Supplemental Tabe S 1 SNPs showing distortion from 1 : 1 in allele ferequency between A58- and Kitaake-type in early- and late- heading groups at $p < 0.05$

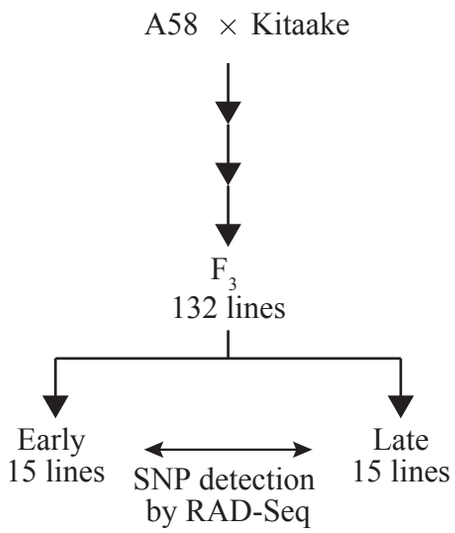
Marker name	Chr	Position *	χ^2	*P*
C1_2871	1	2952301	4.00	0.046
C1_2292	1	25250821	4.02	0.045
C1_2301	1	25270205	4.02	0.045
C1_2745	1	28608975	5.37	0.020
C1_2968	1	30128355	3.88	0.049
C2_10782	2	790734	7.48	0.006
C2_10784	2	790866	7.48	0.006
C2_8013	2	22155575	6.24	0.012
C4_19210	4	29823605	7.05	0.008
C4_19304	4	30511751	9.88	0.002
C4_19390	4	31264195	12.00	0.001
C4_19586	4	32438249	7.76	0.005
C6_29170	6	8746766	3.96	0.047
C6_27238	6	24515347	6.74	0.009
C6_27270	6	24574372	4.55	0.033
C6_27338	6	24978329	6.17	0.013
C6_27340	6	24985031	6.51	0.011
C6_27365	6	25230125	4.57	0.032
C6_27415	6	25515786	5.42	0.020
C7_30353	7	16122146	5.24	0.022
C7_31845	7	26143870	5.84	0.016
C9_39967	9	4630668	3.90	0.048
C9_37661	9	10256209	6.60	0.010
C10_43613	10	593246	4.55	0.033
C10_43829	10	709525	4.57	0.032
C10_43830	10	709622	6.58	0.010
C11_46269	11	22116183	5.31	0.021

*Nucleotide position is based on the Nipponbare genome sequence (IRGSP1.0)

Supplementary Table S2 The effect of the selected SNPs on days to heading (DTH) in F4 lines derived from the cross between A58 and Kitaake in 2015 and 2016

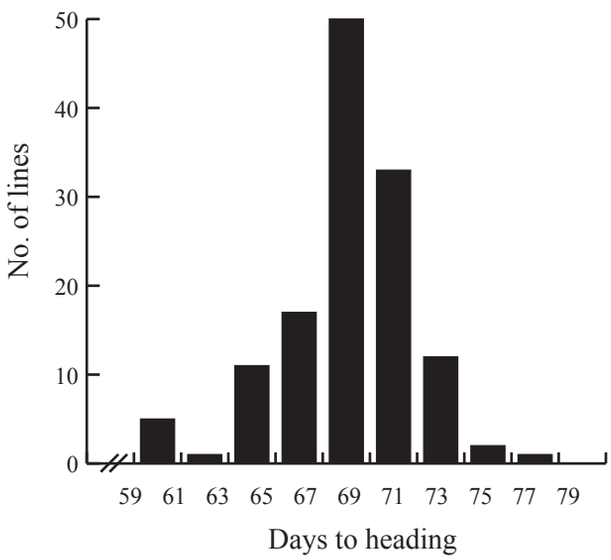
			DTH (2015)			DTH (2016)		
SNP Marker	Chr.	Position	A58-type	Kitaake-type	MGV*	A58-type	Kitaake-type	MGV*
C1_2292	1	25,250,821	68.5±2.02	73.6±1.78	2.6	75.9±1.72	79.3±1.72	1.7
C1_2301	1	25,270,205	68.5±2.02	73.6±1.78	2.6	75.9±1.72	79.3±1.72	1.7
C1_2745	1	28,608,975	68.1±1.85	73.4±1.54	2.7	75.3±1.59	79.0±1.52	1.9
C1_2968	1	30,128,355	66.9±1.96	72.7±1.66	2.9	74.1±1.94	78.1±1.46	2.0
C2_10782	2	790,734	68.1±1.83	71.8±1.59	1.9	74.8±1.65	78.1±1.47	1.7
C2_10784	2	790,866	68.1±1.83	71.8±1.59	1.9	74.8±1.65	78.1±1.47	1.7
C4_19210	4	29,823,605	74.8±1.14	66.6±1.61	4.1	81.9±0.65	73.7±1.34	4.1
C4_19304	4	30,511,751	76.3±1.03	66.1±1.61	5.1	82.1±0.72	73.2±1.43	4.5
C4_19390	4	31,264,195	76.9±1.08	65.1±1.39	5.9	82.5±0.74	72.5±1.3	5.0
C4_19586	4	32,438,249	75.5±1.21	65.7±1.43	4.9	81.6±0.68	72.9±1.31	4.3
C6_27238	6	24,515,347	71.9±1.72	65.7±1.91	3.1	77.2±1.78	73.8±1.62	1.7
C6_27270	6	24,574,372	71.1±1.64	66.6±2.03	2.3	76.5±1.78	75.1±1.51	0.7
C6_27338	6	24,978,329	71.3±1.78	65.2±2.16	3.1	76.9±1.67	73.3±1.92	1.8
C6_27340	6	24,985,031	71.7±1.57	66.0±2.24	2.9	77.6±1.53	74.5±1.74	1.6
C6_27365	6	25,230,125	71.5±1.67	66.9±2.21	2.3	77.3±1.59	75.1±1.67	1.1
C6_27415	6	25,515,786	71.5±1.67	66.6±2.03	2.5	77.3±1.59	75.1±1.51	1.1
C10_43613	10	593,246	71.9±1.68	64.4±1.93	3.8	77.3±1.42	72.1±1.9	2.6
C10_43829	10	709,525	72.5±1.4	65.7±2.28	3.4	78.1±1.22	73.3±2.42	2.4
C10_43830	10	709,622	72.8±1.47	65.7±2.06	3.6	78.2±1.3	73.5±2.2	2.4

