

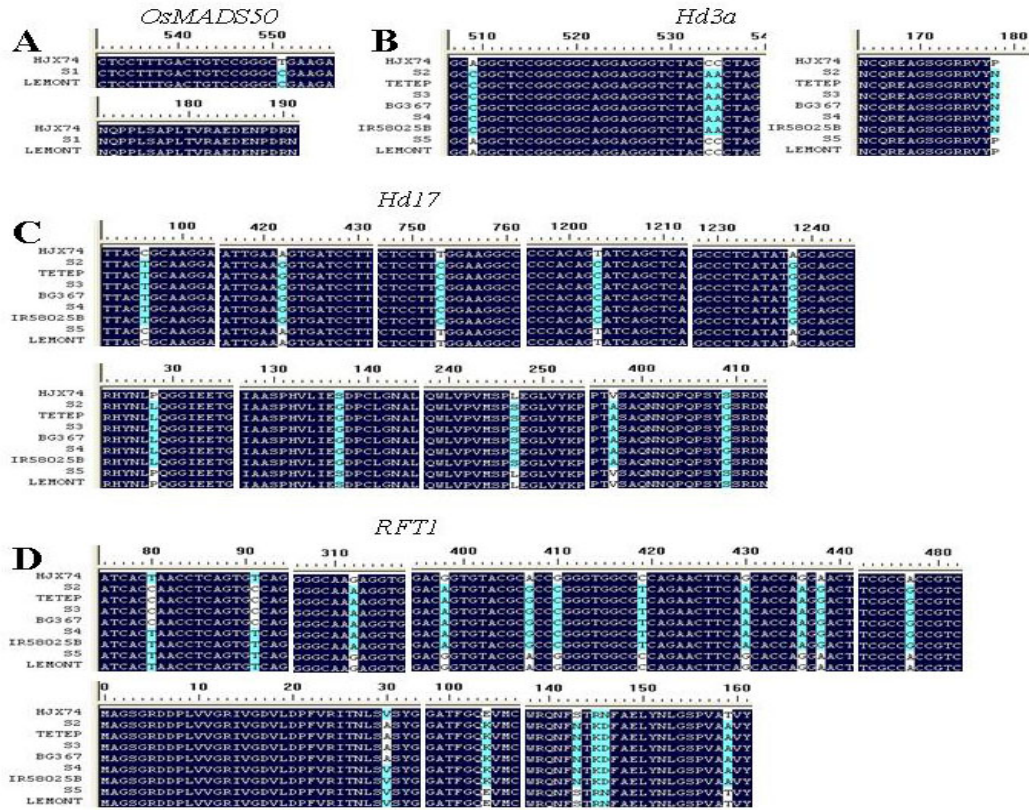
**Appendix A** QTLs for heading date detected with SSSLs under NLD for two cropping seasons (2011 and 2012)

