

Table S2. List of heading date QTLs detected in BC₄F₂ populations derived from crosses between Koshihikari (KSH) and 11 diverse accessions of Asian rice. QTLs written by bold characters indicate those confirmed in BC₄F₃ populations. Abbreviations of rice accessions are defined in Table 1.

Population		Chromo some	Physical position	Marker interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
HAY	10_2237	3	28.8–33.7	RM6329–RM1038	15.3	-6.7	1.9	74.2	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2238	3	28.8–33.7	RM6329–RM1038	6.8	-7.6	0.4	59.9	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2232	3	33.7	RM1038	12.4	-6.0	2.1	86.9	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2249	3	33.7	RM1038	12.5	-6.2	3.6	72.3	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2253	3	33.7	RM1038	4.1	-4.0	-2.7	24.0	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2229	3	33.7–34.0	RM1038–RM2187	12.2	-6.2	2.3	56.6	<i>Hd6</i>	<i>Hd16</i>
HAY	10_2237	6	0.1–10.8	RM19227–RM19835	7.2	-2.2	-1.6	12.8	<i>Hd1</i>	
HAY	10_2238	6	10.8–19.7	RM19835–RM20158	3.0	-3.2	-2.0	15.4		
HAY	10_2240	7	5.0–11.0	RM21137–RM21392	16.7	7.3	4.3	92.0	<i>Ghd7</i>	
HAY	10_2241	7	5.0–17.3	RM21137–RM21577	16.5	7.1	3.4	52.3	<i>Ghd7</i>	
HAY	10_2242	7	15.9–21.2	RM21516–RM21770	3.0	-1.4	0.7	16.1		
HAY	10_2242	7	24.2–29.4	RM6326–RM22164	9.8	2.7	-1.6	81.0		<i>OsPRR37</i>
HAY	10_2253	7	28.7–29.4	RM5720–RM22164	8.1	5.6	-4.1	50.7		<i>OsPRR37</i>
HAY	10_2243	8	0.1–8.6	RM5911–RM22679	10.8	4.1	4.3	83.7	<i>DTH8</i>	
HAY	10_2236	8	4.5–8.6	RM22496–RM22679	14.0	6.5	4.1	89.3	<i>DTH8</i>	
HAY	10_2244	8	4.5–8.6	RM22496–RM22679	12.4	5.3	4.2	91.8	<i>DTH8</i>	

Population		Chromo some	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
QZZ	11_2108	1	0.2–4.1	RM6887–RM8105	5.7	2.2	3.9	66.3		
QZZ	11_2109	1	19.4–21.9	RM11069–RM1196	2.2	0.9	-2.1	34.7		
QZZ	11_2122	1	41.2–42.9	RM5310–RM8137	2.4	1.3	0.1	28.4		
QZZ	11_2112	2	6.7–11.3	RM5897–RM1234	2.0	-1.3	-0.6	32.8		
QZZ	11_2122	3	0.5–9.9	RM4108–RM1371	3.4	-1.7	0.9	37.0		<i>Ehd4</i> , <i>DTH3</i>
QZZ	11_2118	3	5.5–9.9	RM5442–RM1371	4.6	-5.1	2.4	9.7		
QZZ	11_2118	3	26.7–35.6	RM2334–RM3329	7.0	-5.1	2.0	19.1	<i>Hd6</i>	<i>Hd16</i>
QZZ	11_2119	4	4.9–13.1	RM16449–RM5633	2.6	1.2	-1.1	39.4		
