

Table S1. Radish germplasm genotyped for GWAS

No.	Variety (original language)	Variety (pronunciation)	Company	Country	Bolting time	Type
R01	신청일품	Sincheongilpum	Farmhannong	Korea	Late	white
R02	춘강하늘무	Chunganghaneulmu	Danong	Korea	Late	white
R03	탑그린봄무 2 호	Topgreenbommu No. 2	Kwonnong	Korea	Late	white
R04	슈퍼길조무	Supergiljomu	Nongwoo Bio	Korea	Late	white
R05	아시아백춘무	Asiabaegchunmu	Asia Seed	Korea	Late	white
R06	전무후무	Jeonmuhumu	Koregon	Korea	Late	white
R07	백옥무	Baegogmu	Nongwoo Bio	Korea	Late	white
R08	YR 신청장군	YR Sincheongjanggun	Koregon	Korea	Late	white
R09	우리봄무	Ulibommu	Asia Seed	Korea	Late	white
R10	서호무	Seohomu	Nongwoo Bio	Korea	Early	white
R11	국보골드	Guckbogold	Kwonnong	Korea	Early	white
R12	천수무	Cheonsumu	Farmhannong	Korea	Early	white
R13	청풍명월무	Cheongpungmyeongwolmu	Jeilseed Bio	Korea	Early	white
R14	한가을	Hangaeul	Sakata Korea	Korea	Early	white
R15	대보름	Daebolm	Sakata Korea	Korea	Early	white
R16	상황무	Sanghwangmu	PPS	Korea	Early	white
R17	진주대평무	Jinjudaepyongmu	Kyoungshin	Korea	Early	white
R18	하백옥	Habaegock	Hong Kong Qinong	China	Early	white
R19	大地特选白萝卜	Daditexuanbai luobo	Dadi Seed	China	Early	white
R20	耐病夏富士	Taibyonatsufuji	Takayama Seed	Japan	Late	white
R21	高農早生大藏	Konowasedaizo	Takayama Seed	Japan	Early	white
R22	高農みの早生	Konominowase	Takayama Seed	China	Late	white
R23	新天地	Shintenchu	Takayama Seed	Japan	Early	white
R24	白天勇	Hakutenyu	Takayama Seed	Japan	Early	white
R25	耐病貴船	Taibyokifune	Takayama Seed	Japan	Early	white
R26	冬職人	Fuyushokunin	Takayama Seed	Japan	Early	white
R27	耐病東山	Taibyo Higashiyama	Takayama Seed	Japan	Late	white
R28	YR 新富王	YR Shintomioh	Takayama Seed	Japan	Early	white
R29	味職人	Ajishokunin	Takayama Seed	Japan	Late	white
R30	三太郎	Santaro	Nihon Nonsanshubyou	Japan	Late	white
R31	漬物	Zimono	Utane	Japan	Early	white
R32	おでん大根	Oden daikon	Tohoku Seed	Japan	Early	white
R33	耐病青首総太り	Taibyoaokubisofutori	Utane	Japan	Early	white
R34	夏つかさ	Natsutsukasa	Tohoku Seed	Japan	Early	green skin
R35	HC-4	HC-4	Jungwon Seed	Japan	Late	green skin

