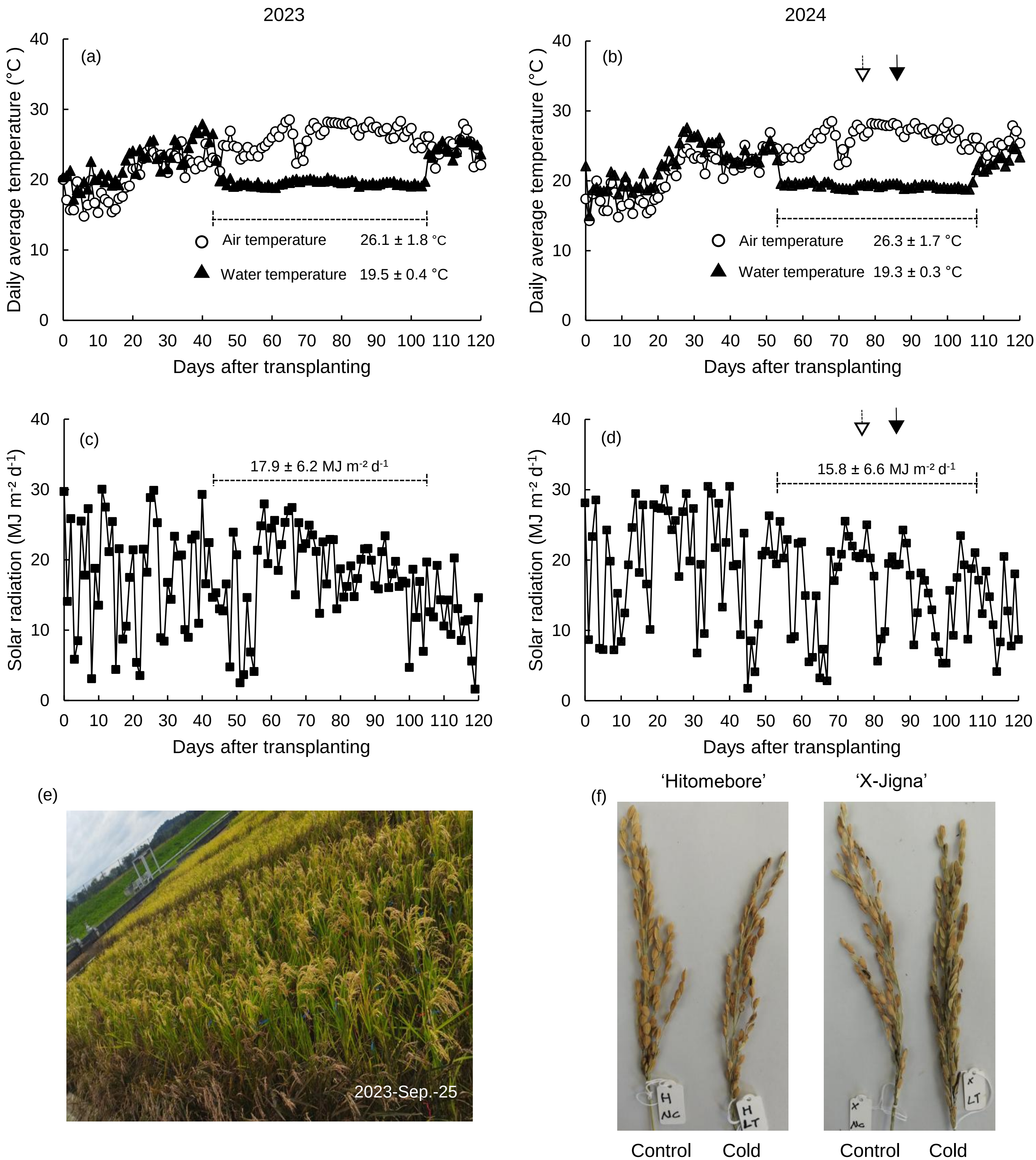
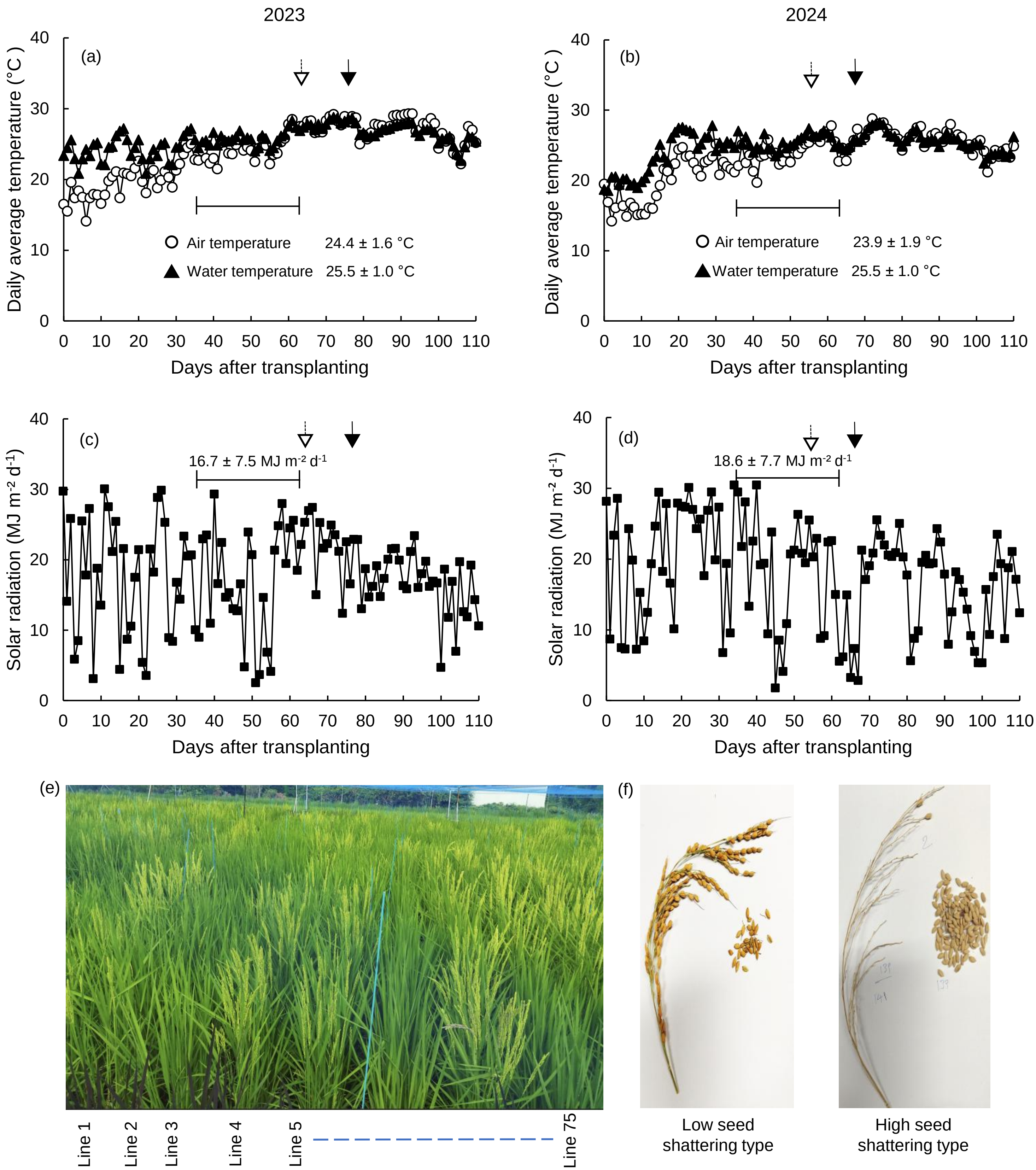
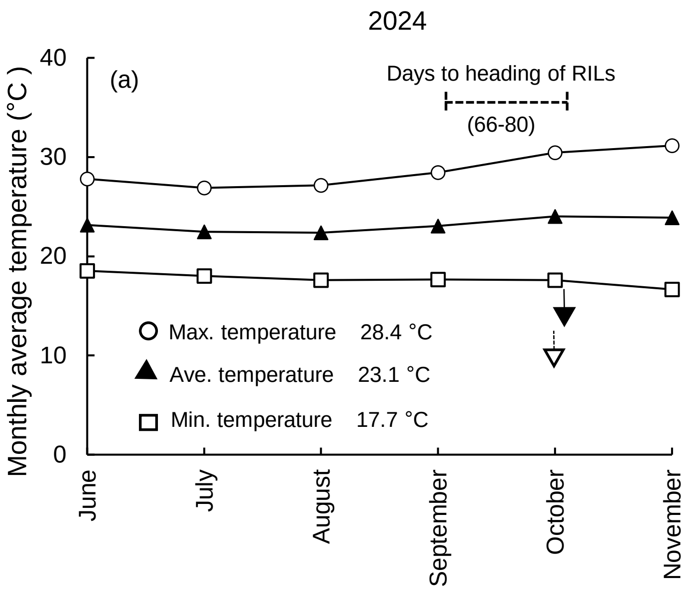


Supplementary Fig. S1. a–d) Daily changes in (a, b) air and water temperatures and in (c, d) solar radiation in (a, c) 2023 and (b, d) 2024; ¦- - -¦ average temperature and solar radiation during cold treatment period (mean ± SD). Arrowheads indicate days to heading of parents: ▽ 'X-Jigna', ▼ 'Hitomebore'. (e) Evaluation of rice RILs and parents under cold irrigation water (19.5 ± 0.4 °C) during the reproductive stage in 2023 at Kitakami, Iwate, Japan. (f) Panicle spikelet fertility of parents