QZZ	11_2121	4	28.8–32.1	RM3916–RM2121	3.8	0.1	-2.0	57.4		
QZZ	11_2131	6	0.2–5.2	RM6467–RM5754	2.0	-1.5	4.2	20.1	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
QZZ	11_2116	6	8.8	RM5963	5.7	7.5	0.6	66.6	<i>Hd1</i>	
QZZ	11_2120	6	8.8	RM5963	7.2	5.3	-2.5	75.4	<i>Hd1</i>	
QZZ	11_2123	6	8.8	RM5963	9.9	6.5	-0.5	85.5	<i>Hd1</i>	
QZZ	11_2125	6	8.8	RM5963	3.8	6.5	2.8	50.2	<i>Hd1</i>	
QZZ	11_2127	6	8.8–20.0	RM5963–RM20176	5.7	6.7	-1.9	69.3	<i>Hd1</i>	
QZZ	11_2132	6	8.8–20.0	RM5963–RM20176	15.9	6.2	-1.2	77.4	<i>Hd1</i>	
QZZ	11_2130	7	3.3–13.4	RM1353–RM7273	16.4	8.2	6.1	72.3	<i>Ghd7</i>	
QZZ	11_2129	7	3.3–26.8	RM1353–RM1364	11.7	10.9	10.5	81.0		<i>OsPRR37</i>
QZZ	11_2117	8	0.4–5.9	RM1381–RM6838	3.9	5.8	3.3	34.3	<i>DTH8</i>	
QZZ	11_2131	8	5.9–12.4	RM6838–RM22839	7.1	5.0	6.4	61.0	<i>DTH8</i>	
QZZ	11_2131	8	18.8–22.5	RM5767–RM23251	3.9	-0.9	6.0	34.0		
QZZ	11_2133	9	15.2–20.5	RM5122–RM3808	2.1	1.5	-0.3	31.2		
QZZ	11_2135	10	6.1–7.6	RM7276–RM25151	3.4	-3.8	-2.7	60.1		
QZZ	11_2138	10	13.4–14.5	RM25302–RM5147	2.6	-3.4	1.1	45.3		
QZZ	11_2132	12	1.0–2.3	RM3323–RM3747	2.5	-1.1	0.1	2.3		
QZZ	11_2139	12	2.3–20.0	RM3747–RM28305	3.4	-1.6	0.6	48.8		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
TUP	10_2153	1	26.8–31.5	RM3143–RM5914	3.0	-1.2	-1.1	28.1		
TUP	10_2179	2	1.9	RM7562	4.9	2.1	-0.8	61.1		
TUP	10_2156	2	6.7–11.3	RM5897–RM1234	3.8	-1.6	0.7	39.1		
TUP	10_2156	2	30.6–35.4	RM3316–RM3850	4.1	-1.6	0.7	44.1		DTH2
TUP	10_2166	3	0.5	RM4108	4.3	-3.9	-1.5	54.3		Ehd4 , DTH3
TUP	10_2158	3	0.5–14.5	RM4108–RM6959	6.4	-3.7	0.6	57.6		Ehd4 , DTH3
TUP	10_2158	3	17.4–25.1	RM1334–RM3513	2.9	-2.9	-1.3	15.9		
TUP	10_2159	3	28.7–32.4	RM1350–RM6970	6.4	-2.8	-2.8	70.3	Hd6	Hd16
TUP	10_2171	3	28.7–32.4	RM1350–RM6970	11.8	-11.2	7.3	63.2	Hd6	Hd16
TUP	10_2172	3	28.7–32.4	RM1350–RM6970	10.9	-12.7	6.5	55.2	Hd6	Hd16
TUP	10_2151	3	32.4–35.6	RM6970–RM3329	5.2	-6.9	7.0	64.6	Hd6	Hd16
TUP	10_2172	5	2.9–6.1	RM6517–RM7118	2.2	2.0	6.1	4.2		
TUP	10_2166	5	23.9–29.5	RM3476–RM3286	2.3	-1.1	2.0	19.1		
TUP	10_2168	6	7.6–15.8	RM19715–RM20023	4.3	2.2	2.2	57.7	Hd1	
TUP	10_2153	6	20.3–24.5	RM7193–RM5957	4.6	-2.0	-1.3	47.5		
TUP	10_2182	6	24.5	RM5957	2.1	-1.6	-0.4	33.8		
TUP	10_2169	7	0.3–3.3	RM20810–RM1353	2.2	-1.6	-0.2	35.3		
TUP	10_2171	7	23.6–29.4	RM5847–RM22164	2.2	-3.9	1.3	10.8		OsPRR37
