

Supplementary Table 1. Descriptive statistics for yield-related traits across two years.

Year	Trait ^z	Mean	SD ^y	CV (%)	Median	Minimum	Maximum	Range	Skew	Kurtosis	SE	Unimodality ^x	Bimodality
2022	HD (DAS)	105.71	2.83	2.68	105.00	102.00	114.00	12.00	0.98	0.26	0.30	TRUE	FALSE
	CL (cm)	85.81	7.95	9.26	87.40	64.70	100.10	35.40	-0.65	-0.24	0.83	TRUE	FALSE
	PL (cm)	21.11	1.01	4.78	21.10	18.80	24.40	5.60	0.30	0.14	0.11	TRUE	FALSE
	PN	10.13	1.07	10.56	10.10	7.00	12.60	5.60	-0.26	-0.24	0.11	TRUE	FALSE
	NS	119.27	14.50	12.16	116.64	91.78	157.69	65.91	0.55	-0.39	1.52	FALSE	TRUE
	TGW (g)	25.54	2.07	8.10	25.94	19.89	29.05	9.16	-0.52	-0.63	0.22	FALSE	TRUE
	RRG (%)	90.62	3.14	3.47	91.25	82.11	96.33	14.21	-0.65	-0.09	0.33	TRUE	FALSE
	BRR (%)	82.23	0.60	0.73	82.20	80.40	83.80	3.40	-0.23	0.31	0.06	TRUE	FALSE
	Yield (g/plant)	28.74	3.44	11.97	28.50	20.23	35.73	15.50	-0.04	-0.65	0.36	TRUE	FALSE
	GL (mm)	5.65	0.36	6.37	5.79	4.91	6.34	1.43	-0.39	-1.14	0.04	FALSE	TRUE
	GW (mm)	3.00	0.07	2.33	3.00	2.76	3.15	0.39	-0.37	0.12	0.01	TRUE	FALSE
	GT (mm)	2.06	0.05	2.43	2.07	1.95	2.20	0.25	-0.02	-0.05	0.01	TRUE	FALSE
	RLW	1.89	0.12	6.35	1.92	1.65	2.08	0.42	-0.29	-1.26	0.01	FALSE	TRUE
2023	HD (DAS)	109.24	1.94	1.78	109.00	104.00	114.00	10.00	0.04	-0.50	0.20	FALSE	TRUE
	CL (cm)	85.96	7.86	9.14	87.80	66.70	100.60	33.90	-0.71	-0.04	0.82	TRUE	FALSE
	PL (cm)	21.21	1.09	5.14	21.20	19.10	23.60	4.50	0.04	-0.82	0.11	FALSE	TRUE
	PN	10.19	1.38	13.54	10.10	7.30	14.20	6.90	0.19	-0.18	0.14	TRUE	FALSE
	NS	120.55	16.02	13.29	116.50	84.55	160.41	75.86	0.58	-0.20	1.68	TRUE	FALSE
	TGW (g)	26.01	2.25	8.65	26.63	19.92	30.28	10.36	-0.40	-0.65	0.24	FALSE	TRUE
	RRG (%)	90.18	3.80	4.21	91.22	74.51	95.53	21.03	-1.52	3.27	0.40	TRUE	FALSE
	BRR (%)	83.31	0.58	0.70	83.36	82.07	84.50	2.43	-0.15	-0.67	0.06	TRUE	FALSE
	Yield (g/plant)	31.70	3.60	11.36	31.50	22.50	40.75	18.25	0.12	0.04	0.38	TRUE	FALSE
	GL (mm)	5.77	0.37	6.41	5.91	5.03	6.38	1.34	-0.42	-1.19	0.04	FALSE	TRUE
	GW (mm)	3.04	0.08	2.63	3.04	2.83	3.21	0.38	-0.04	-0.52	0.01	FALSE	TRUE
	GT (mm)	2.17	0.05	2.30	2.17	2.01	2.28	0.27	-0.36	0.42	0.01	TRUE	FALSE
	RLW	1.90	0.12	6.32	1.91	1.64	2.10	0.46	-0.28	-1.16	0.01	FALSE	TRUE

^zHD: heading date, DAS: days after seeding, CL: culm length, PL: panicle length, PN: number of panicles per hill, NS: number of spikelets per panicle, TGW: 1,000-grain weight, BRR: brown/rough rice ratio, GL: grain length, GW: grain width, GT: grain thickness, RLW: ratio of length to width.