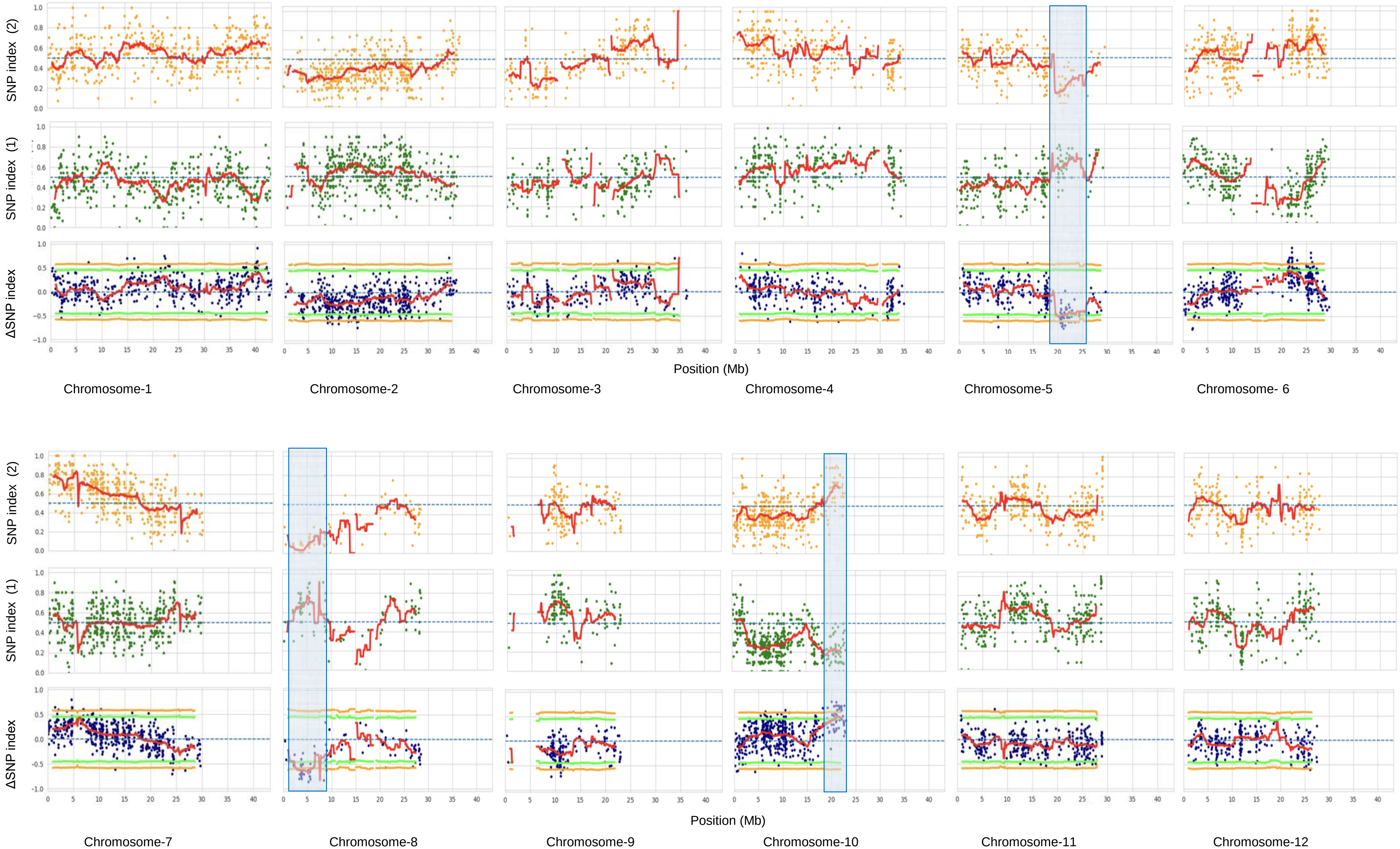


Supplemental Fig. S2. (a–d) Daily changes in (a, b) air and water temperatures and in (c, d) solar radiation in (a, c) 2023 and (b, d) 2024; |—| average temperature and solar radiation (mean ± SD) during reproductive period (30 days before heading of 'X-Jigna'). Arrowheads indicate days to heading of parents: ▽ 'X-Jigna', ▼ 'Hitomebore'. (e) Evaluation of 846 F_5 RILs and parents under normal growing conditions at Morioka, Iwate, Japan. (f) Panicle threshability.

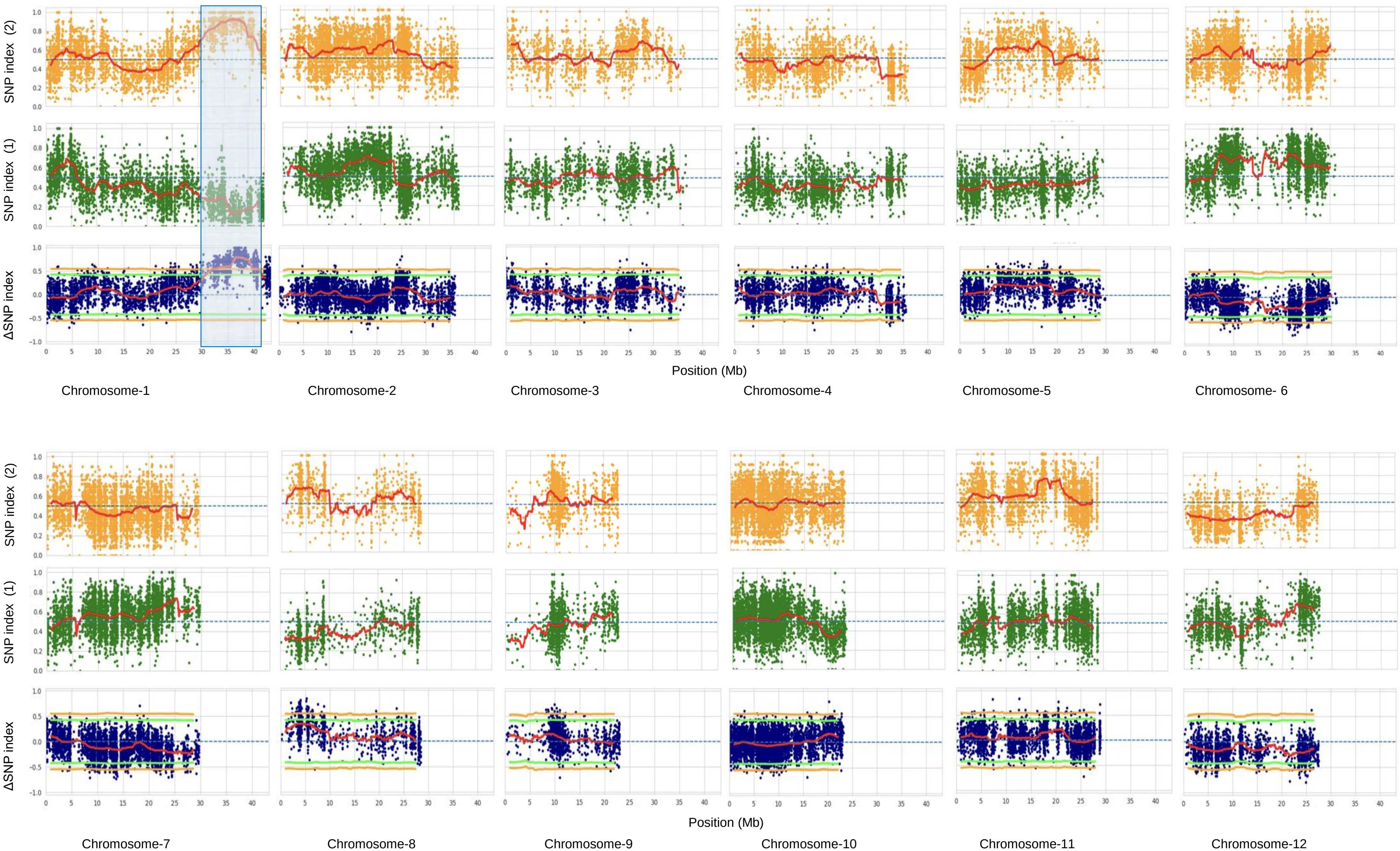


(b)