R36	GR-32	GR-32	Jungwon Seed	Japan	Late	green skin
R37	晩抽春 のいぶき	Wanchuharunoibuki	Hoku seed	Japan	Late	green skin
R38	蒼春	Soshun	Hoku seed	Japan	Late	green skin
R39	삼박자	Sambagja	Farmhannong	Korea	Late	green skin
R40	청두무	Cheongdumu	Asia Seed	Korea	Early	green skin
R41	골드 청라무	Goldcheonglamu	Green Heart Bio	Korea	Early	green skin
R42	CR301	CR301	Nongwoo Bio	China	Late	white
R43	玉山白雪	Yushanbaixue	Nongwoo Bio	China	Late	white
R44	BN132	BN132	Jenong	China	Late	white
R45	BN1308	BN1308	Jenong	China	Late	white
R46	NA1202	NA1202	Jenong	China	Late	white
R47	BN151	BN151	Jenong	China	Late	white
R48	BN147	BN147	Jenong	China	Late	white
R49	RT5012	RT5012	Dayi Seed	China	Late	white
R50	춘득	Chundeuk	Dayi Seed	China	Late	white
R51	扬州圆白萝卜	Yangzhuuyuanbai luobo	Yangzhou Bangda Seed	China	Early	white
R52	潍县萝卜	Weixian luobo	-	China	Early	green skin
R53	琴萌青二号	Qinmengqing No. 2	-	China	Early	green skin
R54	创丰抗热 40 天	Chuangfengkangre 40 tian	-	China	Early	green skin
R55	绿宝	Lubao	-	China	Early	green skin
R56	民权红	Minquanhong	-	China	Early	red skin
R57	粉皮脆	Fenpicui	-	China	Early	red skin
R58	沈春青萝卜	Shenchunqingluobo	-	China	Early	green skin
R59	北京翠红	Beijingcuihong	-	China	Early	green skin, red flesh
R60	心里美	Xinlimei	-	China	Early	green skin, red flesh

Table S4. Linkage map of F₂ populations after 2 and 3 weeks of vernalization treatment.

Chromosome	Length (bp)	2 week			3 week		
		No. of SNPs	Number of bin	Length (cM)	No. of SNPs	Number of bin	Length (cM)
RSAskrl.0R1	27,719,058	1034	99	152.7	1252	85	104.2
RSAskrl.0R2	42,944,316	1246	151	287.9	1354	131	177.6
RSAskrl.0R3	31,410,669	891	107	161.5	1363	94	142.5
RSAskrl.0R4	56,498,296	1251	182	309	1644	149	147.2
RSAskrl.0R5	42,357,306	1474	168	171.7	1855	150	119.9
RSAskrl.0R6	53,940,652	1698	207	302.7	2129	169	200.8
RSAskrl.0R7	28,108,325	915	98	155.7	1177	88	87.3
RSAskrl.0R8	28,319,830	794	102	122.6	1038	81	78.6
RSAskrl.0R9	38,520,653	972	140	176.1	1229	116	143.9
Total	349,819,105	10,275	1254	1839.9	13,041	1063	1202.0

Table S9. Summary of resequencing data for 60 radish germplasms used for GWAS

Sample ID	Total bases(bp)	Total reads	GC(%)	AT(%)	Q20(%)	Q30(%)
R1	6,692,196,784	44,319,184	37.3	62.7	96.5	91.1
R2	5,000,556,468	33,116,268	37.5	62.5	96.1	90.4
R3	6,971,216,094	46,166,994	37.1	62.9	96.5	91.1
R4	5,785,895,690	38,317,190	37.4	62.6	96.5	91.2
R5	6,568,126,426	43,497,526	37.2	62.8	96.5	91.2
R6	5,751,240,586	38,087,686	37.2	62.8	96.6	91.3
R7	5,593,806,174	37,045,074	37.4	62.6	96.3	90.7
R8	6,778,226,014	44,888,914	37.4	62.6	96.1	90.3
R9	6,272,745,964	41,541,364	37.2	62.8	96.6	91.4
R10	7,263,654,170	48,103,670	37.6	62.4	96.4	91
R11	5,827,221,068	38,590,868	37.7	62.3	96.5	91.2
R12	5,670,241,770	37,551,270	37.5	62.5	96.1	90.3
R13	6,775,748,708	44,872,508	37.4	62.6	96.4	91.1
R14	5,671,629,762	37,560,462	37.4	62.6	96.6	91.4
R15	5,522,591,554	36,573,454	37.7	62.3	96.3	90.8
R16	6,418,825,176	42,508,776	37.6	62.4	96.2	90.6
R17	5,562,798,626	36,839,726	37.8	62.2	96.3	90.8
R18	6,109,385,406	40,459,506	37.4	62.6	96.6	91.4
R19	7,476,001,242	49,509,942	37.6	62.4	96.5	91.1
R20	5,468,905,014	36,217,914	37.6	62.4	96.5	91.3
R21	6,717,024,204	44,483,604	37.6	62.4	96.4	91.2
R22	6,254,450,804	41,420,204	37.4	62.6	96.5	91.1
R23	6,925,343,200	45,863,200	37.4	62.6	96.5	91.2
R24	5,388,086,492	35,682,692	37.5	62.5	96.3	90.9
R25	7,292,245,416	48,293,016	37.9	62.1	96.2	90.7
R26	7,033,506,010	46,579,510	37.4	62.6	96.4	91.1
R27	5,812,541,452	38,493,652	37.3	62.7	96.2	90.7
R28	5,888,672,330	38,997,830	37.1	62.9	96	90.1
R29	5,597,831,230	37,071,730	37.2	62.8	95.9	90
R30	7,061,537,650	46,765,150	37.6	62.4	96.5	91.1
R31	6,773,179,896	44,855,496	37.8	62.2	96.5	91.2
R32	6,455,952,452	42,754,652	37.4	62.6	96.4	91.1
R33	7,457,574,410	49,387,910	37.6	62.4	96.4	91.1
R34	6,194,399,614	41,022,514	37.8	62.2	96.5	91.2
R35	6,827,993,500	45,218,500	37.4	62.6	96.1	90.4
R36	6,202,109,976	41,073,576	37.5	62.5	96.5	91.2
R37	7,276,663,424	48,189,824	37.2	62.8	96.3	90.7
R38	5,975,466,526	39,572,626	37.5	62.5	96.7	91.6
R39	7,095,038,812	46,987,012	37.1	62.9	96.4	91.1