^ySD: standard deviation, CV: coefficient of variation, SE: standard error.

^xUnimodality and bimodality were determined using the LaplacesDemon package in R.

Supplementary Table 2. Sequence analysis of nucleotide variations involved in the function of Candidate genes.

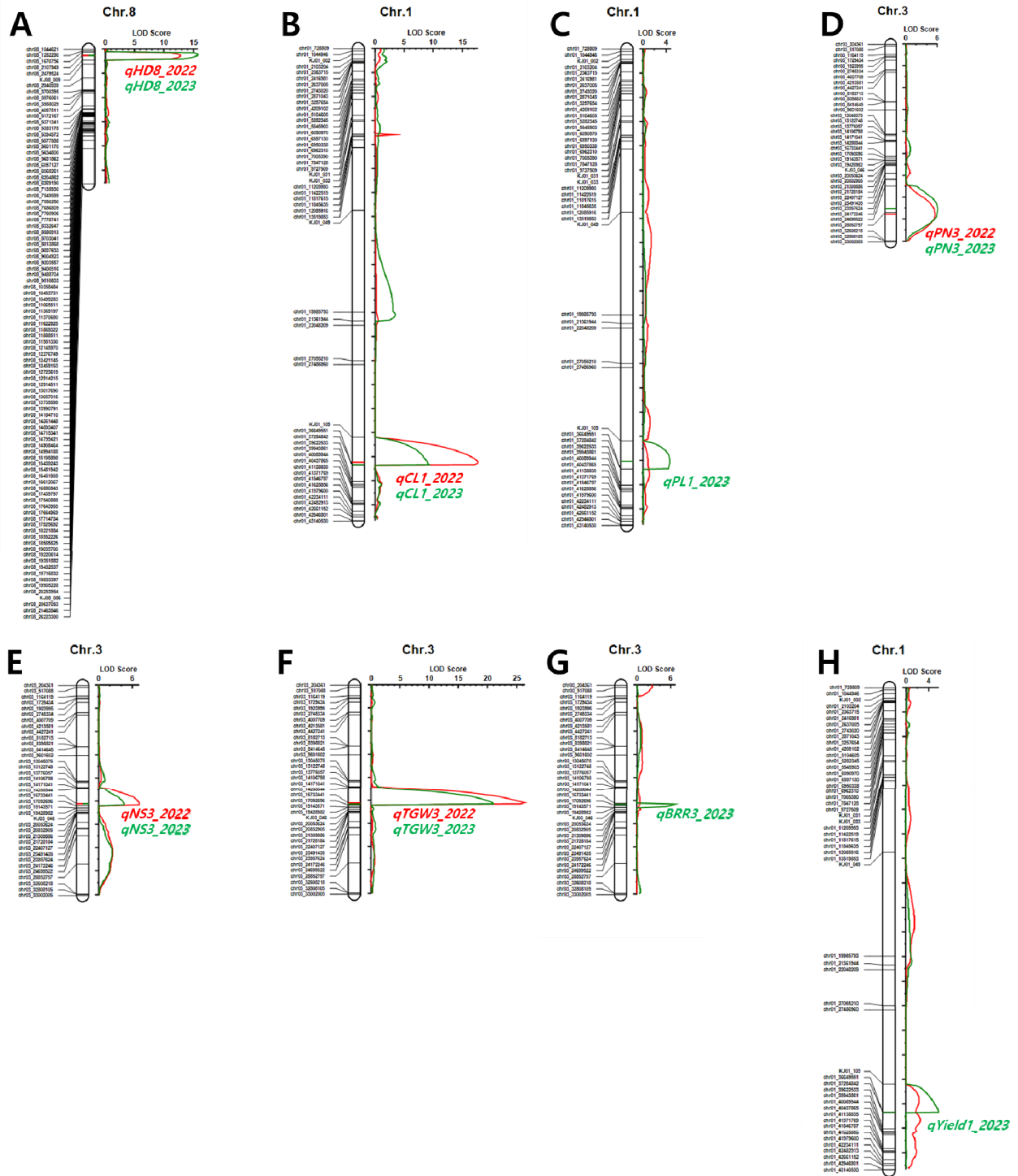
ID	Variants type	Chromosome	Position (bp)	Reference allele	Alternative allele	Chamdongjin genotype	Younghojimi genotype	Candidate gene
08_2388554	snp	chr08	2,388,554	T	C	ref. allele	C/C	<i>Hd18</i>
03_16733441	snp	chr03	16,733,441	G	T	T/T	ref. allele	<i>GS3</i>
03_28428721	indel	chr03	28,428,721	C	CTGTG	C/CTGTG	ref. allele	<i>OsTBI</i>