* MGV (marker genotype value) is an indication of the effect of each SNP locus based on DTH as described in the Materials and methods.

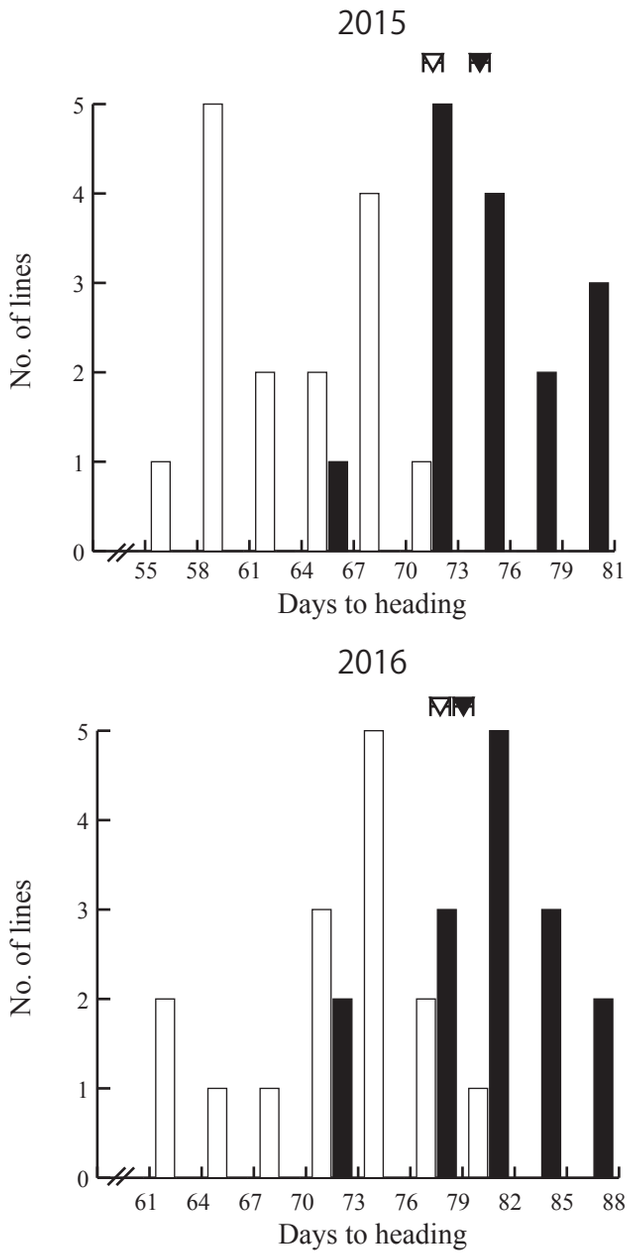


Supplementary Figure S1: Experimental scheme of this study.

The ddRAD-Seq analysis was completed to detect differences in the allele frequency of genome-wide SNPs between early- and late-heading F4 lines.