Sample ID	Total bases(bp)	Total reads	GC(%)	AT(%)	Q20(%)	Q30(%)
R40	6,629,770,364	43,905,764	37.6	62.4	96.2	90.5
R41	7,161,950,838	47,430,138	37.5	62.5	96.5	91.3
R42	6,169,574,610	40,858,110	37.6	62.4	96.3	90.8
R43	6,962,361,756	46,108,356	37.3	62.7	96.2	90.5
R44	5,744,230,864	38,041,264	37.1	62.9	96.2	90.6
R45	6,735,432,916	44,605,516	37.3	62.7	96.3	90.9
R46	5,469,317,848	36,220,648	36.6	63.4	96.7	91.4
R47	5,716,675,478	37,858,778	37.4	62.6	96.6	91.5
R48	5,769,998,410	38,211,910	37.6	62.4	96.5	91.1
R49	7,283,125,016	48,232,616	37.4	62.6	96.5	91.2
R50	5,424,831,134	35,926,034	37.6	62.4	96.4	91
R51	6,167,648,152	40,845,352	37.3	62.7	96.5	91.2
R52	6,669,667,584	44,169,984	49	51	96.4	90.8
R53	5,692,466,252	37,698,452	37.3	62.7	96.3	90.7
R54	6,941,824,246	45,972,346	37.3	62.7	96.5	91.1
R55	6,949,028,456	46,020,056	37.2	62.8	96.3	90.8
R56	5,983,834,342	39,628,042	37.4	62.6	96.6	91.4
R57	6,817,630,068	45,149,868	37.2	62.8	96.6	91.4
R58	7,038,152,884	46,610,284	37.6	62.4	96.3	90.8
R59	5,848,700,818	38,733,118	37.4	62.6	96.5	91.3
R60	6,221,906,680	41,204,680	37.3	62.7	96.3	90.8

Table S10. Summary of significant SNPs used for GWAS

Chromosome	Length (bp)	Number of SNPs	Average distance between SNPs
RSAsk1.0R1	27,719,058	6,153	4,505
RSAsk1.0R2	42,944,316	9,141	4,698
RSAsk1.0R3	31,410,669	6,777	4,635
RSAsk1.0R4	56,498,296	11,302	4,999
RSAsk1.0R5	42,357,306	9,904	4,277
RSAsk1.0R6	53,940,652	11,817	4,565
RSAsk1.0R7	28,108,325	6,052	4,644
RSAsk1.0R8	28,319,830	6,206	4,563
RSAsk1.0R9	38,520,653	7,500	5,136
Total	349,819,105	74,852	4,673

Table S11. Candidate genes located at loci associated with bolting time.

