	AGAAAGTACATTAAATA AGGGTGTGATTC	ATTACCTCTAATTAA CCTCTCTCTCACTT
10	2,760,140	KJ10_009	[29]	GATTTCGGTCCCTCCCTTCT TCT	CGGTCCCTCCCTTCTTCC	CATAAATTTAGGAAA GTAATACGGTGCCAA
10	6,305,120	id10002069	[30]	AAACCATAAAGCTGCTTG ACAGATTAAAT	AACCATAAAGCTGCTTG ACAGATTAAAG	GGTTACCTTACATTCA TGCAACATGGAA
10	10,730,617	id10002842	[30]	GAATGAGTCAGTCAGGC AGTGTA	TGAGTCAGTCAGGCAGT GTG	GCAAACATAAACTAAA AAATATGTCTGACAG TCTCA
10	15,128,495	KJ10_019	[29]	GTAACCTCTCCAGTCGTT ATAGAATACAT	AACTTCTCCAGTCGTTA TAGAATACAG	CATGTTAGAGGGTAA AAACTTAATCGGCAT
10	16,412,329	cmb1016.4	[30]	AACTGCAATTCTAGGAGT GGCT	AACTGCAATTCTAGGAG TGGCA	CGAGGCTATGTTATG TTCTATGTTTCACT
10	19,917,460	wd10003790	[30]	TCTAGGTGCAAATGGTGT TGTC	CTAGGTGCAAATGGTGT TGTC	GGAAGCATGGCACTC TTGAAAGT
10	20,358,666	KJ10_039	[29]	AGAGCTCGGCTGCTCGA GA	AGAGCTCGGCTGCTCGA GC	GCCTGCCTCCATTCTT TTACTTCGAA
10	21,047,555	KJ10_041	[29]	ACACTAATAATTAGATAC TTTGTAGGGTAAAAT	CACTAATAATTAGATAC TTTGTAGGGTAAAAG	GAAACATGTATAGTTT CTTGTTGCACCAAA
10	21,389,928	KJ10_043	[29]	ATCTCACTCTACACTTTGT AGGCTG	CATCTCACTCTACACTTT GTAGGCTA	GCTGGAACAAAGAAT CGAGTGTGTATATA

