

Supplementary Table 1. Descriptive statistics of yield and grain-related traits in the population of 89 RILs derived from a cross between 'Koshihikari' and 'IS592BB' across two years.

Year	Trait	Mean	SD ^y	CV (%)	median	min	max	range	skew	kurtosis	SE	Unimodality ^z	Bimodality
2023	HD ^z (DAS)	94.3	5.24	5.56	92.5	85.5	110.0	24.5	0.57	-0.52	0.56	FALSE	TRUE
	CL (cm)	82.4	6.82	8.28	81.8	63.4	98.9	35.5	0.17	-0.09	0.72	TRUE	FALSE
	PL (cm)	21.7	1.01	4.65	21.5	19.2	24.1	4.9	0.19	-0.42	0.11	TRUE	FALSE
	PN	11.3	0.88	7.78	11.4	8.6	13.0	4.4	-0.32	-0.17	0.09	TRUE	FALSE
	NS	124.0	21.26	17.15	121.9	79.4	183.9	104.5	0.50	-0.05	2.25	TRUE	FALSE
	TGW (g)	22.2	1.13	5.09	22.4	19.6	24.5	4.9	-0.14	-0.82	0.12	TRUE	FALSE
	RRG (%)	84.6	6.78	8.01	85.6	62.8	95.5	32.7	-0.96	0.58	0.72	FALSE	TRUE
	BRR (%)	79.7	1.23	1.54	79.7	75.7	82.8	7.0	-0.25	0.35	0.13	FALSE	TRUE
	Yield (g/plant)	25.4	3.94	15.50	25.1	18.6	36.4	17.7	0.41	-0.32	0.42	TRUE	FALSE
2024	HD (DAS)	94.4	5.80	6.14	94.0	84.5	109.5	25.0	0.51	-0.28	0.61	FALSE	TRUE
	CL (cm)	86.3	6.72	7.79	85.9	68.3	102.3	34.0	0.10	0.04	0.71	TRUE	FALSE
	PL (cm)	21.7	0.94	4.34	21.5	19.7	23.7	4.0	0.08	-0.48	0.10	FALSE	TRUE
	PN	11.3	1.01	8.93	11.2	8.4	15.2	6.8	0.50	2.06	0.11	TRUE	FALSE
	NS	124.9	20.24	16.21	124.1	86.9	192.9	106.0	0.76	0.73	2.15	TRUE	FALSE
	TGW (g)	21.5	1.11	5.16	21.6	19.2	23.3	4.1	-0.25	-0.98	0.12	FALSE	TRUE
	RRG (%)	77.7	7.57	9.74	79.4	56.2	89.4	33.2	-0.77	-0.07	0.80	FALSE	TRUE
	BRR (%)	78.4	1.27	1.62	78.6	75.0	81.3	6.3	-0.23	-0.28	0.13	TRUE	FALSE
	Yield (g/plant)	25.8	2.61	10.12	25.8	20.0	32.0	12.0	0.26	-0.14	0.28	TRUE	FALSE

^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, RRG: ratio of ripened grain, BRR: brown/rough rice ratio.

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

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

Supplementary Table 2. Chromosomal distribution and density of SNP markers polymorphic between 'Koshihikari' and 'IS592BB' used for QTL analysis.

Chr.	No. of markers	Chr. size (Mbp)	Marker density (markers/Mbp)
1	63	43.2	1.5
2	34	35.9	0.9
3	33	36.4	0.9
4	58	35.5	1.6
5	29	29.9	1.0
6	57	31.2	1.8
7	52	29.7	1.8
8	68	28.4	2.4
9	37	23	1.6
10	29	23.2	1.3
11	105	29	3.6
12	26	27.5	0.9
Total	591	372.9	1.6