TUP	10_2172	7	23.6–29.4	RM5847–RM22164	2.5	-5.8	1.6	7.8		OsPRR37
TUP	10_2172	8	0.1–2.9	RM6369–RM22380	4.1	-1.3	-2.1	15.2		
TUP	10_2173	8	5.9–16.0	RM6838–RM22934	2.3	-1.2	2.4	36.0	DTH8	
TUP	10_2174	8	22.9–27.4	RM7556–RM3480	3.8	1.1	0.0	52.7		
TUP	10_2175	9	7.8–9.2	RM1328–RM23941	2.0	0.9	0.4	32.8		
TUP	10_2176	9	7.8–9.2	RM1328–RM23941	2.8	0.8	0.0	42.2		
TUP	10_2163	10	2.0	RM24944	2.6	-1.2	0.6	40.5		
TUP	10_2177	10	11.7–17.4	RM4455–RM5620	4.4	-1.4	-1.9	55.5		Ehd1
TUP	10_2181	11	0.3	RM5716	2.1	1.5	-1.1	33.2		
TUP	10_2180	11	10.0–14.5	RM4862–RM5824	2.9	0.8	0.6	25.7		
TUP	10_2184	12	20.0–24.4	RM28305–RM5479	4.9	-0.6	-3.1	62.5		
TUP	10_2178	12	24.4–27.4	RM5479–RM2197	3.5	-1.3	0.5	49.2		
TUP	10_2168	12	27.4	RM2197	2.1	-0.6	2.0	13.9		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
MUH	10_2369	3	0.5	RM4108	8.6	-1.6	0.1	51.9		Ehd4 , DTH3
MUH	10_2349	3	0.5–2.7	RM4108–RM14391	6.6	-3.5	-0.4	68.8		Ehd4 , DTH3
MUH	10_2352	3	26.7–35.0	RM2334–RM16153	10.8	-9.3	7.0	61.0	Hd6	Hd16
MUH	10_2351	3	26.7–35.6	RM2334–RM3329	15.5	-8.4	7.5	90.9	Hd6	Hd16
MUH	10_2355	5	8.3–15.8	RM2744–RM18419	3.2	1.2	-0.4	44.0		
MUH	10_2357	5	23.9–27.9	RM3476–RM5784	2.8	-1.5	0.4	5.3		
MUH	10_2342	6	5.2–8.1	RM5754–RM19725	9.0	3.8	-3.3	78.9	Hd1	
MUH	10_2372	6	8.1	RM19725	7.0	5.9	-1.9	76.0	Hd1	
MUH	10_2356	6	8.1–20.3	RM19725–RM7193	10.1	7.1	-2.5	82.1	Hd1	
MUH	10_2357	6	8.1–20.3	RM19725–RM7193	14.3	5.9	-0.8	78.5	Hd1	
MUH	10_2359	6	8.1–20.3	RM19725–RM7193	10.4	4.6	-2.1	82.9	Hd1	
MUH	10_2361	6	8.1–20.3	RM19725–RM7193	14.0	9.2	-1.8	89.3	Hd1	
MUH	10_2358	6	15.8–24.5	RM20023–RM5957	6.2	4.8	-0.9	69.3		
MUH	10_2362	8	0.1–6.8	RM6369–RM22617	7.8	-5.7	0.2	74.4	DTH8	
MUH	10_2344	8	6.8–15.7	RM22617–RM22921	8.4	-3.9	-0.1	76.5		
MUH	10_2373	8	10.3–19.1	RM3395–RM23055	2.3	-3.1	-0.3	39.4		
MUH	10_2364	8	28.2	RM4997	2.4	0.6	-0.3	27.4		
MUH	10_2364	9	7.5–9.2	RM1328–RM23928	2.5	1.1	-0.4	28.7		
MUH	10_2369	10	7.6–11.7	RM25151–RM4455	3.0	-0.9	0.2	8.0		
MUH	10_2369	10	17.4–23.1	RM5620–RM6673	4.3	0.9	-0.4	12.7		Ehd1
MUH	10_2348	11	3.8–8.1	RM5599–RM3701	2.3	-1.3	0.7	34.5		
MUH	10_2370	12	24.4–27.4	RM5479–RM2197	2.5	-1.1	1.0	42.0		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
BAS	10_2304	1	12.1–18.7	RM10764–RM11033	3.3	-2.6	26.6	46.7		