10	21,598,545	ah10001182	[30]	CGAAAGAGAGGGGACTAC TATTTATTTATGATGTC	CGAAAGAGAGGGGACTA CTATTTATTTATGATGTA	TGGACGGAGCTAGCA TTGTCAT
10	21,823,138	KJ10_045	[29]	GGAAGCTCCTCGCTCCGG	GGAAGCTCCTCGCTCC GA	CTCTTTTCCACCGCCA CCAAGCTT
10	22,128,982	KJ10_047	[29]	GCCAGAAAGGAACCGAG AATTGC	GCCAGAAAGGAACCGA GAATTGT	ATTGTTCCAGCTTATT TCTCGCCCTTTT
10	22,459,939	KJ10_049	[29]	ACTAAATGGATGCACATA TTTAATAACTTTAAA	ACTAAATGGATGCACAT ATTTAATAACTTTAAG	GTTGTTCCGGATTGATA TCATTTCAAACCAT
10	23,690,908	id10007384	[30]	CTTCTCAAATCGCTCAAA TGATCCT	CTTCTCAAATCGCTCAA ATGATCCA	TCCATGGCCAAGATG GGGT
11	680,665	id11000131	[30]	ATTTGATAAAATCGTCAT CCAAACCGT	TTGATAAAATCGTCATC CAAACCGC	GGCCAACACAAGATC CCCAG
11	2,455,283	KJ11_005	[29]	GAGAATTTGATGAGTTTA ATTGCTGTTAGAA	GAGAATTTGATGAGTTT AATTGCTGTTAGAT	AATCCAAGTAGTATC ACAGTTTGGGGAAA
11	2,669,824	cmb1102.6	[30]	TGAGGGCAATGCATTTGT GATACTA	AGGGCAATGCATTTGTG ATACTG	CCATCAATAATGCATG GAGTCATGATGAG
11	4,667,865	cmb1104.6	[30]	GTTGCGTGAAGACCTCAG AAATTTA	TTGCGTGAAGACCTCAG AAATTTG	GTTGTTTTCTTCCCGG TATAAATCACTGT
11	5,007,156	KJ11_013	[29]	TACATAAAAGTGCAATGT GAAAACCCTA	ACATAAAAGTGCAATGT GAAAACCCTG	GAGTGAAAATGACTT ACATAGGATATGTTA
11	5,628,396	id11002336	[30]	GTAATCGACAATAATCTC AAGTTGCCG	GTAATCGACAATAATCT CAAGTTGCCA	GACTGTTCAACTTCAG CAGGCA
11	7,109,268	cmb1107.1	[30]	AATTTAGATTTTCATCCAG AATTGAGTTGCA	AAATTTAGATTTTCATCC AGAATTGAGTTGCT	CTGGATTGATTGATAT ATAGATATGTTTGATT GCTTATTA
11	9,670,517	wd11000649	[30]	CAATTTTCTGTGAGTCTTT GCGGA	AATTTTCTGTGAGTCTTT GCGGG	AAGCCTGAGGGTGCG TACA
11	9,835,830	cmb1109.8	[30]	TTGGATTTTGTCAAAGAC AAATGGTCA	TGGATTTTGTCAAAGAC AAATGGTCG	ACGAGTCCATCAAAG ATGAGTGAGG
11	10,335,474	KJ11_033	[29]	GAAATTAATGATGTACTT GTTCCGTTTTTCAAT	AATTAATGATGTACTTG TTCCGTTTTTCATG	CAAGGGACGTTATAA TCACATGACCAAAA
11	21,212,729	id11006897	[30]	TTTCTGAGTCTTGCCCTGT GT	TCTGAGTCTTGCCCTGT GC	GATCCTTGTGCTCTCC AGCCT
11	21,935,946	cmb1121.9	[30]	AATGACAATTAAGCACAA ACCTGAAAGATA	TGACAATTAAGCACAAA CCTGAAAGATG	GAGGCTGCCACTTGC ACA
11	25,372,661	id11008929	[30]	TGCAGTAGAAAGATACAC CGCC	ATGCAGTAGAAAGATA CACCGCA	GATCAGATGTGGAGT TTTTGTCACTTCAA