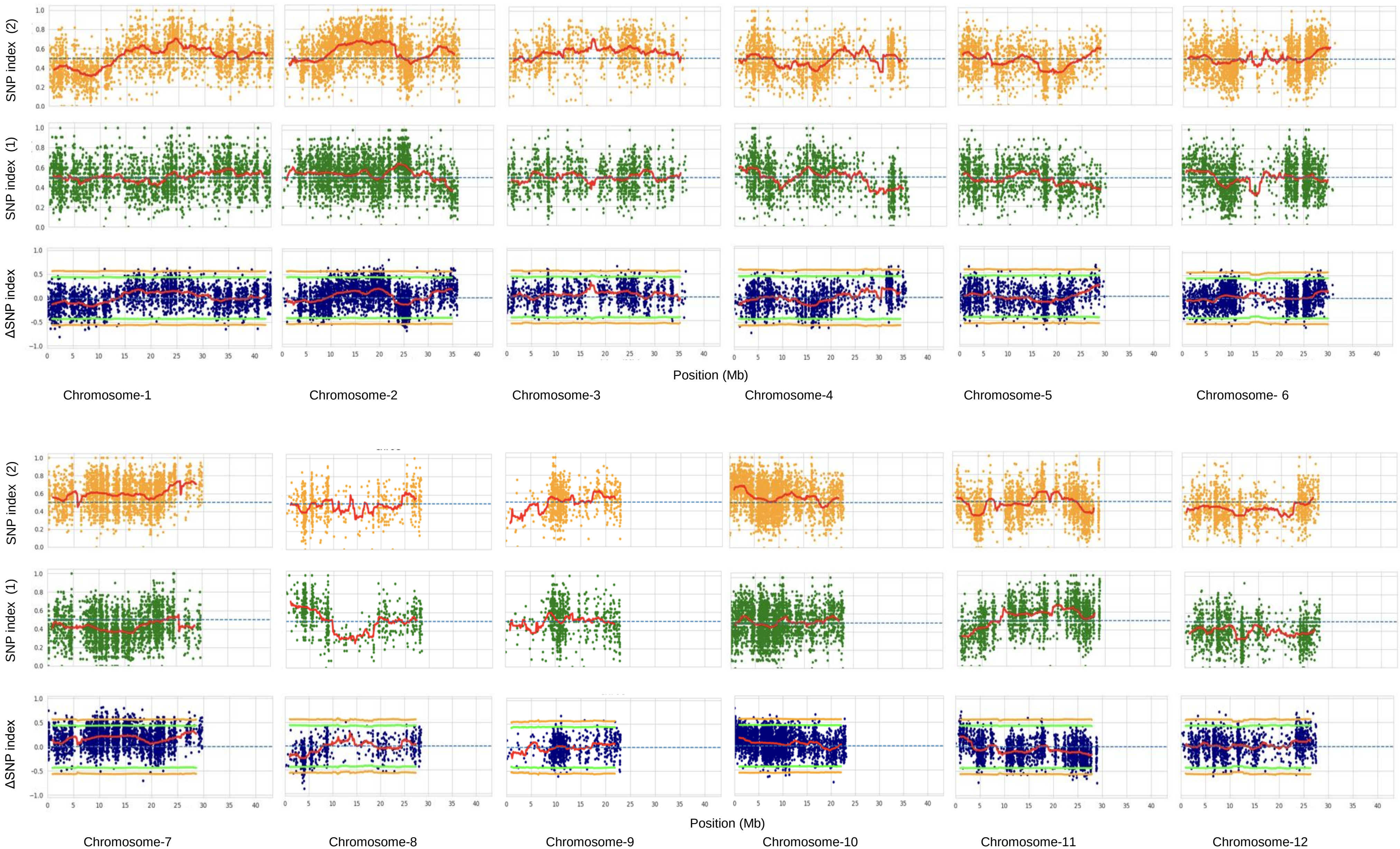
Supplemental Fig. S3. (a) Monthly temperatures during reproductive stage (30 days before heading of 'X-Jigna') in Fogera, Ethiopia; arrowheads indicate days to heading of parents: ▽ 'X-Jigna' (1 Oct 2024), ▼ 'Hitomebore' (2 Oct 2024). ¦- - -¦ Heading dates of RILs: 27 Sep – 11 Oct 2024. (b) Evaluation of 52 F_6 rice RILs and parents.



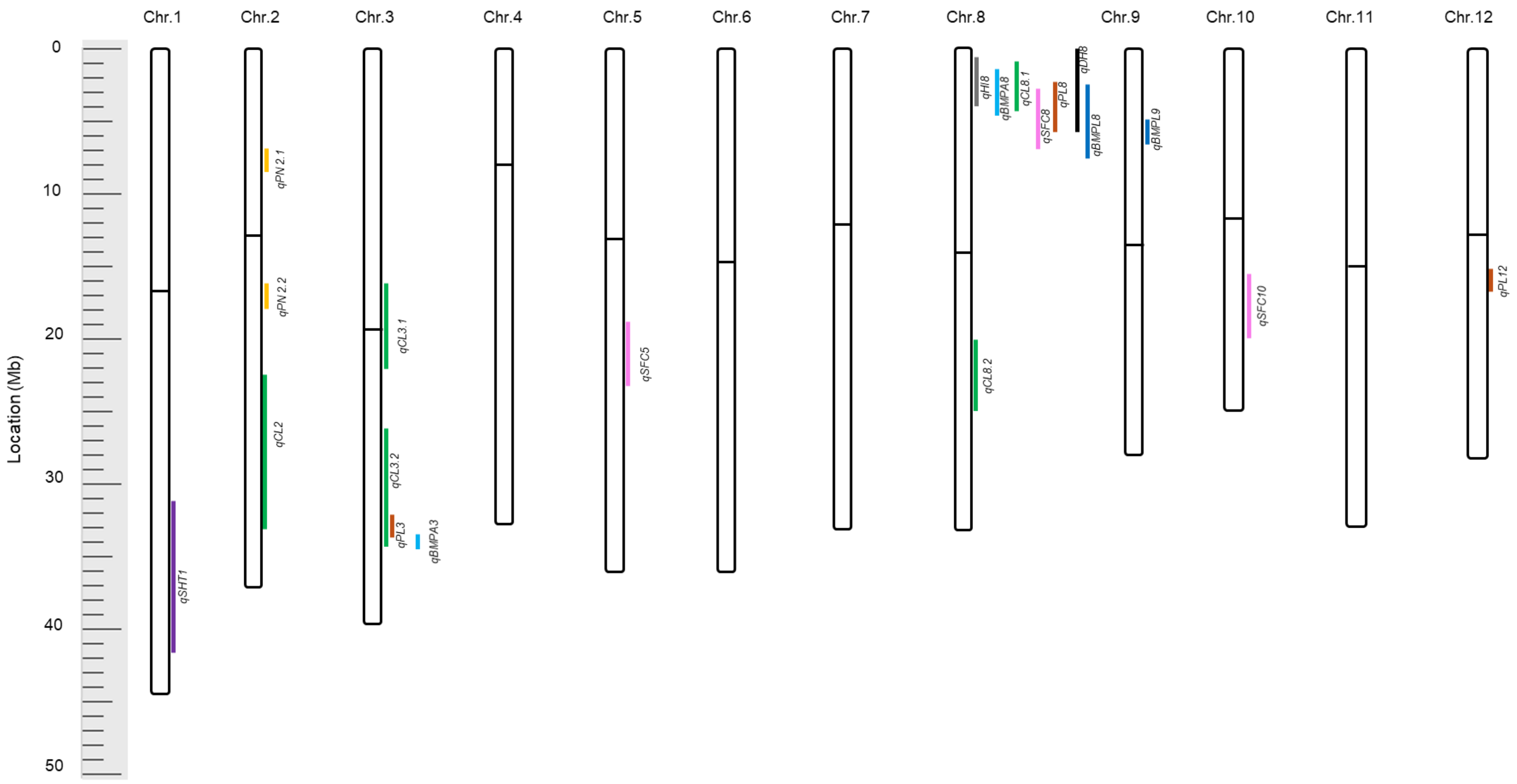
Supplemental Fig. S4. QTL mapping through QTL-seq approach for rice spikelet fertility (*qSFC5 (*20.0–20.4 Mb); *qSFC8 (*2.4–7.4 Mb); *qSFC10 (*20.7–21.9 Mb)) using 846 F_5 RILs of 'X-Jigna' × 'Hitomebore' under cold irrigation water at Iwate in 2023. SNP indexes 1 and 2 identify the low and high spikelet fertility bulks, respectively; ΔSNP index is the difference between the two bulks. Colored horizontal bars indicate statistical confidence intervals: green, *P* < 0.05; orange; *P* < 0.01. The rectangle highlighted region indicates the detected QTL region.



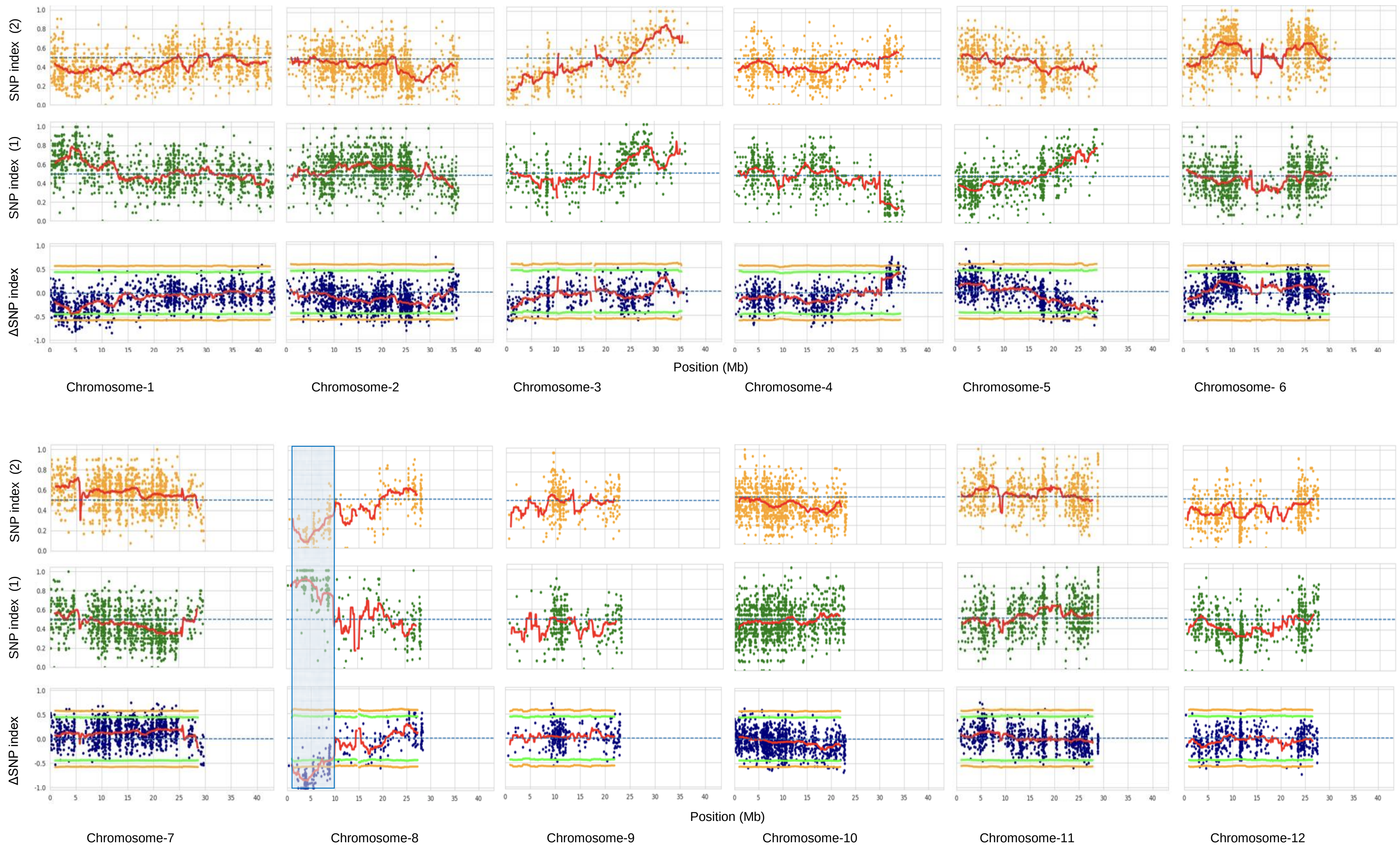
Supplementary Fig. S5. QTL mapping through QTL-seq approach for seed shattering in rice (*qSHT1* (30.8- 41.5 Mb) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and high seed shattering bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively



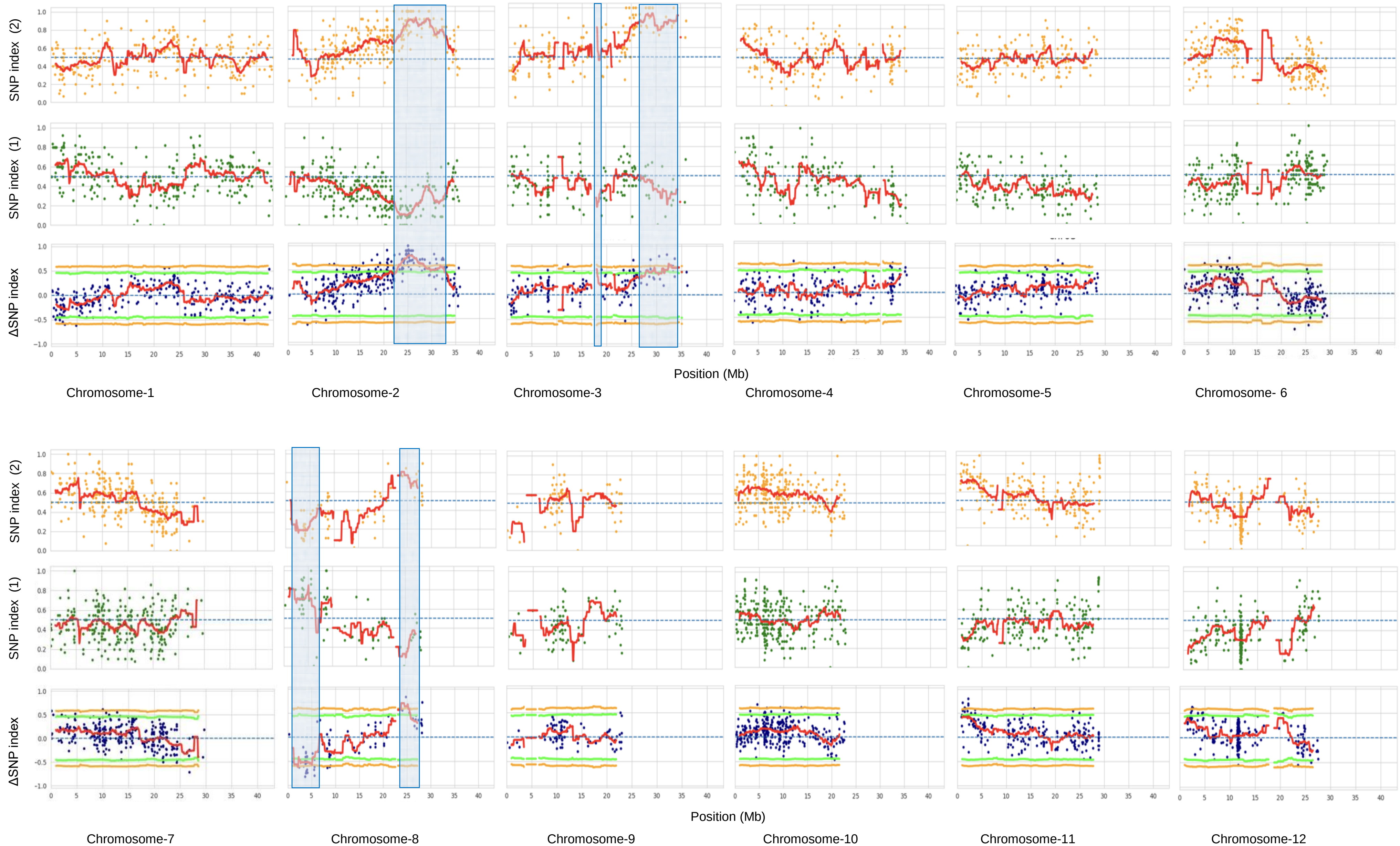
Supplementary Fig. S6. QTL mapping through QTL-seq approach for grain yield per plant in rice (No QTL is detected) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at *P* < 0.05 and *P* < 0.01, respectively



Supplementary Fig. S7. QTLs for nine agronomic traits (*qSHT* = seed shattering, *qPN* = panicle number, *qCL* = culm length under normal condition, *qPL* = panicle length, *qDH* = days to heading, *qSFC* = spikelet fertility under cold condition, *qBMPA* = biomass per panicle, *qHI* = harvest index, *qCLC* = culm length cold, *qBMPL* = biomass per plant) identified by QTL-seq analysis of 846 F_5 RILs of 'X-Jigna' × 'Hitomebore' at Iwate, Japan, in 2023.

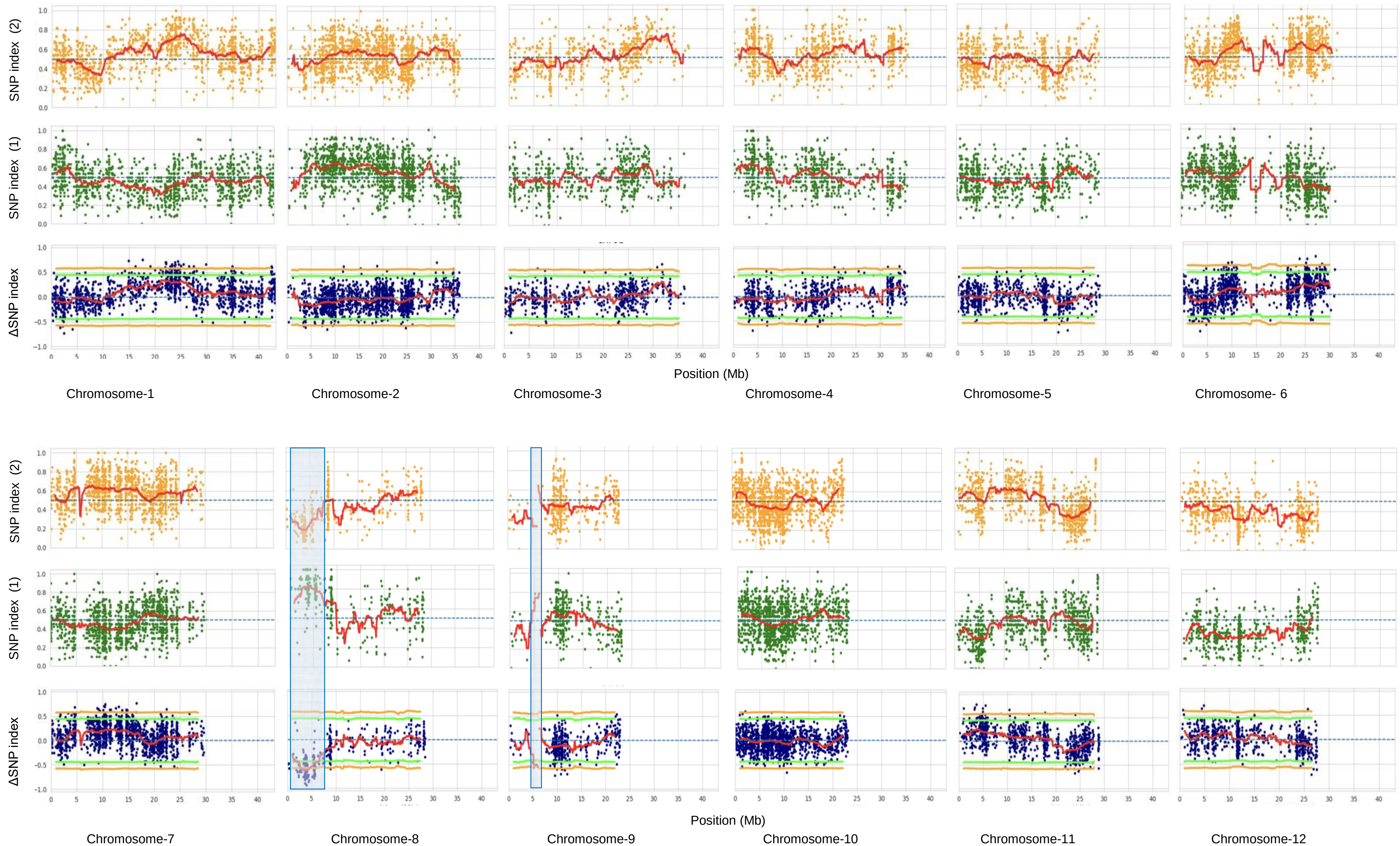


Supplementary Fig. S8. QTL mapping through QTL-seq approach for days to heading in rice (*qDH8* (1-9 Mb) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively

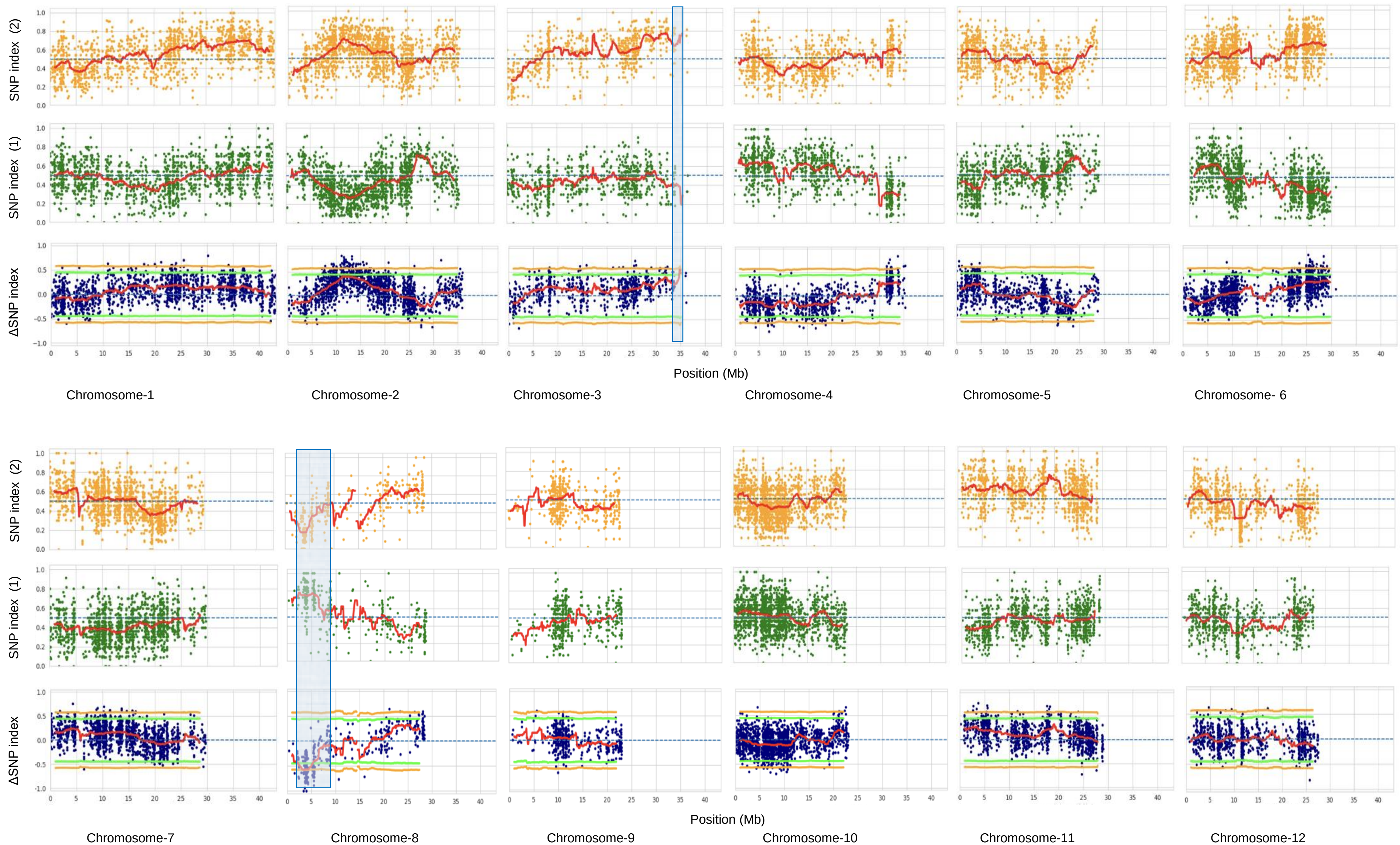


Supplementary Fig. S9. QTL mapping through QTL-seq approach for culm length in rice (*qCL2* (21.3-32.6 Mb), *qCL3.1* (18-21.6 Mb), *qCL3.2* (27.8-35.1Mb), *qCL8.1* (1.3-5.1 Mb), *and qCL8.2* (23.1-25.7Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at P < 0.05 and P < 0.01, respectively

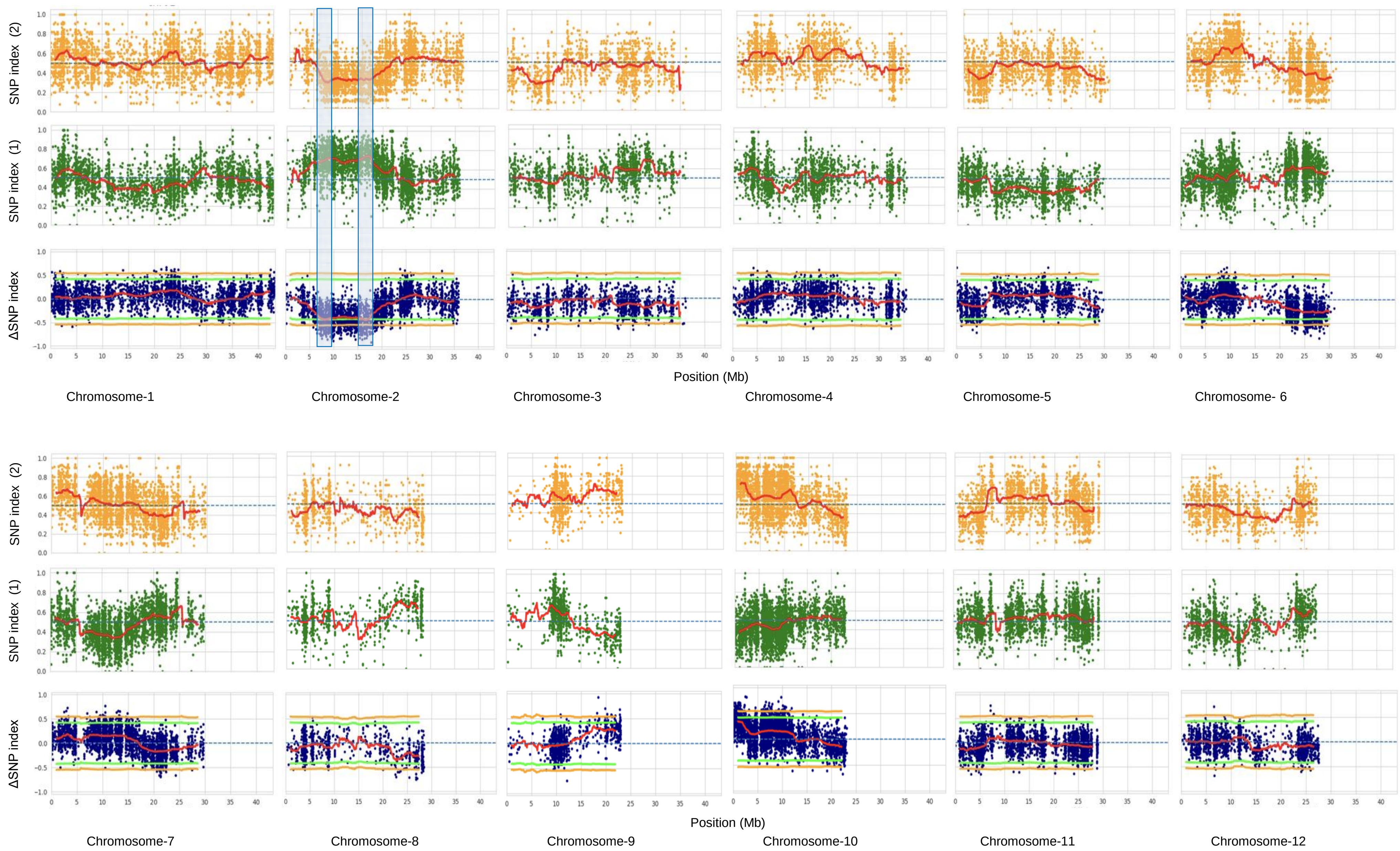
Supplementary Fig. S10. QTL mapping through QTL-seq approach for panicle length in rice through the QTL-seq approach (*qPL3* (33.1-34.6 Mb), *qPL8* (1.6- 7.1Mb), and *qPL12* (17.5- 18Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively



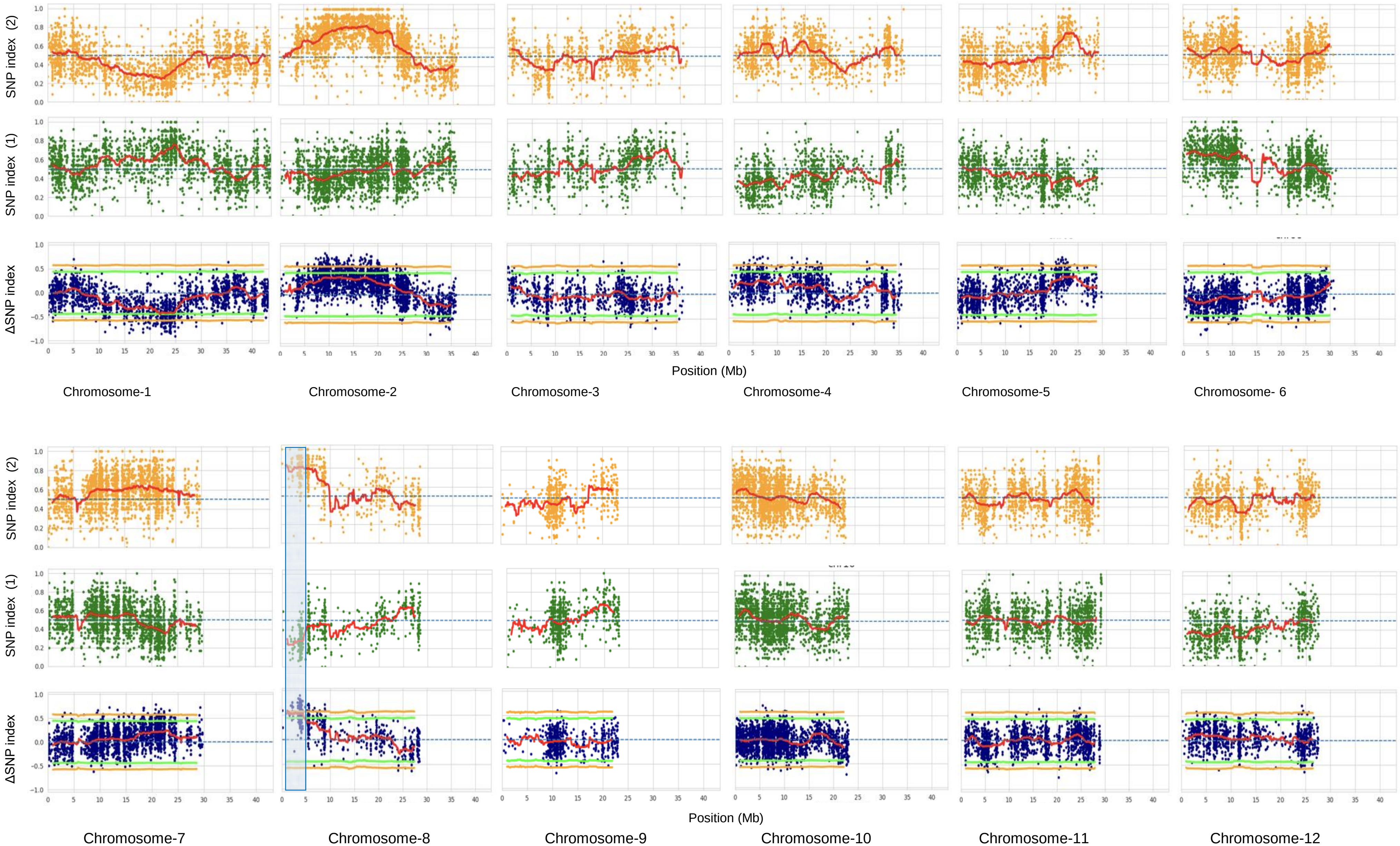
Supplementary Fig. S11. QTL mapping through QTL-seq approach for biomass per plant in rice (*qBMPL8* (1.6-6.5 Mb), *qBMPL9* (5.2-6.1 Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively



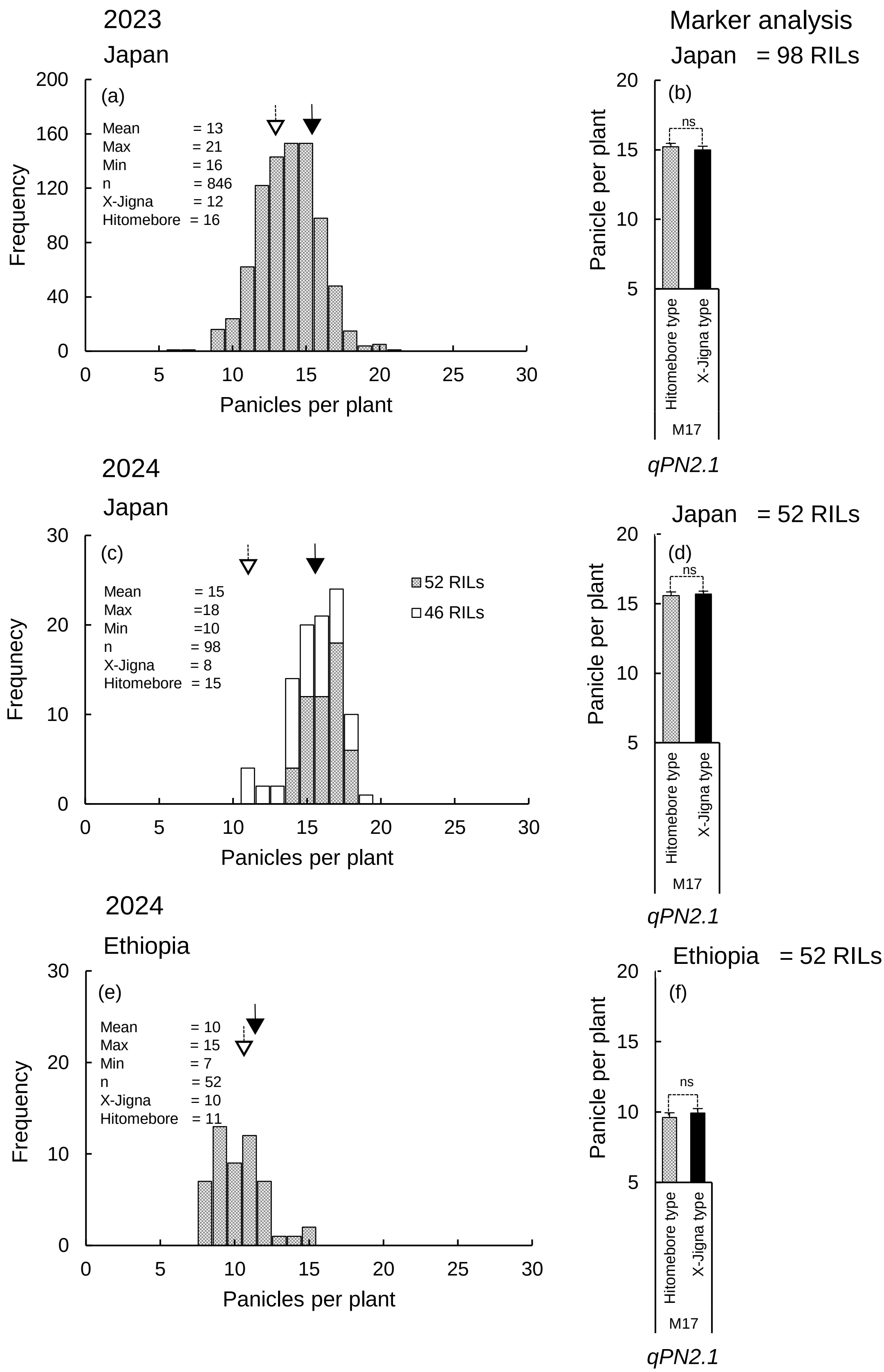
Supplementary Fig. S12. QTL mapping through QTL-seq approach for biomass per panicle in rice (*qBMPA3* (34.8-35.1 Mb) and *qBMPA8* (2.2 -5.2 Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at *P* < 0.05 and *P* < 0.01, respectively