Code	QTL	2011				2012			
		HD (Day) <sup>1)</sup>	P-value	Difference from HJX74 (Day)	A (Day) <sup>2)</sup>	HD (Day) <sup>1)</sup>	P-value	Difference from HJX74 (Day)	A (Day) <sup>2)</sup>
<b>S1</b>	<b><i>qHD3</i></b>	<b>73.5±2.1</b>	<b>2.1E-41</b>	<b>-41.0</b>	<b>-20.5</b>	<b>71.2±1.9</b>	<b>4.1E-42</b>	<b>-43.4</b>	<b>-21.7</b>
S1-1	<i>qHD3</i>	72.5±3.8	2.6E-40	-41.8	-20.9	71.9±1.9	5.8E-42	-42.7	-21.4
S1-2	<i>qHD3</i>	71.6±1.9	6.1E-42	-42.9	-21.5	72.0±2.9	8.8E-41	-42.6	-21.3
S1-3	<i>qHD3</i>	74.3±1.8	4.2E-37	-40.2	-20.1	73.8±2.9	7.9E-37	-40.8	-20.4
S1-4	<i>qHD3</i>	73.9±1.2	7.3E-42	-40.6	-20.3	72.3±3.8	2.4E-38	-42.3	-21.2
S1-5	<i>qHD3</i>	70.2±2.7	7.5E-40	-44.3	-22.2	71.2±2.3	2.4E-40	-43.4	-21.7
S1-6	<i>qHD3</i>	71.3±3.2	3.3E-38	-43.2	-21.6	70.9±1.8	2.4E-42	-43.7	-21.9
S1-7		115.4±3.1	5.2E-02	0.9		114.1±2.7	6.2E-01	-0.5	
S1-8		112.5±2.3	3.1E-03	-2.0		113.2±4.1	5.7E-01	-1.4	
<b>S2</b>	<b><i>qHD6</i><sup>W01</sup></b>	<b>132.8±1.5</b>	<b>5.4E-28</b>	<b>18.3</b>	<b>9.2</b>	<b>133.9±1.1</b>	<b>1.7E-28</b>	<b>19.3</b>	<b>9.7</b>
S2-1	<i>qHD6</i> <sup>W01</sup>	131.7±2.5	6.0E-31	17.2	8.6	132.0±3.4	1.6E-25	17.4	8.7
S2-2	<i>qHD6</i> <sup>W01</sup>	133.8±3.7	1.1E-30	19.3	9.7	132.7±0.9	2.9E-26	18.1	9.1
S2-3		114.9±3.5	6.3E-01	0.4		115.6±3.5	7.9E-02	1.0	
<b>S3</b>	<b><i>qHD6</i><sup>W04</sup></b>	<b>131.8±2.8</b>	<b>2.1E-28</b>	<b>17.8</b>	<b>8.9</b>	<b>133.9±2.6</b>	<b>1.0E-29</b>	<b>19.3</b>	<b>9.7</b>
S3-1	<i>qHD6</i> <sup>W04</sup>	131.2±1.9	4.4E-27	17.2	8.6	132.8±3.4	2.4E-27	18.2	9.1
S3-2	<i>qHD6</i> <sup>W04</sup>	131.5±2.9	1.6E-27	17.5	8.8	133.6±1.9	1.0E-29	19.0	9.5
S3-3	<i>qHD6</i> <sup>W04</sup>	130.7±2.5	1.1E-26	16.7	8.3	131.5±2.6	2.4E-26	16.9	8.5
S3-4		111.9±4.1	7.9E-03	-2.6		113.8±2.8	3.3E-01	-0.8	
<b>S4</b>	<b><i>qHD6</i><sup>W12</sup></b>	<b>132.1±2.1</b>	<b>6.1E-29</b>	<b>17.7</b>	<b>8.8</b>	<b>131.7±3.7</b>	<b>1.1E-27</b>	<b>17.1</b>	<b>8.6</b>
S4-1	<i>qHD6</i> <sup>W12</sup>	132.8±2.9	2.3E-27	18.3	9.2	132.5±1.9	5.2E-27	17.9	9.0
<b>S5</b>	<b><i>qHD6</i><sup>W23</sup></b>	<b>105.8±2.8</b>	<b>9.9E-17</b>	<b>-8.7</b>	<b>-4.4</b>	<b>106.4±1.4</b>	<b>4.6E-17</b>	<b>-8.2</b>	<b>-4.1</b>
S5-1	<i>qHD6</i> <sup>W23</sup>	103.4±1.9	6.9E-18	-11.1	-5.6	106.2±2.6	3.6E-16	-8.4	-4.2
S5-2	<i>qHD6</i> <sup>W23</sup>	104.8±3.8	2.4E-15	-9.7	-4.9	105.5±2.8	3.6E-15	-9.1	-4.6
S5-3		115.7±2.9	6.2E-02	1.2		114.7±3.6	2.4E-02	0.1	
HJX74		114.5±2.8				114.6±2.0			

<sup>1)</sup>The data of heading date of each line represents mean values and standard errors of twenty plants.