11	27,413,918	cmb1127.4	[30]	GCTGGCATCCGACGAAG G	GCTGGCATCCGACGAA GA	AGTGTTCGTTGTGC TGCC
11	27,579,717	KJ11_099	[29]	AAAAAGAAAAATCATGG GGAAATGATAAGC	AAAAAGAAAAATCATG GGGAAATGATAAGT	CTGTCTCTCATATGT TTCCTCTTTCAAT
11	27,843,952	KJ11_101	[29]	CACCTCGCCAGCAGCTTC G	CCACCTCGCCAGCAGCT TCA	GCGACGACCGGGAGG ACGAA
11	31,063,738	id11011607	[30]	TTGGCCCATCGCAGAAGA T	TGGCCCATCGCAGAAG AC	TGACCTCTGGAGTTTC AGTGCTC
12	264,373	id12000076	[30]	CTCGTCACAGCATTAGCA TATACTCT	TCGTCACAGCATTAGCA TATACTCC	AGGCTATGCGCCTAT GCCA
12	2,420,416	cmb1202.4	[30]	CGTACCATCATTATTGA TTCATGCG	CGTACCATCATTATTG ATTCATGCA	TGGACAATGGTGACC CGATGT
12	3,791,039	KJ12_007	[29]	TGCAGACTGACAGGGGC AAC	GCAGACTGACAGGGGC AAG	CGTACACAAGTACAC ACAACGGCTT
12	4,662,617	id12002113	[30]	ACACACCATGCTCTAATG GCTC	ACACACCATGCTCTAAT GGCTT	AGGATCGTGGCTCAG CATGT
12	6,810,046	KJ12_017	[29]	CGCGTGCGCACGACA	CTCGCGTGGCGCACGAC G	GTGAGGGTGCAGCAT CGGCTT
12	9,135,012	id12003700	[30]	AGAGCTTCTTGGCTCCAA GAAT	AGAGCTTCTTGGCTCCA AGAAC	GGCCAGAGCTACCTG ACCT
12	10,955,863	KJ12_027	[29]	AATGAAGAGATAAATTAA ATGTTTAATTGAAAC	AATGAAGAGATAAATTA AATGTTTAATTGAAAT	CACATGCAGCCAATG ACTATTTAGATGAT
12	14,646,923	id12005212	[30]	GGAGTTGTGGGCTTAACT TTTCTC	GGAGTTGTGGGCTTAAC TTTTCTT	CCGGCCTCAAGATGC TCCA
12	15,328,542	KJ12_041	[29]	TACAGATTTTCATCCGCAA GCGCAT	CAGATTTTCATCCGCAAG CGCAC	CTCTCGGGGTGAAAT ATTACAATGGTATA
12	15,839,951	KJ12_043	[29]	GGAAGCTAAAAATCACTA GCCAACC	AGGAAGCTAAAAATCA CTAGCCAAC	AGGTGGAATGTGTAT GAGGCCCAT
12	18,468,907	id12006155	[30]	GCATCGACAGAGATCCG AAATGAC	GCATCGACAGAGATCC GAAATGAT	GCGACAGATGAAATA CTGGACAAGC
12	23,255,904	KJ12_059	[29]	CAGATGCTCCCAGAATTT TGATCCAA	CAGATGCTCCCAGAATT TTGATCCAT	ATGGCGATGGTTTTTT GGAACGTAGTTTT
12	24,056,822	cmb1224.0	[30]	GGAATTTCTTGTGCTCAT CGCT	GGAATTTCTTGTGCTCA TCGCC	TGGCAGAATCGTAAT AATCTATTTAACGAG GG
12	26,032,801	cmb1226.0	[30]	CAGCAACTTGAGGGAAG CG	TCAGCAACTTGAGGGA AGCA	CTCCTTTTCCACCTCT AACTAGACGG

12

27,582,487

id12010130

[30]

GGGGCCACTTGTTTTCAA
TCA

GGGGCCACTTGTTTTCA
ATCC

GGGAAGTGTTCCCTC
CAGGT

Table S3. Information on the physical distance between SNP markers.

Chr.	Number of Markers	Number of Deviated Markers	Average Physical Distance
1	31	4	1,441,042
2	17	7	2,154,523
3	19	11	1,956,945
4	20	6	1,792,173
5	17	11	1,752,824
6	15	0	1,218,538
7	26	8	1,166,360
8	17	7	1,642,445
9	21	2	1,118,326
10	16	4	1,480,682
11	17	0	1,827,279
12	14	9	1,970,178
Total	230	69	1,526,957

Table S4. Distribution of flowering time of DH population according to the genotype of *qFG3*.

	Cultivation seasons			
	Early 2018	Normal 2019	Normal 2021	Late 2018
93-11	Sep. 9	Sep. 6	Aug. 10	Oct. 1
Milyang352	Aug. 21	Aug. 26	Jul. 31	Sep. 19
DH population with 93-11 allele of <i>qFG3</i>	Aug. 22–Sep. 13	Aug. 25–Sep. 15	Aug. 02–Aug. 24	Sep. 22–Oct. 20
DH population with Milyang352 allele of <i>qFG3</i>	Aug. 18–Sep. 2	Aug. 20–Sep. 8	Jul. 29–Aug. 11	Sep. 15–Sep. 30

Table S5. List of candidate genes.