BAS	10_2307	1	26.8–31.5	RM3143–RM5914	3.8	-1.8	0.9	49.9		
BAS	10_2316	2	18.5–24.0	RM1211–RM3515	2.7	-3.9	-6.1	27.2		
BAS	10_2313	2	33.0–35.4	RM7286–RM3850	4.2	-2.2	-1.3	15.2		<i>DTH2</i>
BAS	10_2316	3	0.5–3.8	RM4108–RM14462	2.8	0.2	5.4	17.7		<i>Ehd4</i> , <i>DTH3</i>
BAS	10_2311	3	10.1–25.1	RM14778–RM3513	3.4	-2.0	-0.3	44.5		
BAS	10_2313	3	10.1–14.5	RM14778–RM6959	2.3	-1.2	-0.9	7.0		
BAS	10_2312	3	32.4–35.6	RM6970–RM3329	15.1	-10.3	7.6	90.6	<i>Hd6</i>	<i>Hd16</i>
BAS	10_2314	3	32.4–35.6	RM6970–RM3329	11.6	-10.2	7.8	85.0	<i>Hd6</i>	<i>Hd16</i>
BAS	10_2337	3	32.4–35.6	RM6970–RM3329	13.1	-9.3	6.9	88.1	<i>Hd6</i>	<i>Hd16</i>
BAS	10_2315	5	8.3–10.1	RM2744–RM18222	2.6	0.8	-1.5	37.9		
BAS	10_2315	5	14.9–23.9	RM6742–RM3476	2.7	0.9	-1.5	38.6		
BAS	10_2316	5	23.9–29.4	RM3476–RM19193	3.1	-4.9	-1.1	33.3		
BAS	10_2317	5	23.9–29.4	RM3476–RM19193	2.1	-1.1	0.2	31.9		
BAS	10_2318	6	5.2–8.8	RM5754–RM5963	3.7	6.4	-2.8	48.9		
BAS	10_2319	6	5.2–15.8	RM5754–RM20023	13.1	6.1	-0.9	89.3	<i>Hd1</i>	
BAS	10_2323	7	11.0–16.0	RM21392–RM21521	2.6	-1.5	-0.2	39.9		
BAS	10_2313	7	29.4	RM22164	7.8	-3.2	0.3	50.3		<i>OsPRR37</i>
BAS	10_2318	8	0.4–5.9	RM1381–RM6838	2.5	-4.1	2.5	39.6	<i>DTH8</i>	
BAS	10_2326	9	3.4–10.5	RM23736–RM24075	2.4	1.3	-0.1	35.6		
BAS	10_2334	11	14.5–25.1	RM5824–RM2191	3.5	1.1	0.7	49.2		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
DPZ	11_2004	1	2.2–7.3	RM5423–RM3598	3.0	2.0	0.1	41.5		
DPZ	11_2006	1	21.9–26.8	RM1196–RM3143	4.1	-1.9	0.8	59.3		
DPZ	11_2019	2	13.4–18.4	RM13101–RM1211	4.1	1.0	-1.9	32.7		
DPZ	11_2005	2	18.4–24.0	RM1211–M3515	2.7	0.6	-5.5	10.8		
DPZ	11_2017	2	24.0	RM3515	2.1	2.7	-4.5	7.1		
DPZ	11_2009	2	29.3–33.0	RM6933–RM7286	2.3	-1.9	-1.2	34.6		<i>DTH2</i>
DPZ	11_2007	2	33.0–35.4	RM7286–RM3850	5.3	-3.0	0.2	63.2		<i>DTH2</i>
DPZ	11_2010	3	0.1–1.5	RM14243–RM3372	3.3	-1.8	1.0	44.9		<i>Ehd4</i> , <i>DTH3</i>
DPZ	11_2031	3	19.2–21.4	RM15289–RM5488	2.6	-2.4	0.8	17.3		
DPZ	11_2019	3	25.1	RM3513	3.5	-1.7	0.2	41.6		
DPZ	11_2031	3	25.1–27.3	RM3513–RM6736	2.1	-2.7	-0.8	14.4		
DPZ	11_2011	3	27.3–35.6	RM6736–RM3329	13.0	-11.7	7.7	89.2	<i>Hd6</i>	<i>Hd16</i>
DPZ	11_2014	5	23.9–27.9	RM3476–RM5784	2.8	-1.6	1.5	15.4		
DPZ	11_2013	6	0.2	RM6467	3.8	-3.1	-3.4	49.7		