Supplementary Table 3. Yield-related traits of the selected prominent line 'CY_RIL_79' with *sd1* allele.

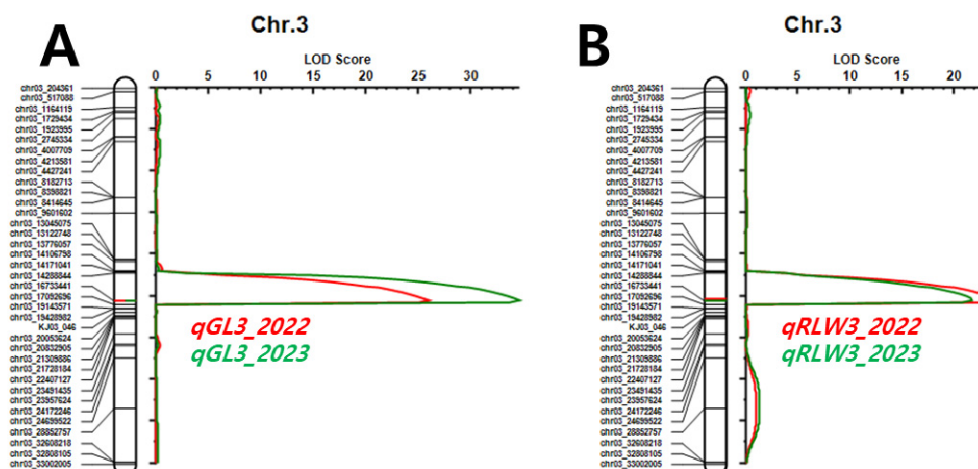
Line	Allele combination	HD ^z (DAS)	CL (cm)	PL (cm)	PN	NS	TGW (g)	RRG (%)	BRR (%)	Yield (g/plant)
Chamdongjin	<i>Hd18-SD1-gs3-OsTBI</i> ^{TGTG}	105b ^y	85a	22.1a	10.4b	143a	27.6a	91.3a	83.4a	31.6a
Younghojimi	<i>hd18-sd1-GS3-OsTBI</i>	111a	78b	19.5b	11.0a	107b	22.4b	88.0b	81.6b	28.1b
CY_RIL_79	<i>Hd18-sd1-gs3-OsTBI</i> ^{TGTG}	106b	75b	19.6b	10.1b	111b	27.0a	92.9a	83.5a	28.0b

^zHD: heading date, DAS: days after seeding, CL: culm length, PL: panicle length, PN: number of panicles per hill, NS: number of spikelets per panicle, TGW: 1,000-grain weight, BRR: brown/rough rice ratio.