Gene ID	Description	Chr.	Position (bp)	Linked loci	Previous studies
RSAskr1.0R2g32110	FLC2 protein	2	23,950,482– 23,954,575	<i>R2_24501949</i>	Wang et al. [19]
RSAskr1.0R2g34815	Zinc finger protein CONSTANS-LIKE 1	2	37,215,497– 37,216,874	<i>RsBT2.1</i>	Nie et al. [39]
RSAskr1.0R2g34893	Protein ULTRAPETALA 1	2	37,565,538– 37,567,631	<i>RsBT2.1</i>	Nie et al. [39]
RSAskr1.0R2g35823	Floral homeotic protein APETALA 2 isoform X1	2	41,623,918– 41,626,879	<i>RsBT2.2</i>	Nie et al. [39]
RSAskr1.0R4g44495	Zinc finger protein CONSTANS-LIKE 4 isoform X2	4	11,775,331– 11,777,352	<i>RsBT4.3</i> , <i>R4_11119288</i>	Hu et al. [20], Nie et al. [39]
RSAskr1.0R4g44851	FRIGIDA-like protein	4	13,458,898– 13,462,290	<i>RsBT4.4</i>	Nie et al. [39]
RSAskr1.0R4g44858	Glucose-1-phosphate adenyltransferase	4	13,492,509– 13,495,000	<i>RsBT4.4</i>	Li et al. [40]
RSAskr1.0R4g44863	Zinc finger protein CONSTANS-LIKE 10- like	4	13,522,655– 13,524,938	<i>RsBT4.4</i>	Hu et al. [20], Li et al. [40], Nie et al. [39]
RSAskr1.0R4g44990	FACT complex subunit SSRP1-like	4	14,145,118– 14,148,836	<i>RsBT4.4</i>	Li et al. [40]
RSAskr1.0R4g50522	E3 ubiquitin-protein ligase HOS1	4	44,202,308– 44,207,349	<i>RsBT4.1</i>	Li et al. [40]
RSAskr1.0R4g50705	Squamosa promoter- binding-like protein 9	4	45,099,463– 45,102,239	<i>RsBT4.1</i>	Jung et al. [38], Li et al. [40], Nie et al. [39]
RSAskr1.0R5g57099	Squamosa promoter- binding-like protein 8	5	22,636,835– 22,638,726	<i>RsBT5.1</i>	Jung et al. [38], Nie et al. [39]
RSAskr1.0R7g73042	Nuclear transcription Factor Y subunit A-10 isoform X1	7	5,776,959– 5,778,657	<i>RsBT7.2</i>	Jung et al. [38]
RSAskr1.0R7g73342	Agamous-like MADS- box protein AGL62	7	7,034,934– 7,036,969	<i>RsBT7.2</i>	Nie et al. [39]

Table S12. Primer sequences for HRM analysis

Primer name	Sequence (5'→3')
RsBT4.3_11.4 M-F	GGATGGGAAGAGCTGTTTGAAG
RsBT4.3_11.4 M-R	TTCCAATCATCATCTCCCCAGT
RsBT4.3_12.1 M-F	TCTCGTGCTTTGCTTGTAGA
RsBT4.3_12.1 M-R	CCGTCTAGCAAAGGTTTCATCA

Figure S1. Bolting time of parental lines with four different vernalization treatments.