<sup>2)</sup>The additive effect. The superscript of *qHD6* represents different donor segment on corresponding SSSL. <sup>W01</sup>, <sup>W04</sup>, <sup>W12</sup> and <sup>W23</sup> as the superscript of *qHD6* represent 4 donors, 'Tetep', 'BG367', 'IR58025B' and 'Lemont', respectively.

**Appendix B** Comparisons of the cDNA and the deduced amino acid sequences of *OsMADS50*, *Hd3a*, *Hd17* and *RFT1*. (A) Sequence alignment of *OsMADS50* among the recipient 'HJX74', P-SSSL S1 and its donor 'Lemont'. (B to D) Sequence alignments of *Hd3a*, *Hd17* and *RFT1* among 'HJX74', P-SSSLs S2 to S5 and their donor 'Tetep', 'BG367', 'IR58025B' and 'Lemont'. The sequences were aligned using the DNAMAN software.



**Appendix C** Means of heading date of nine sub-populations with different genotypes between *qHD3* and *qHD6* in four F<sub>2</sub> populations derived from crosses between P-SSSLs

Genotype <sup>1)</sup>	Cross combinations			
	S1/S2	S1/S3	S1/S4	S1/S5
aabb	113.6±1.9	114.2±2.1	113.6±3.2	112.8±2.1
aaBb	116.5±3.6	117.3±4.5	115.5±6.3	109.6±5.3
aaBB	131.7±5.2	132.1±3.4	130.5±5.4	104.8±6.5
AAbb	72.0±5.3	73.5±4.4	70.4±2.7	74.3±6.9
AABb	75.7±3.7	77.0±6.8	78.3±5.4	76.4±4.6
AABB	75.1±7.3	78.9±4.1	77.7±7.2	75.6±6.7
Aabb	82.1±5.6	85.5±6.3	83.2±4.4	76.6±4.1
AaBb	87.8±4.1	89.6±5.2	86.3±6.1	78.7±6.7
AaBB	98.8±5.4	97.3±7.5	95.1±6.3	83.5±3.8
<i>P</i> -A×a	1.9E-19	3.8E-21	4.5E-23	6.6E-21
<i>P</i> -B×a	1.9E-15	3.8E-14	4.5E-17	6.6E-8
<i>P</i> -A×B	2.6E-9	1.7E-8	3.2E-10	7.8E-9

<sup>1)</sup> Each genotype is represented by the closely linked marker loci, RM3894 and RM14314 for *qHD3*, RM19410 and RM204 for *qHD6*. *P*-value was calculated by two-way ANOVA. “A ”and “a” indicate homologous genotype of donor ‘Lemont’ allele and the recipient ‘HJX74’ at *qHD3* locus, respectively; “B”and “b” indicate genotype of the donors (‘Tetep’, ‘BG367’, ‘IR58025B’ and ‘Lemont’) alleles and the recipient ‘HJX74’ at *qHD6* locus, respectively. *P*-value was calculated by ANOVA. *P*-A×a, *P*-B×a and *P*-A×B represent the *P* values for *qHD3* locus, *qHD6* locus and interaction between *qHD3* and *qHD6*, respectively.

**Appendix D** Codes, names, origin of donors and substituted chromosomes of P-SSSLs

SSSL code	P-SSSL	Donor	Donor code	Donor origin	Ecotype	Chromosome
S1	W23-03-08-9-1	Lemont	W23	America	<i>Japonica</i>	3
S2	W01-42-42-8-02-2	Tetep	W01	Vietnam	<i>Indica</i>	6
S3	W04-47-68-5-4-5	BG367	W04	Bangladesh	<i>Indica</i>	6
S4	W12-28-58-03-19-2	IR58025B	W12	Philippines	<i>Indica</i>	6
S5	W23-07-6-02-14(t)	Lemont	W23	America	<i>Japonica</i>	6