DPZ	11_2031	6	0.2–6.0	RM6467–RM2615	3.8	-2.8	-2.7	40.2	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
DPZ	11_2005	6	0.2–8.1	RM6467–RM19725	7.1	-11.3	1.5	71.4	<i>Hd1</i>	
DPZ	11_2014	6	6.0–8.1	RM2615–RM19725	10.5	-6.2	3.4	63.4	<i>Hd1</i>	
DPZ	11_2016	6	6.0–8.1	RM2615–RM19725	9.6	-5.7	2.2	81.5	<i>Hd1</i>	
DPZ	11_2017	6	6.0–8.1	RM2615–RM19725	8.5	-11.7	0.6	75.0	<i>Hd1</i>	
DPZ	11_2018	6	6.0–8.1	RM2615–RM19725	11.6	-6.8	3.7	85.5	<i>Hd1</i>	
DPZ	11_2008	6	8.1	RM19725	10.4	-8.0	3.0	82.8	<i>Hd1</i>	
DPZ	11_2026	6	8.1–11.0	RM19725–RM3330	6.4	-6.7	1.5	73.0	<i>Hd1</i>	
DPZ	11_2020	7	5.0–16.2	RM21137–RM5481	10.4	-3.1	1.7	82.9	<i>Ghd7</i>	
DPZ	11_2021	7	8.8–16.2	RM21324–RM5481	7.3	-3.9	1.8	25.3	<i>Ghd7</i>	
DPZ	11_2021	7	28.1–29.4	RM22105–RM22164	6.6	-5.5	1.0	34.5		<i>OsPRR37</i>
DPZ	11_2022	8	5.5–10.3	RM22550–RM3395	10.8	6.3	5.6	89.0	<i>DTH8</i>	
DPZ	11_2032	10	17.5–20.7	RM5620–RM25771	5.1	2.2	2.0	59.6		<i>Ehd1</i>
DPZ	11_2031	12	1.0–2.3	RM3323–RM3747	2.1	-4.1	-0.2	19.1		
DPZ	11_2023	12	21.2–26.0	RM1986–RM1300	3.8	-2.2	1.8	40.7		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
KMK	10_2095	2	9.5–15.6	RM12921–RM13165	6.2	-1.3	-1.5	56.9		
KMK	10_2108	2	26.1–33.0	RM13679–RM7286	2.1	0.8	0.7	33.5		DTH2
KMK	10_2095	3	0.4	RM7332	2.1	-0.6	0.9	16.3		Ehd4 , DTH3
KMK	10_2090	3	3.2–9.9	RM4683–RM1371	3.1	-1.9	-1.6	45.9		
KMK	10_2093	3	32.4–36.2	RM6970–RM7389	16.1	-9.9	2.1	92.2		Hd6 , Hd16
KMK	10_2096	5	4.7–6.8	RM17990–RM18107	2.2	0.6	-0.5	35.1		
KMK	10_2098	5	23.9–29.8	RM3476–RM19221	4.9	-3.4	-9.7	53.4		
KMK	10_2085	5	27.9–29.8	RM5784–RM19221	2.7	-1.2	-1.0	41.0		
KMK	10_2099	6	0.1–8.1	RM19227–RM19725	3.6	-3.5	-1.8	41.8	RFT1, Hd3a	Hd17
KMK	10_2099	6	17.1–20.3	RM20084–RM7193	2.1	2.4	0.7	12.5		
KMK	10_2105	7	0.1	RM5911	3.1	2.5	1.2	23.7		
KMK	10_2088	8	3.0	RM4955	5.7	-2.5	0.6	66.5		
KMK	10_2105	8	3.0	RM4955	5.1	-1.3	1.4	62.7		
KMK	10_2106	8	3.0–8.5	RM4955–RM22674	3.5	-2.5	0.2	47.4	DTH8	
KMK	10_2106	8	19.5–24.6	RM23068–RM5891	2.5	1.3	1.7	17.0		
KMK	10_2107	8	24.6–28.2	RM5891–RM4997	3.3	1.0	-1.5	49.0		
KMK	10_2094	10	0.1	RM7492	2.5	-0.5	-1.3	38.9		
KMK	10_2084	10	11.7–13.6	RM4455–RM1859	3.3	-0.7	-0.5	49.4		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
NAB	11_2046	2	34.7	RM3789	2.1	-1.5	0.7	24.0		DTH2
NAB	11_2043	3	0.5–5.5	RM4108–RM5442	2.3	-4.2	0.2	19.7		Ehd4 , DTH3