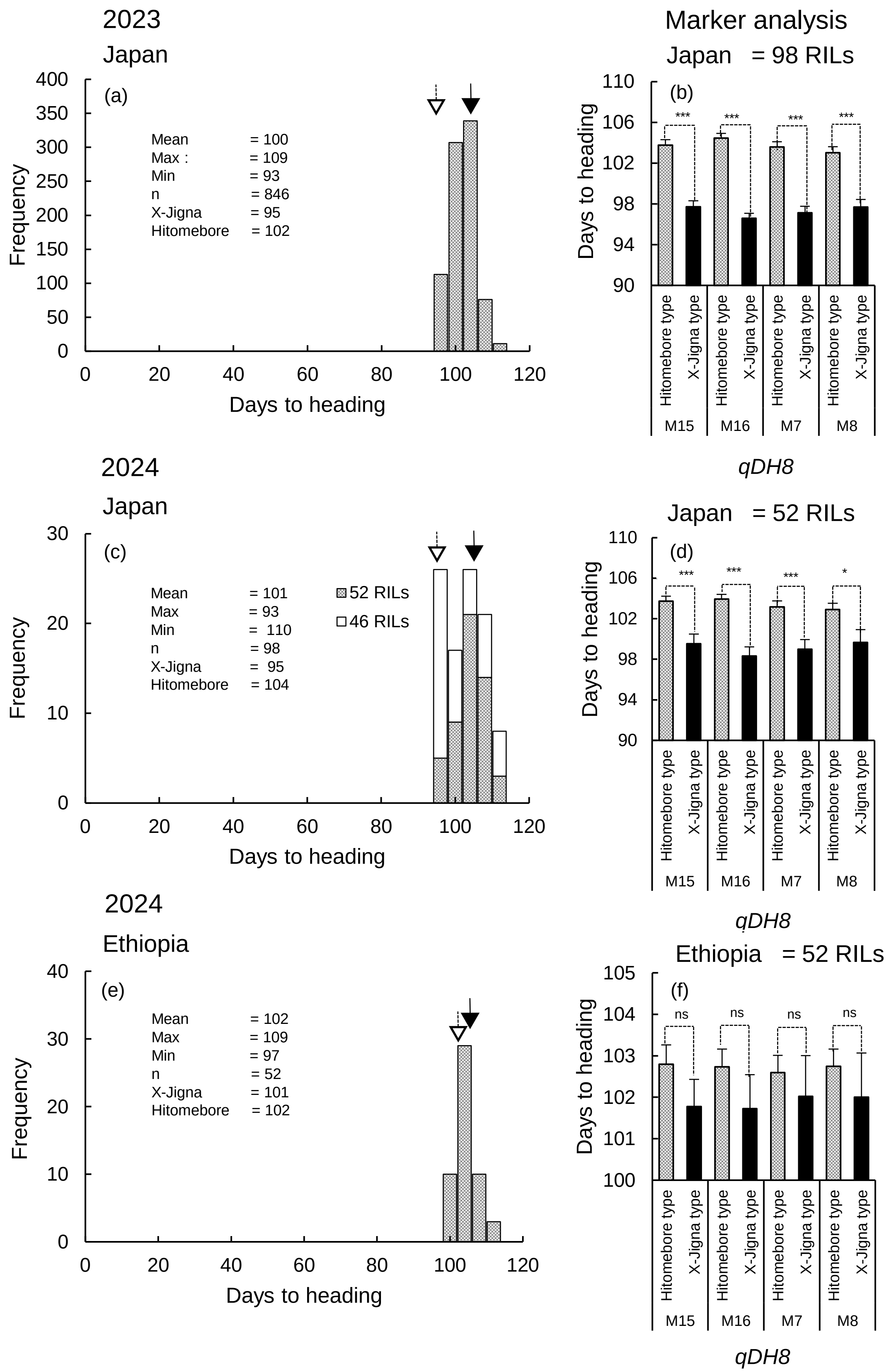
Supplementary Fig. S13. QTL mapping through QTL-seq approach for panicle number in rice through the QTL-seq approach (*qPN2.1* (8.1-8.4 Mb) and *qPN2.2* (16.1-17.1 Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively



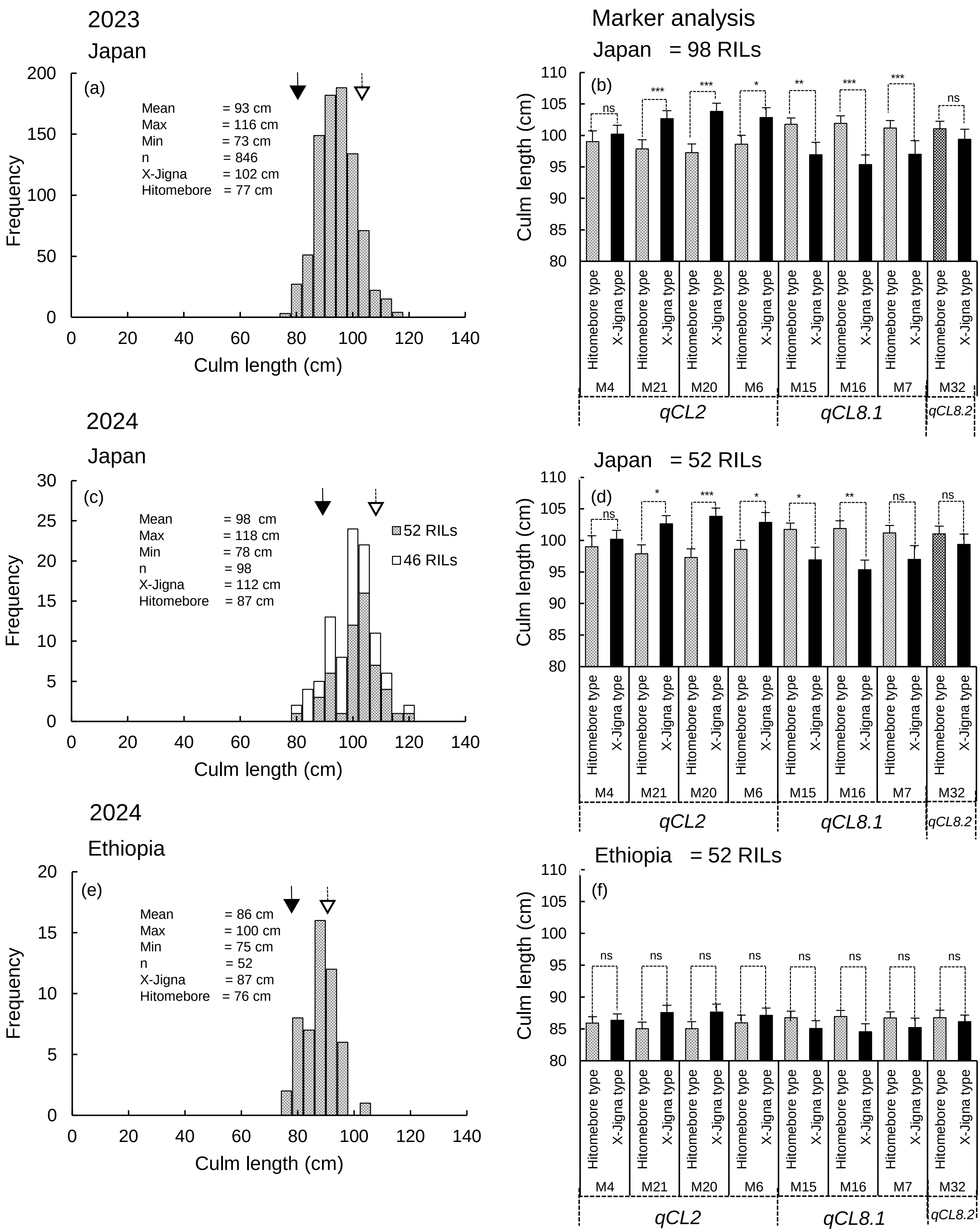
Supplementary Fig. S14. QTL mapping through QTL-seq approach for harvest index in rice (*qHI8* (1.0- 4.7 Mb)) using 846 F_5 RILs developed from 'X-Jigna' and 'Hitomebore' at Iwate, Japan, in 2023. SNP index1 and SNP index2 refer to the low and the high spikelet fertility bulks, respectively, while ΔSNP index refers to the difference between the two bulks. The green and orange lines indicate statistical confidence intervals at $P < 0.05$ and $P < 0.01$, respectively



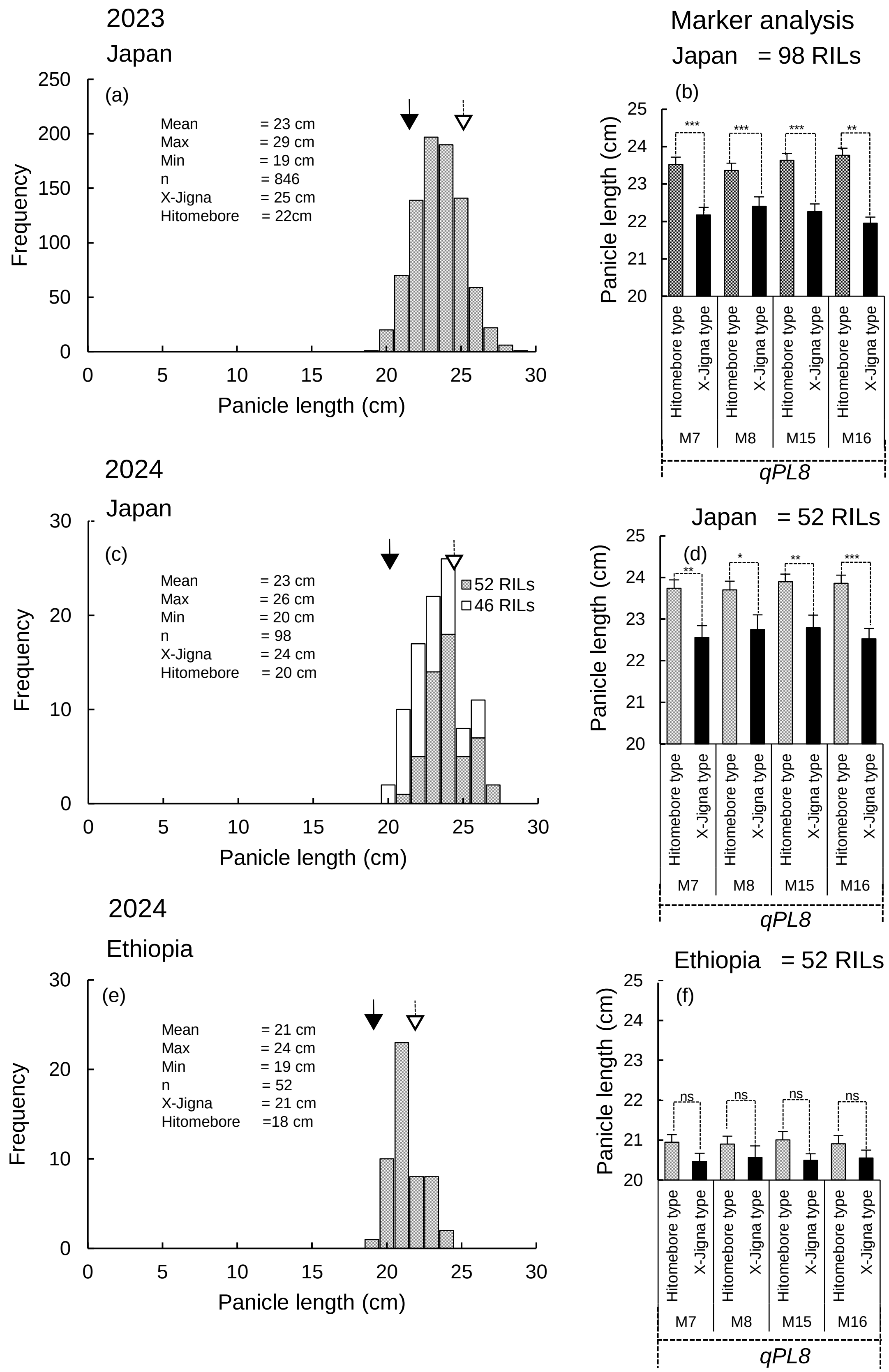
Supplementary Fig. S15. Histograms of rice RILs developed from 'X-Jigna' and 'Hitomebore' for panicles per plant in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = 'Hitomebore', ns refers to non-significant, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical with the RILs in Ethiopia



