

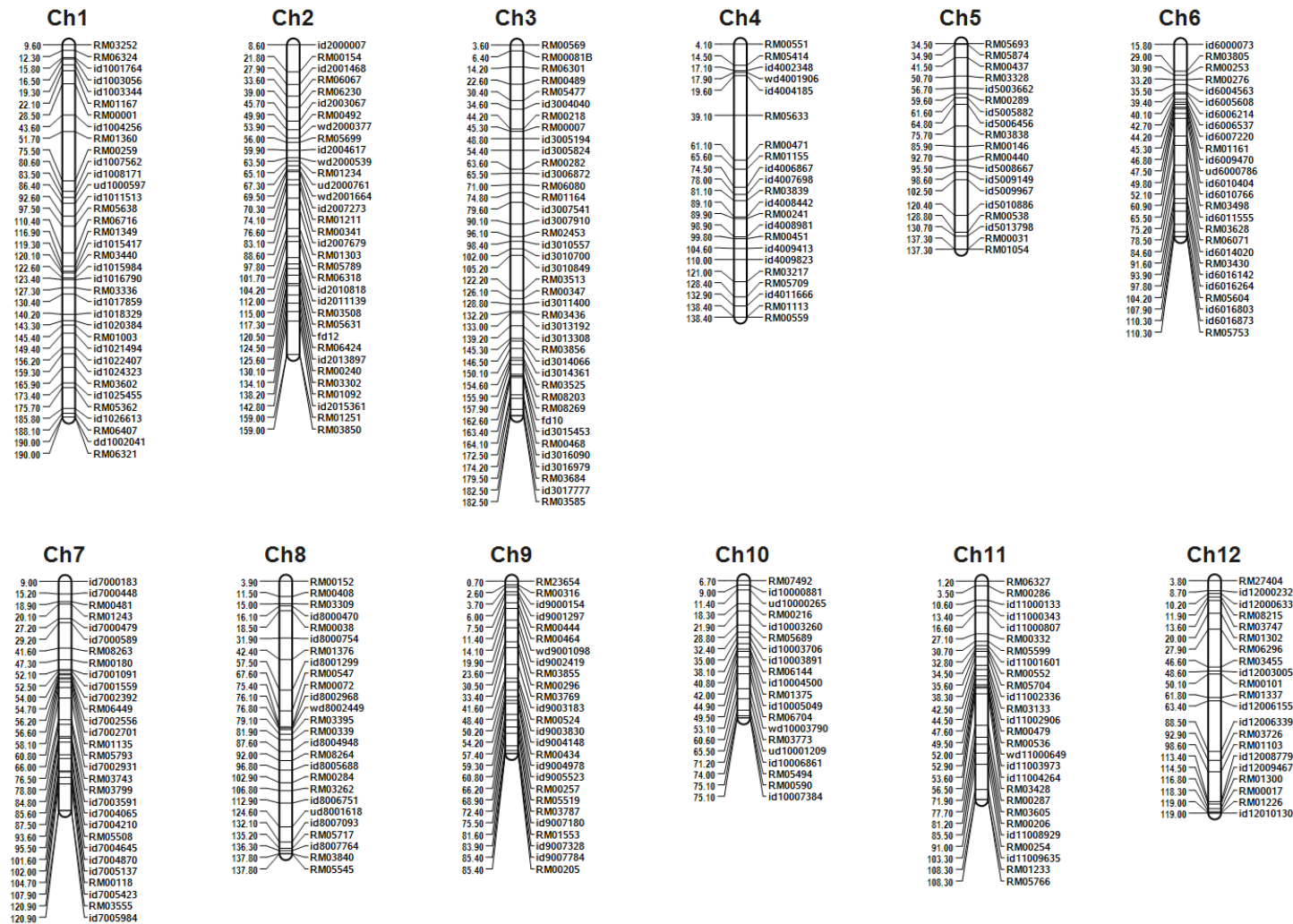


Figure S1. Linkage map from the Milyang23 × Giho RIL population using 168 SSR and 159 SNP markers. The numbers on the left of each chromosome indicate genetic distances (cM), and those on the right indicate the names of the markers.

Table S1. QTL for spikelet fertility and other agronomic traits under control condition without cold treatment determined by composite interval mapping.

Trait ^a	Chr.	Marker interval	Position (Mb) ^b	Position (cM)	LOD ^c	R ^{2d}	Additive effect ^e
SF (field)	6	id6004563–id6005608	7.1–8.7	36	2.7	9.3	-6.5
SF (pot)	4	wd4001906–id4004185	13.0–14.1	18	2.7	8.0	-3.9
DH	2	RM5699–id2004617	9.0–9.6	58	3.1	3.7	1.2
	3	RM8269–fd10	31.4–31.5	159	4.8	6.0	1.6
	4	id4011666–RM1113	33.5–34.3	134	3.9	4.9	1.4
	6	id6004563–id6005608	7.1–8.7	39	24.8	41.9	-8.5
CL	1	id1024323–RM3602	38.3–39.0	166	32.9	51.5	-9.9
	3	id3010849–RM3513	24.4–25.1	122	2.9	2.7	2.3
	6	id6014020–RM3430	26.0–27.4	87	4.8	5.1	3.2
	8	id8007764–RM3840	27.8–27.9	137	4.0	3.9	2.8
	10	RM1375–id10005049	16.7–17.6	43	8.2	8.3	-4.1
PL	1	RM1360–RM259	6.2–7.4	75	3.6	4.8	-0.5
	1	RM3440–id1015984	27.2–27.6	121	6.4	8.7	0.7
	1	RM3602–id1025455	39.0–40.0	173	3.4	4.5	-0.5
	2	RM5789–RM6318	22.4–24.4	102	4.6	6.0	-0.6
	3	RM7–id3005194	9.8–10.0	46	7.0	9.6	0.7
	3	id3011400–RM3436	27.1–27.4	130	3.7	4.9	0.5
	6	id6016264–RM5604	28.5–29.0	98	5.5	7.2	0.6
	7	RM180–id7001091	5.7–6.8	48	2.8	3.6	0.4
	8	RM8264–id8005688	19.8–20.8	96	8.4	12.3	-0.8
PEX	1	RM3602–id1025455	39.0–40.0	168	9.5	19.5	-1.7
	5	id5009967–id5010886	22.7–24.0	108	5.9	12.2	1.3
	5	id5013798–RM31	28.1–28.7	134	3.3	6.0	-0.9

^a Trait abbreviations are as follows. SF (field): spikelet fertility in the field as control; SF (pot): spikelet fertility in the pot experiment as control; DH: days to heading (d); CL: culm length (cm); PL: panicle length (cm); PEX: panicle exertion (cm). DH, CL, PL, and PEX were evaluated only in the field.

^b Os-Nipponbare-Reference-IRGSP 1.0.

^c LOD experiment-wise $P=0.05$ was equivalent to the critical LOD score threshold of 2.5.

^d Percent phenotypic variance explained by the QTL.

^e Negative values indicate additive effects from Giho.

Chromosomal regions highlighted in bold were identified in both the control and cold-water-irrigated plots (see Table 6 and Fig. 2).