NAB	11_2044	3	9.9–15.0	RM1371–RM3204	4.8	-2.5	-0.5	61.0		
NAB	11_2040	3	30.4–35.6	RM3199–RM3329	7.4	-8.5	5.4	84.0	Hd6	Hd16
NAB	11_2045	3	30.4–35.6	RM3199–RM3329	10.5	-7.9	4.0	51.0	Hd6	Hd16
NAB	11_2046	4	2.0–4.9	RM5414–RM16449	2.4	2.0	0.3	29.0		
NAB	11_2049	5	4.2–8.3	RM3777–RM2744	2.4	-2.3	-1.2	39.0		
NAB	11_2051	6	2.2–6.0	RM8112–RM2615	3.2	-1.6	-1.8	47.0	RFT1, Hd3a	Hd17
NAB	11_2052	6	2.2–6.0	RM8112–RM2615	4.5	3.6	3.8	14.0	RFT1, Hd3a	Hd17
NAB	11_2052	6	8.8–15.8	RM5963–RM20023	6.2	8.0	-1.8	34.0	Hd1	
NAB	11_2067	6	8.8–20.3	RM5963–RM7193	14.2	8.1	-0.6	86.0	Hd1	
NAB	11_2043	6	13.0–23.3	RM19951–RM1340	5.3	6.9	3.2	55.4		
NAB	11_2053	6	13.0–20.3	RM19951–RM7193	8.4	5.9	-0.7	79.0		
NAB	11_2055	7	5.7–16.2	RM6728–RM5481	4.0	-7.0	-0.3	54.0	Ghd7	
NAB	11_2054	7	5.7–16.2	RM6728–RM5481	7.5	-5.3	1.9	75.0	Ghd7	
NAB	11_2055	7	25.7–29.4	RM1330–RM22164	7.4	-6.2	0.1	32.0		OsPRR37
NAB	11_2045	8	1.8–5.9	RM22321–RM6838	7.4	-6.9	2.2	40.0	DTH8	
NAB	11_2056	8	5.9–12.4	RM6838–RM22839	9.1	-5.6	1.3	81.0	DTH8	
NAB	11_2057	8	5.9–18.8	RM6838–RM5767	5.4	-4.6	1.8	65.0	DTH8	
NAB	11_2037	10	0.1	RM7492	2.1	-0.8	-1.9	34.0		
NAB	11_2061	10	18.8–23.1	RM6737–RM6673	2.2	2.2	1.7	35.0		
NAB	11_2040	12	3.8–4.9	RM27627–RM3455	2.2	-4.4	-5.6	16.0		
NAB	11_2067	12	4.9–16.3	RM3455–RM28112	3.4	-1.8	-0.7	5.0		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
BKH	10_2046	1	41.2–42.9	RM5310–RM8137	2.5	1.3	0.1	38.3		
BKH	10_2053	3	0.5	RM4108	2.9	-1.3	2.8	42.9		<i>Ehd4</i> , <i>DTH3</i>
BKH	10_2068	3	0.5	RM4108	5.3	-7.8	-2.3	36.7		<i>Ehd4</i> , <i>DTH3</i>
BKH	10_2049	3	0.5–9.9	RM4108–RM1371	5.8	-4.6	2.2	67.0		<i>Ehd4</i> , <i>DTH3</i>
BKH	10_2050	3	21.4–25.1	RM5488–RM3513	2.4	-1.8	-0.9	37.6		
BKH	10_2051	3	27.3–32.4	RM6736–RM6970	8.7	-8.6	7.3	80.0	<i>Hd6</i>	<i>Hd16</i>
BKH	10_2056	5	0.1–5.9	RM1248–RM18055	4.2	-3.0	0.9	25.0		
BKH	10_2058	5	20.1–22.3	RM1386–RM3295	2.7	2.3	1.9	15.2		
BKH	10_2058	5	22.3–27.9	RM3295–RM5784	4.7	-5.2	0.1	41.9		