QTL	locus name	description	<i>Biological process/ Molecular function</i>
<i>qFG3</i>	LOC_Os03g46190	parafibromin, putative, expressed	flower development
	LOC_Os03g46200	acetyltransferase, GNAT family, putative, expressed	transferase activity
	LOC_Os03g46250	acetyltransferase, GNAT family, putative, expressed	transferase activity
	LOC_Os03g46325	pattern formation protein, putative, expressed	post-embryonic development, transporter activity
	LOC_Os03g46400	UDP-glucuronosyl and UDP-glucosyl transferase domain containing protein, expressed	transferase activity, metabolic process
	LOC_Os03g46910	pyruvate kinase, putative, expressed	lipid metabolic process
	LOC_Os03g47070	RXW8, putative, expressed	lipid metabolic process
	LOC_Os03g47530	glycosyl transferase 8 domain containing protein, putative, expressed	reproduction
	LOC_Os03g47770	ubiquitin-conjugating enzyme E2 W, putative, expressed	flower development
<i>qFG5-1</i>	LOC_Os05g08850	Cytochrome P450, putative, expressed	catalytic activity
	LOC_Os05g08920	late embryogenesis abundant protein, putative, expressed	molecular_function
	LOC_Os05g08930	chloroplast lumen common family protein, putative, expressed	biological_process
	LOC_Os05g08950	phosphoribosyl transferase, putative, expressed	post-embryonic development
	LOC_Os05g08960	ubiquitin-conjugating enzyme, putative, expressed	reproduction
	LOC_Os05g08970	SSRP1-like FACT complex subunit, putative, expressed	reproduction
	LOC_Os05g08990	glutaminyI-tRNA synthetase, putative, expressed	flower development
	LOC_Os05g09020	WRKY67, expressed	response to stress
	LOC_Os05g09370	kinase, pfkB family, putative, expressed	carbohydrate metabolic process
	LOC_Os05g10730	ABC transporter, ATP-binding protein, putative, expressed	transport
	LOC_Os05g10810	O-acyltransferase, putative, expressed	reproduction
	LOC_Os05g10940	metal cation transporter, putative, expressed	transport

	LOC_Os05g11130	cytochrome P450, putative, expressed	flower development
	LOC_Os05g11360	DTDP-D-glucose 4,6-dehydratase, putative, expressed	transport, catalytic activity
	LOC_Os05g11380	OsMADS66 - MADS-box family gene with MIKCC type-box, expressed	flower development
	LOC_Os05g11414	OsMADS58 - MADS-box family gene with MIKCC type-box, expressed	flower development
	LOC_Os05g11510	B-box zinc finger family protein, putative, expressed	secondary metabolic process, post-embryonic development
<i>qFG5-2</i>	LOC_Os05g44910	dual specificity protein phosphatase, putative, expressed	carbohydrate metabolic process
	LOC_Os05g44922	6-phosphofructokinase, putative, expressed	carbohydrate metabolic process
	LOC_Os05g45080	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45090	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45100	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45110	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45120	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45140	glucosyl transferase, putative, expressed	transferase activity
	LOC_Os05g45150	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45170	glucosyl transferase, putative, expressed	transferase activity
	LOC_Os05g45180	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45200	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	transferase activity
	LOC_Os05g45230	WRKY58, expressed	biosynthetic process
	LOC_Os05g45730	ubiquinone oxidoreductase, putative, expressed	generation of precursor metabolites and energy
	LOC_Os05g45740	mitochondrial ATP synthase g subunit family protein, putative, expressed	transport
	LOC_Os05g45760	EMB1796, putative, expressed	embryo development
	LOC_Os05g45860	glucan endo-1,3-beta-glucosidase precursor, putative, expressed	carbohydrate metabolic process

LOC_Os05g45950	outer mitochondrial membrane porin, putative, expressed	transport, post-embryonic development
LOC_Os05g45954	AP2 domain containing protein, expressed	carbohydrate metabolic process
LOC_Os05g46020	WRKY7, expressed	response to stress
LOC_Os05g46030	myosin head family protein, expressed	post-embryonic development, cell differentiation
LOC_Os05g46200	beta-galactosidase 8 precursor, putative, expressed	carbohydrate metabolic process
LOC_Os05g46220	mitochondrial carrier protein, putative, expressed	flower development
LOC_Os05g46480	late embryogenesis abundant protein, group 3, putative, expressed	embryo development
LOC_Os05g46510	polygalacturonase, putative, expressed	carbohydrate metabolic process
LOC_Os05g46520	polygalacturonase, putative, expressed	carbohydrate metabolic process
LOC_Os05g47560	serine/threonine-protein kinase SNT7, chloroplast precursor, putative, expressed	photosynthesis
LOC_Os05g47640	threonine synthase, chloroplast precursor, putative, expressed	biosynthetic process
LOC_Os05g47650	B3 DNA binding domain containing protein, expressed	embryo development
LOC_Os05g47780	E3 ubiquitin ligase, putative, expressed	embryo development
LOC_Os05g47850	chloroplastic group IIA intron splicing facilitator CRS1, chloroplast precursor, putative, expressed	embryo development
LOC_Os05g47980	ATP synthase, putative, expressed	transport
LOC_Os05g48200	glutamate synthase, chloroplast precursor, putative, expressed	biosynthetic process
LOC_Os05g48240	dynamamin family protein, putative, expressed	embryo development
LOC_Os05g48410	50S ribosomal protein L21, chloroplast precursor, putative, expressed	reproduction