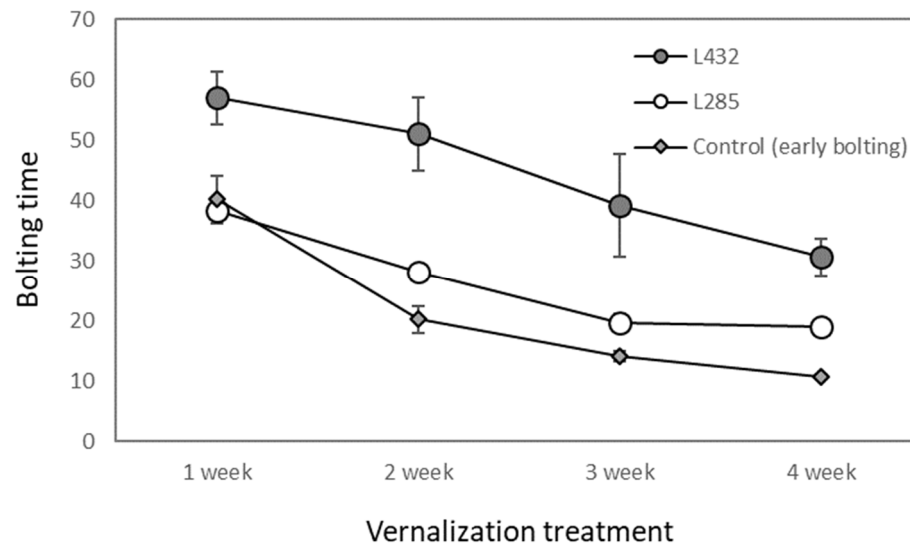
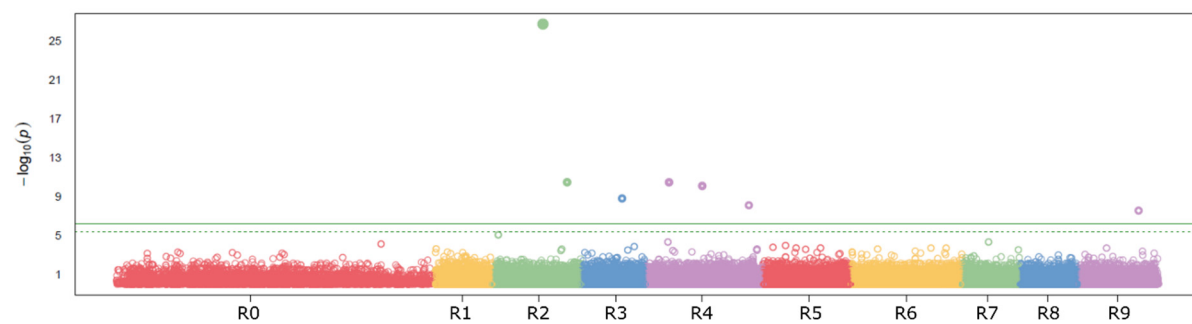
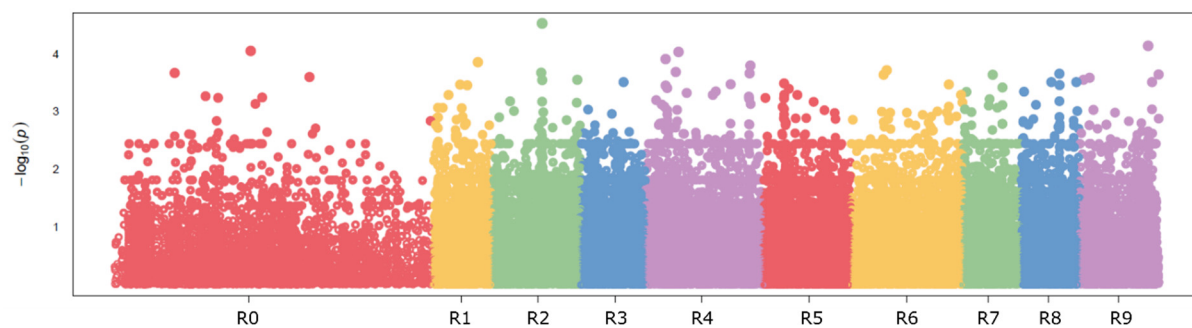


Figure S2. Manhattan plot of GWAS for bolting time by (A) BLINK, (B) MLM, and (C) GLM methods.