BKH	10_2056	6	0.2–5.2	RM6467–RM5754	5.8	-3.2	-1.7	33.7	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2057	6	0.2–5.2	RM6467–RM5754	4.9	-5.0	-3.8	18.1	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2058	6	0.2–5.2	RM6467–RM5754	4.4	-4.0	0.8	36.5	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2059	6	0.2–5.2	RM6467–RM5754	5.3	-7.3	-3.5	22.2	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2071	6	0.2–5.2	RM6467–RM5754	4.8	-4.8	-2.3	60.1	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2045	6	0.2–9.0	RM6467–RM19771	6.9	-11.7	-4.3	68.6	<i>Hd1</i>	
BKH	10_2068	6	5.2	RM5754	7.4	-4.8	-3.5	47.0	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2073	6	5.2	RM5754	4.5	-8.7	-6.7	58.0	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BKH	10_2057	6	5.2–9.0	RM5754–RM19771	7.8	-9.1	4.4	35.7	<i>Hd1</i>	
BKH	10_2059	6	5.2–9.0	RM5754–RM19771	10.2	-9.4	4.5	60.7	<i>Hd1</i>	
BKH	10_2075	6	5.2–9.0	RM5754–RM19771	5.4	-11.0	-0.9	66.0	<i>Hd1</i>	
BKH	10_2076	6	5.2–9.0	RM5754–RM19771	9.2	-15.1	-5.2	81.4	<i>Hd1</i>	
BKH	10_2074	6	5.2–11.0	RM5754–RM3330	2.9	-9.7	-4.4	42.9	<i>Hd1</i>	
BKH	10_2060	6	9.0–20.3	RM19771–RM7193	11.6	-8.1	4.1	80.5	<i>Hd1</i>	
BKH	10_2063	7	5.7–13.4	RM6728–RM7273	4.9	-4.9	0.2	60.9		
BKH	10_2080	7	5.7–28.4	RM6728–RM22120	4.5	1.4	3.0	58.1		
BKH	10_2062	7	5.7–23.6	RM6728–RM5847	7.2	-3.6	-0.6	74.3	<i>Ghd7</i>	
BKH	10_2052	7	13.4–18.4	RM7273–RM6394	4.2	-3.4	1.1	56.1		
BKH	10_2065	8	10.3–14.7	RM3395–RM22896	5.2	4.2	2.0	63.5		
BKH	10_2073	10	17.4–20.7	RM5620–RM25771	4.2	0.8	-7.5	55.6		<i>Ehd1</i>
BKH	10_2076	10	23.1	RM6673	2.2	3.5	1.0	3.2		
BKH	10_2078	12	5.5–10.1	RM27723–RM6973	2.0	-0.9	1.3	36.5		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
KNJ	10_2208	1	2.2	RM5423	2.1	-1.4	0.1	11.5		
KNJ	10_2205	1	14.0–18.7	RM10850–RM11033	2.1	0.6	0.6	24.1		
KNJ	10_2194	3	3.2–7.8	RM4683–RM14674	2.1	-1.0	-1.0	33.3		
KNJ	10_2195	3	14.5–21.4	RM6959–RM5488	3.2	-3.4	-3.2	46.7		
KNJ	10_2209	3	25.1–28.7	RM3513–RM1350	2.9	1.3	0.5	20.2		
KNJ	10_2193	3	28.7–32.4	RM1350–RM6970	7.6	-8.8	5.1	44.4	<i>Hd6</i>	<i>Hd16</i>
KNJ	10_2196	3	28.7–32.4	RM1350–RM6970	17.9	-10.8	6.7	93.2	<i>Hd6</i>	<i>Hd16</i>
KNJ	10_2202	5	20.1–23.9	RM1386–RM3476	5.2	-2.2	-1.4	63.3		
KNJ	10_2203	6	0.1–16.1	RM19227–RM20045	5.2	-6.9	0.8	63.4	<i>Hd1</i>	
KNJ	10_2204	6	6.0–11.8	RM2615–RM19882	8.8	-8.5	1.3	80.3	<i>Hd1</i>	
KNJ	10_2208	7	26.8–29.4	RM1364–RM22164	5.6	-2.9	1.1	66.1		<i>OsPRR37</i>
KNJ	10_2192	8	0.1–3.7	RM6369–RM1148	4.0	-2.3	1.3	54.1		
KNJ	10_2209	8	0.7–3.7	RM22258–RM1148	5.6	-2.3	-0.2	57.6		