Table S6. Putative candidate genes located within *qFG3*.

No.	MSU ID	Description	Biological process	Molecular function	Cellular component	Similar papers
1	LOC_Os03g44420	Tubulin/FtsZ domain containing protein, putative, expressed; Similar to Plastid division protein ftsZ1 precursor	Chloroplast fission; cell division; protein polymerization; obsolete GTP catabolic process	GTPase activity; identical protein binding; GTP binding	Protein complex; chloroplast stroma; cytoplasm	[33,34]
2	LOC_Os03g44440	Cyclic nucleotide-gated ion channel	Potassium ion transport; transmembrane transport	Voltage-gated potassium channel activity; ion channel activity	Integral component of membrane	-
3	LOC_Os03g44484	DNA-directed RNA polymerase II subunit RPB2, beta subunit, protrusion domain containing	Reproduction; embryo development; post-embryonic development; transcription	Transferase activity; DNA-directed 5'-3' RNA polymerase activity	Cytosol;	-
4	LOC_Os03g44500	Serine/threonine protein phosphatase	Metabolic process	Binding; hydrolase activity	Cytosol; plasma membrane	-
5	LOC_Os03g44540	Nuclear transcription factor Y (Nf-Y-A) subunit	Regulation of transcription, DNA-templated	Sequence-specific DNA binding transcription factor activity	Nucleus; nucleoplasm	-
6	LOC_Os03g44580	Protein of unknown function DUF266, plant family protein	-	Acetylglucosaminyltransferase activity	Membrane	[51, 52]
7	LOC_Os03g44610	IQ calmodulin-binding motif domain containing protein	-	Protein binding	Plasma membrane	[53-55]
8	LOC_Os03g44620	Chaperone protein DnaJ	Flower development; response to abiotic stimulus; protein folding	Unfolded protein binding; nucleotide binding; heat shock protein binding;	cell wall; nucleolus; cytosol	[33,34]
9	LOC_Os03g44630	Plastocyanin-like domain containing protein, putative, expressed; Cupredoxin domain containing protein	Transport; response to biotic stimulus; response to abiotic stimulus;	Copper ion binding; electron transfer activity	Membrane; plasma membrane; vacuole	-

10	LOC_Os03g44636	Zinc finger, C3HC4 type domain containing protein	-	Zinc ion binding; protein binding	Cell	-
11	LOC_Os03g44660	Cytosolic 5-nucleotidase III, putative, expressed; Similar to Pyrimidine 5'-nucleotidase family protein, expressed; HAD-superfamily subfamily IE hydrolase protein.	Cellular process	Magnesium ion binding; hydrolase activity; 5'-nucleotidase activity	Cytosol; cytoplasm	
12	LOC_Os03g44710	OsSh1, YABBY domain containing protein, Similar to Yabby9 protein	Cell differentiation	Sequence-specific DNA binding transcription factor activity; metal ion binding	Nucleus	[35-37]
13	LOC_Os03g44740	Cytochrome P450 family protein, putative, expressed	Oxidation-reduction process; Secondary metabolic process; response to endogenous stimulus	Heme binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	-	[38-44]
14	LOC_Os03g44760	SWI1, Similar to ameiotic 1, putative, expressed	DNA metabolic process; cell cycle; cellular component organization	Hydrolase activity	Nucleus	-
15	LOC_Os03g44780	Translation elongation factor EFG/EF2, C-terminal domain containing protein. Tu family protein, putative, expressed	Translational elongation; catabolic process; obsolete GTP catabolic process	Translation elongation factor activity, GTPase activity; nucleic acid binding; GTP binding	Cytosol	-
16	LOC_Os03g44820	Glutamyl-tRNA ^{Gln} amidotransferase, C subunit family protein, putative, expressed	Translation; regulation of translational fidelity	Ligase activity; nucleotide binding; ATP binding	Plastid	[45]
17	LOC_Os03g44830	OsRhmbd9, Peptidase S54, rhomboid domain containing protein, Putative Rhomboid homologue, expressed	-	Serine-type endopeptidase activity	Integral component of membrane	[56]
18	LOC_Os03g44890	Anthranilate phosphoribosyltransferase, C2	-	Transferase activity, transferring glycosyl groups; protein binding	-	[57]