(A)



(B)



(C)

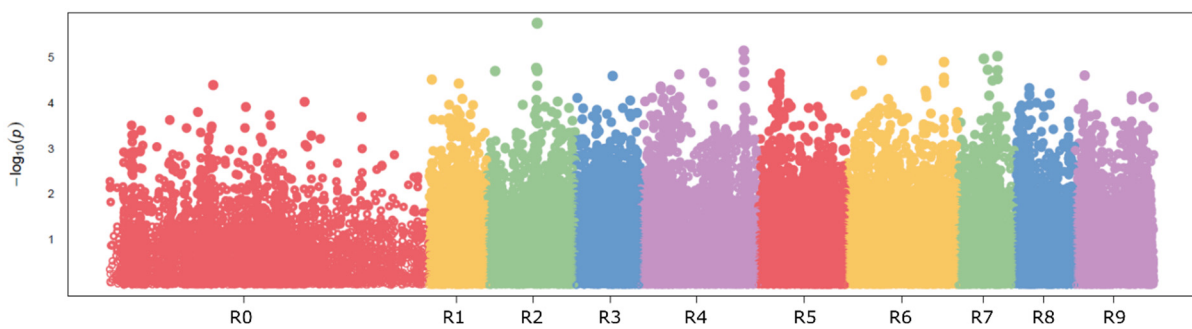


Figure S3. Distribution of bolting time in the 'H16' \times 'red' F_2 population after three weeks of vernalization treatment. H16 is a late-bolting Korean radish, and red is an early-bolting radish with a red root skin color.

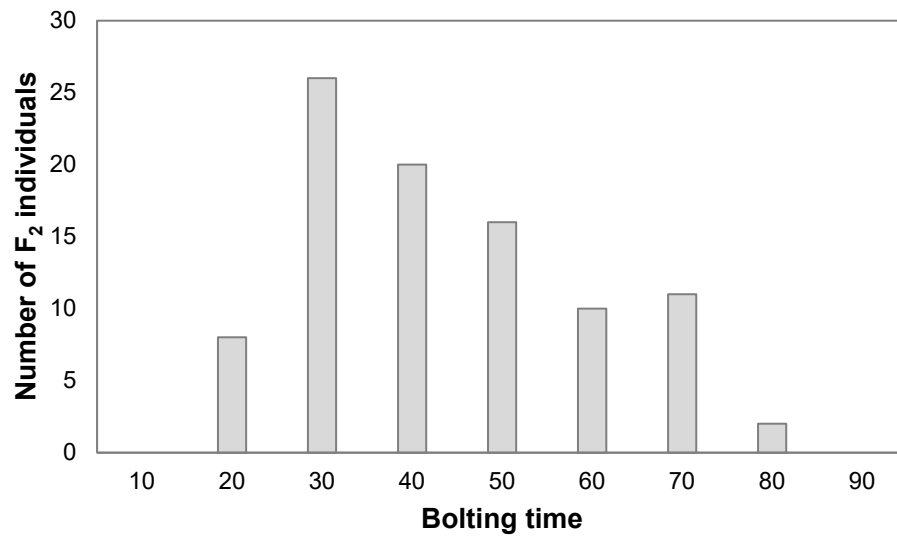


Table S (in Excel form)

Table S2. Bolting time of 'L432' × 'L285' F₂ plants after 2 weeks of vernalization treatment.

Table S3. Bolting time of 'L432' × 'L285' F₂ plants after 3 weeks of vernalization treatment.

Table S5. Genotype of SNPs detected from 'L432' × 'L285' F₂ plants after 2 weeks of vernalization treatment.

Table S6. Genotype of SNPs detected from 'L432' × 'L285' F₂ plants after 3 weeks of vernalization treatment.

Table S7. Genotype and genetic position of bin markers of 'L432' × 'L285' F₂ plants after 2 weeks of vernalization treatment.

Table S8. Genotype and genetic position of bin markers of 'L432' × 'L285' F₂ plants after 3 weeks of vernalization treatment.

Table S13. HRM analysis results of the 'L432' × 'L285' and 'H16' × 'red' F₂ populations.

Table S14. SNPs located in FLC2 and COL4, detected from GWAS population