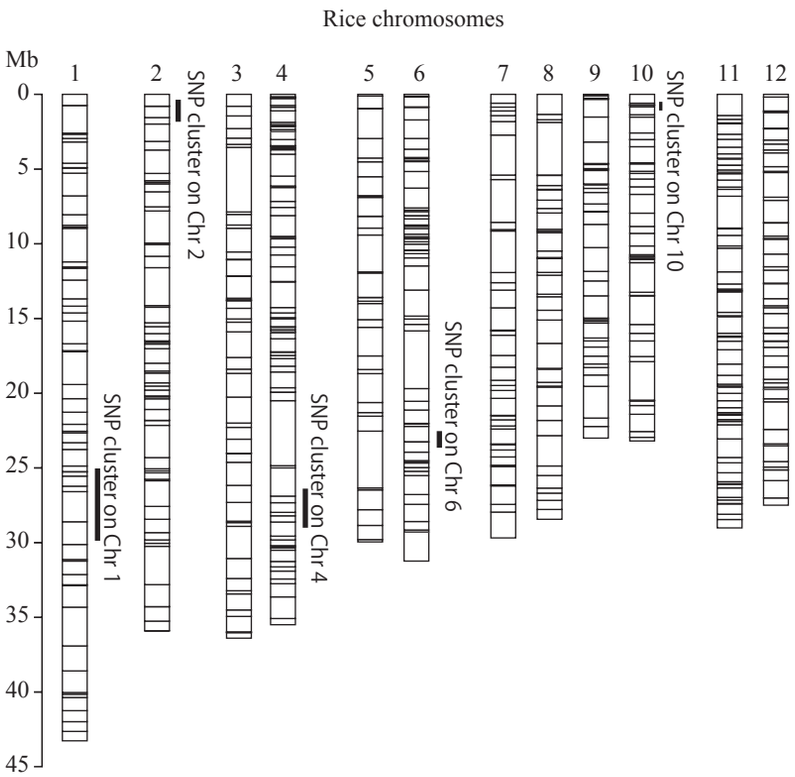


Supplementary Figure S2: Frequency distribution of DTH in the F3 population derived from the A58 × Kitaake cross.



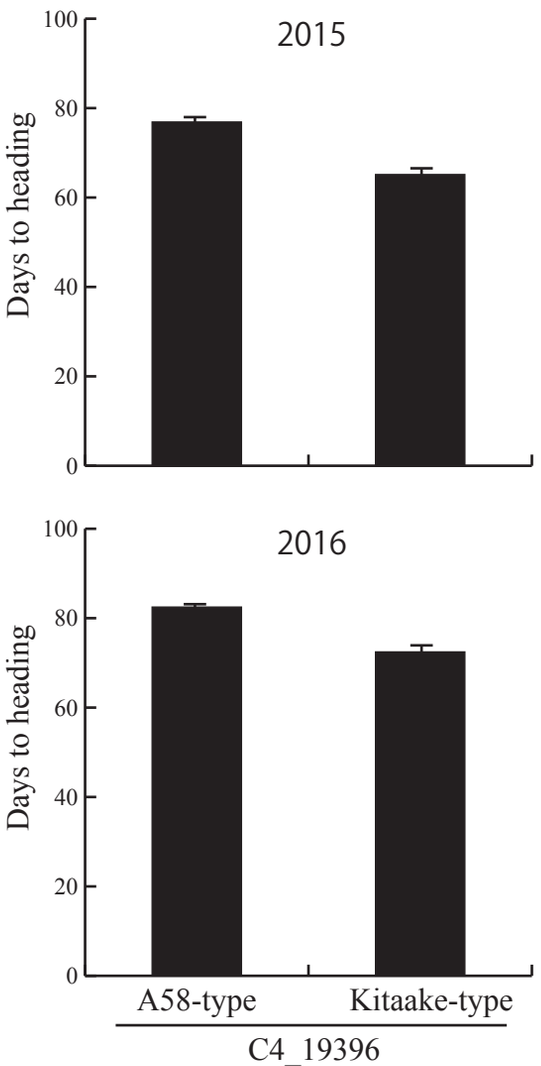
Supplementary Figure S3: Frequency distribution of DTH in early- and late-heading F4 lines derived from the A58 × Kitaake cross in 2015 and 2016.

The DTH of the 15 early-heading and 15 late-heading F4 lines was examined in 2015 and 2016. Early- and late-heading lines are indicated by white and black, respectively. Kitaake and A58 DTH are indicated by white and black arrowheads, respectively, with bars representing the standard error.