19	LOC_Os03g44900	domain containing protein, putative, expressed CCR4-NOT transcription factor, NOT complex component, N-terminal domain containing protein, putative, expressed	Regulation of transcription, DNA-templated	Sequence-specific transcription factor activity	Nucleus	[46]
20	LOC_Os03g44950	LTPL91 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	-	-	-	[58,59]
21	LOC_Os03g45194	Oxidoreductase, short chain dehydrogenase/reductase family domain containing protein, Similar to Myb-like DNA-binding domain, SHAQKYF class family protein, expressed expressed	Chlorophyll catabolic process; PSII associated light-harvesting complex II catabolic process; oxidation-reduction process; protein metabolic process;	Chlorophyll(ide) b reductase activity; oxidoreductase activity; protein binding	Plastid; thylakoid; chloroplast thylakoid membrane; chloroplast	[47-49]
22	LOC_Os03g45260	Vesicle transport v-SNARE protein, Similar to Membrin 11 (AtMEMB11) (Golgi SNAP receptor complex member 2-1) (27 kDa Golgi SNARE protein); putative, expressed	Cellular component organization; protein transport	Protein binding	Golgi apparatus; Golgi membrane; Golgi stack	-
23	LOC_Os03g45320	OsIPMDH, dehydrogenase, Similar to 3-isopropylmalate dehydrogenase 2; putative, expressed	Leucine biosynthetic process; oxidation-reduction process	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; magnesium ion binding	Plastid; cytoplasm	[50]
24	LOC_Os03g45370	Sodium/calcium exchanger protein, Similar to K-exchanger-like protein, putative, expressed	Transmembrane transport	Transporter activity	Cell; integral component of membrane	-

25	LOC_Os03g45390	Glucan endo-1,3-beta-glucosidase precursor, putative, expressed	Carbohydrate metabolic process	Hydrolase activity, acting on glycosyl bonds;hydrolyzing O-glycosyl compounds	Anchored component of plasma membrane	-
26	LOC_Os03g45400	Antitermination NusB/RsmB/TIM44 domain containing protein, putative, expressed	Positive regulation of transcription, DNA-templated transcription, termination; aromatic amino acid family biosynthetic process; stomatal complex morphogenesis	RNA binding	Plastid; chloroplast	-
27	LOC_Os03g45420	Armadillo/beta-catenin repeat family protein, putative, expressed	Regulation of chlorophyll biosynthetic process; regulation of abscisic acid biosynthetic process; protein ubiquitination; leaf senescence	Ubiquitin-protein transferase activity; protein binding; catalytic activity	Plasma membrane; ubiquitin ligase complex	-
28	LOC_Os03g45450	WRKY60, expressed	Regulation of transcription, DNA-templated	Sequence-specific DNA binding transcription factor activity	-	-
29	LOC_Os03g45619	Cytochrome P450 family protein, putative, expressed	Oxidation-reduction process	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; electron transfer activity; metal ion binding	-	-
30	LOC_Os03g45920	Ankyrin repeat domain-containing protein 50, putative, expressed	-	-	Cell wall	[60,61]