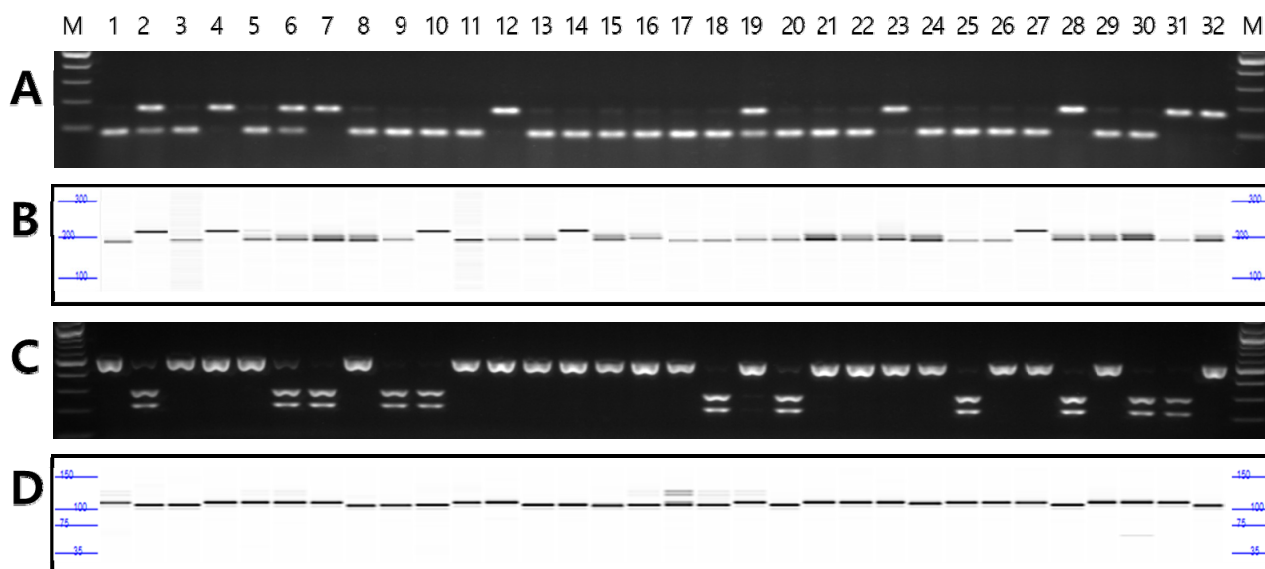
^yMeans with same letters in a column are not significantly different at $p < 0.05$ (ANOVA followed by DMRT).



Supplementary Fig. 1. Genetic map showing the LOD scores and locations of QTLs associated with yield-related traits in the population of 91 RILs derived from a cross between 'Chamdongjin' and 'Younghojinmi' across two years. A: heading date (HD), B: culm length (CL), C: panicle length (PL), D: number of panicles per hill (PN), E: number of spikelets per panicle (NS), F: 1,000-grain weight (TGW), G: brown/rough rice ratio (BRR). The red and green curves represent LOD scores for the years 2022 and 2023, respectively. The red and green horizontal lines and symbols indicate the positions and names of QTLs for the years 2022 and 2023, respectively.



Supplementary Fig. 2. Genetic map showing the LOD scores and locations of QTLs associated with grain-related traits in the population of 91 RILs derived from a cross between 'Chamdongjin' and 'Younghojinmi' across two years. A: grain length (GL), B: ratio of length to width (RLW). The red and green curves represent LOD scores for the years 2022 and 2023, respectively. The red and green horizontal lines and symbols indicate the positions and names of QTLs for the years 2022 and 2023, respectively.



Supplementary Fig. 3. Genotype of *Hd18* (A), *SD1* (B), *GS3* (C), and *OsTB1* (D). PCR analysis to confirm the allele type of parents and CY_RIL using gene specific DNA markers. *Hd18*, *SD1*, *GS3*, and *OsTB1* were confirmed by PCR product amplified with primer, Hd18_ID011 (HD18_AF, GF, R), sd1 (cleaved by *Sac* I), *GS3* (*Pst* I), and *OsTB1*_HRM, respectively. The genotypes of *SD1* and *OsTB1* were analyzed using capillary electrophoresis with the ZAG DNA analyzer system (Agilent Technologies, Santa Clara, CA, USA). M: size marker, 1: Chamdongjin, 2: Younghojinmi, 3-32: CY_RIL1-CY_RIL30.