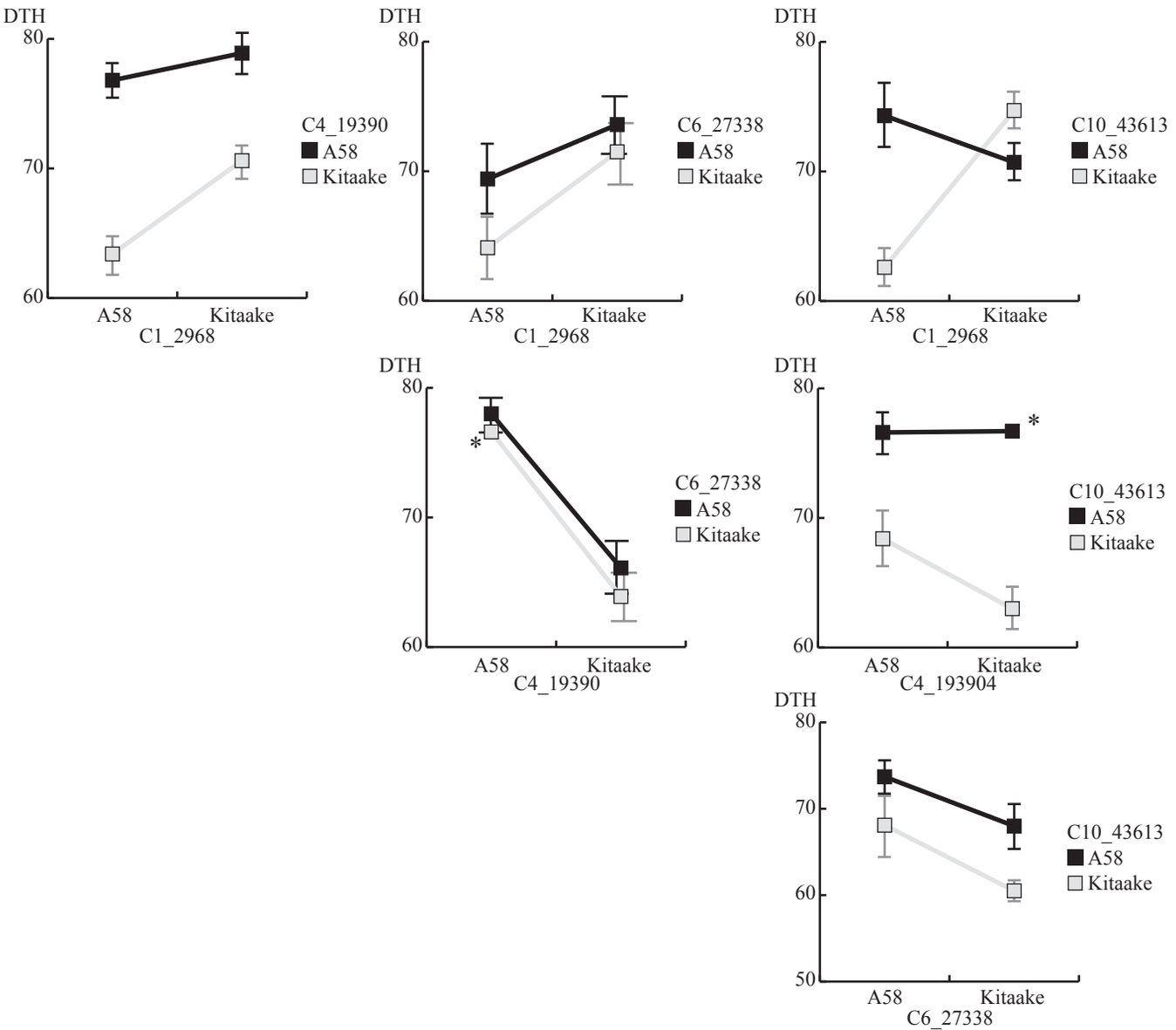
Supplementary Figure S4: Chromosomal positions of five SNP clusters.

Physical map positions of each SNP detected by ddRAD-Seq are specified by horizontal bars in each chromosome. Positions of SNP clusters that exhibited significant differences in allele frequency between early- and late-heading populations are indicated by vertical bars on the right side of each chromosome.



Supplementary Figure S5: Effect of the chromosome 4 SNP cluster on DTH in 2015 and 2016.

Average DTH values of the F4 lines with homozygous A58- and Kitaake-type alleles at the SNP cluster on chromosome 4, which is represented by the central SNP in the cluster, C4_19396. Significant differences ($P < 0.01$) between average DTH values were observed in 2015 and 2016.



Supplementary Figure S6: Genetic interactions between SNP clusters on chromosomes 1, 4, 6, and 10 relative to DTH in 2015.

Average DTH values (y-axis) of F4 lines with each genotype are presented in squares. Six combinations of any two loci among the SNP clusters on chromosomes 1, 4, 6, and 10 are depicted. The A58-type alleles (black line) and Kitaake-type alleles (gray line) are paired with another locus corresponding to A58-type alleles (left side) or Kitaake-type alleles (right side) (x-axis), respectively. An allelic interaction (non-additive interaction) is indicated by the crossing of the black and gray lines.