KNJ	10_2210	8	12.4–16.6	RM22837–RM22965	2.3	-1.0	1.4	36.7		
KNJ	10_2190	9	7.4–9.2	RM23920–RM1328	2.5	-1.1	0.4	39.4		
KNJ	10_2214	10	0.1–9.8	RM7492–RM1126	3.6	-1.4	-1.0	50.8		
KNJ	10_2216	11	6.3–8.1	RM4469–RM3701	2.7	0.8	-1.2	41.3		

Population		Chromosome	Physical position	Marker Interval	LOD ^a	Additive effect ^b	Dominance effect ^c	PVE (%) ^d	Corresponding gene ^e	Located near gene ^f
BLE	11_2078	1	31.5–35.5	RM5914–RM7594	2.6	-1.6	0.0	39.8		
BLE	11_2080	2	9.0–13.4	RM5699–RM13101	2.6	-3.4	0.9	11.8		
BLE	11_2098	2	35.4	RM3850	2.2	-1.7	0.5	35.5		<i>DTH2</i>
BLE	11_2100	3	0.5	RM4108	5.6	-5.2	-0.6	65.7		<i>Ehd4</i> , <i>DTH3</i>
BLE	11_2079	3	0.5–5.5	RM4108–RM5442	3.2	-2.8	0.2	25.0		<i>Ehd4</i> , <i>DTH3</i>
BLE	11_2080	3	26.7–35.6	RM2334–RM3329	12.7	-7.4	4.5	70.6	<i>Hd6</i>	<i>Hd16</i>
BLE	11_2088	3	30.4–35.6	RM3199–RM3329	6.5	-4.5	4.0	24.3	<i>Hd6</i>	<i>Hd16</i>
BLE	11_2073	5	0.1–4.2	RM1248–RM3777	2.0	-1.5	0.5	32.5		
BLE	11_2084	5	0.1–4.2	RM1248–RM3777	2.6	-0.7	2.7	40.4		
BLE	11_2085	5	23.9–27.9	RM3476–RM5784	2.5	-1.6	2.4	39.4		
BLE	11_2086	6	0.1–2.2	RM19227–RM8112	2.2	-2.3	-1.1	48.5	<i>RFT1</i> , <i>Hd3a</i>	<i>Hd17</i>
BLE	11_2087	6	8.8–20.3	RM5963–RM7193	13.5	-8.1	2.3	89.8	<i>Hd1</i>	
BLE	11_2088	6	20.3–23.3	RM7193–RM1340	5.0	-4.1	-0.1	24.8		
BLE	11_2089	7	2.6–7.1	RM5752–RM21251	2.2	-1.8	-0.5	35.2		
BLE	11_2090	7	7.1–18.4	RM21251–RM6394	10.2	-4.5	0.8	84.2	<i>Ghd7</i>	
BLE	11_2091	7	29.0–29.4	RM7601–RM22164	7.0	-4.2	3.1	73.4		<i>OsPRR37</i>
BLE	11_2102	7	29.4	RM22164	5.7	-3.6	1.0	70.6		<i>OsPRR37</i>
BLE	11_2092	8	0.1–5.9	RM6369–RM6838	10.1	-6.4	1.8	83.8		
BLE	11_2101	10	23.1	RM6673	2.7	2.2	-0.5	41.9		
BLE	11_2103	12	22.7–24.3	RM28450–RM28580	2.0	-1.1	-0.8	32.4		

^a Log-likelihood value. LOD threshold to detect QTLs was determined in each BC₄F₂ population.

^b Additive effect of KSH allele on days to heading

^c Dominance effect of KSH allele on days to heading

^d Percentage of phenotypic variance explained by QTL

^e Previously identified heading date genes corresponding to the QTLs detected in this study based on their physical positions on IRGSP 1.0.

^f Previously identified heading date genes located near the QTLs detected in this study based on their physical positions on IRGSP 1.0.