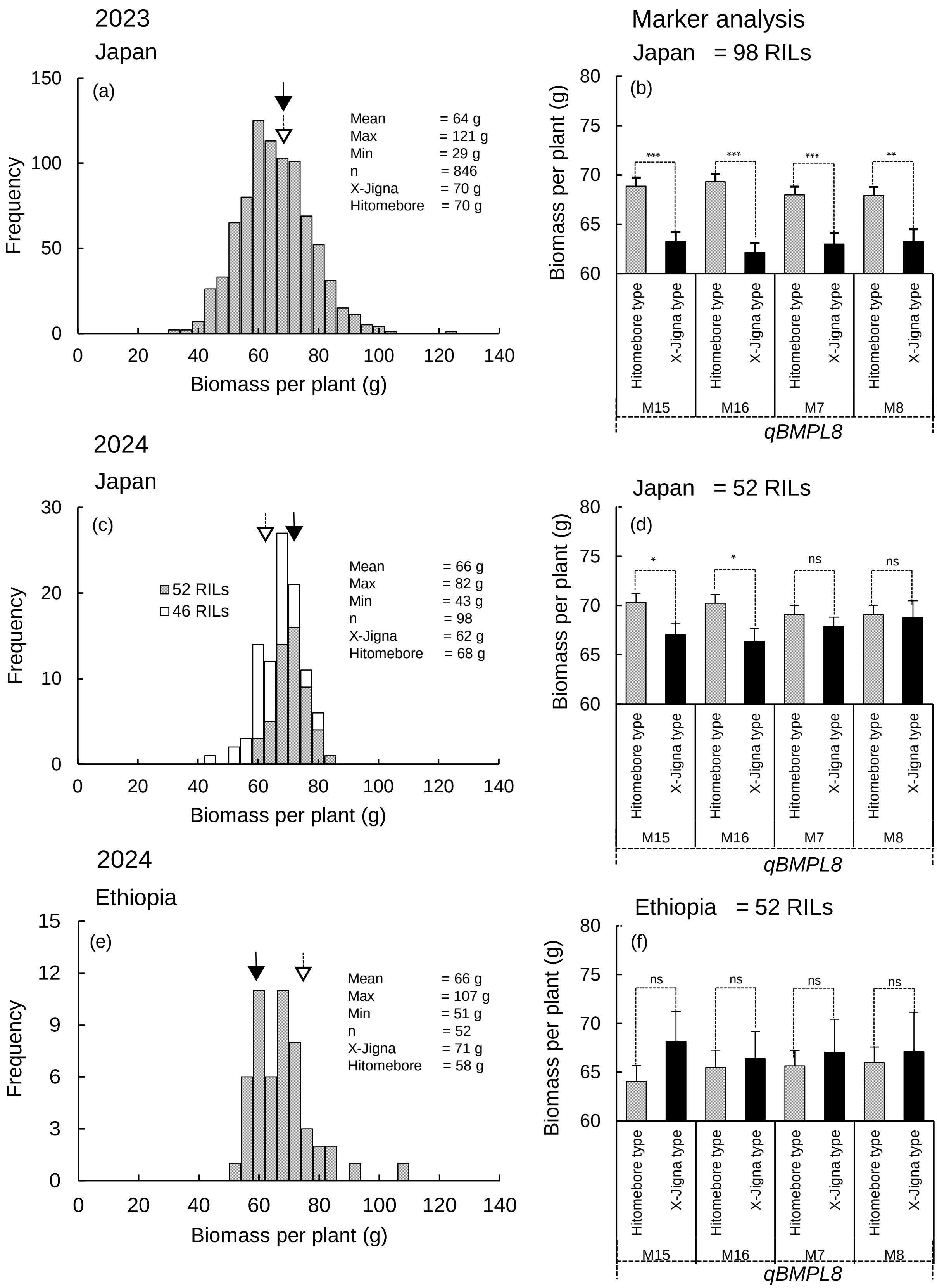
Supplementary Fig. S16. Histograms of rice RILs developed from ‘X-Jigna’ and ‘Hitomebore’ for days to heading in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = ‘Hitomebore’, *, *** and ns refers significant level at p<0.05, p<0.001 and non-significant respectively, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical to the RILs in Ethiopia



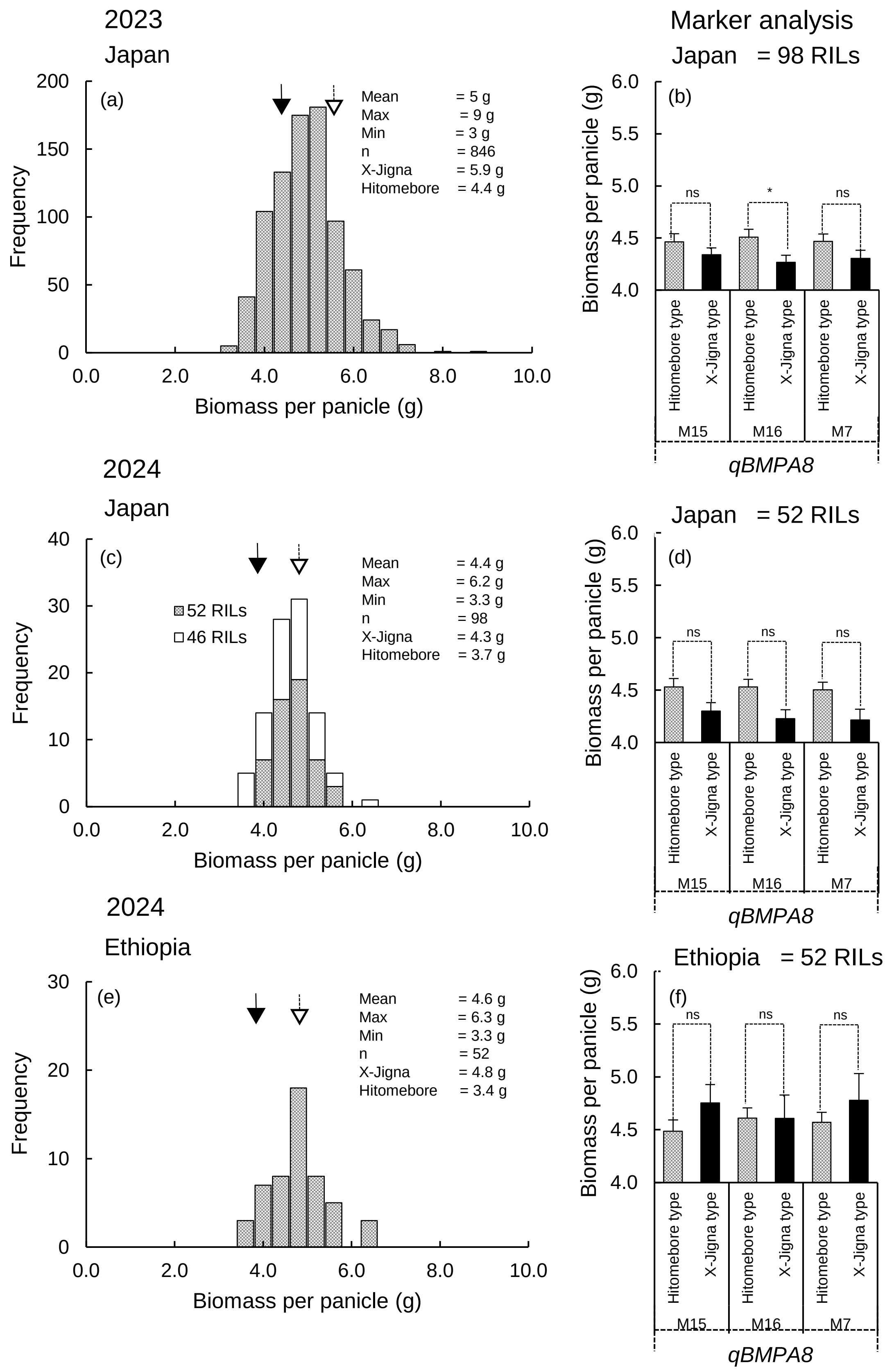
Supplementary Fig. S17. Histograms of rice RILs developed from 'X-Jigna' and 'Hitomebore' for culm length (cm) in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = 'Hitomebore', *, **, *** and ns refers significant level at p<0.05, p<0.01, p<0.001 and non-significant respectively, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical to the RILs in Ethiopia



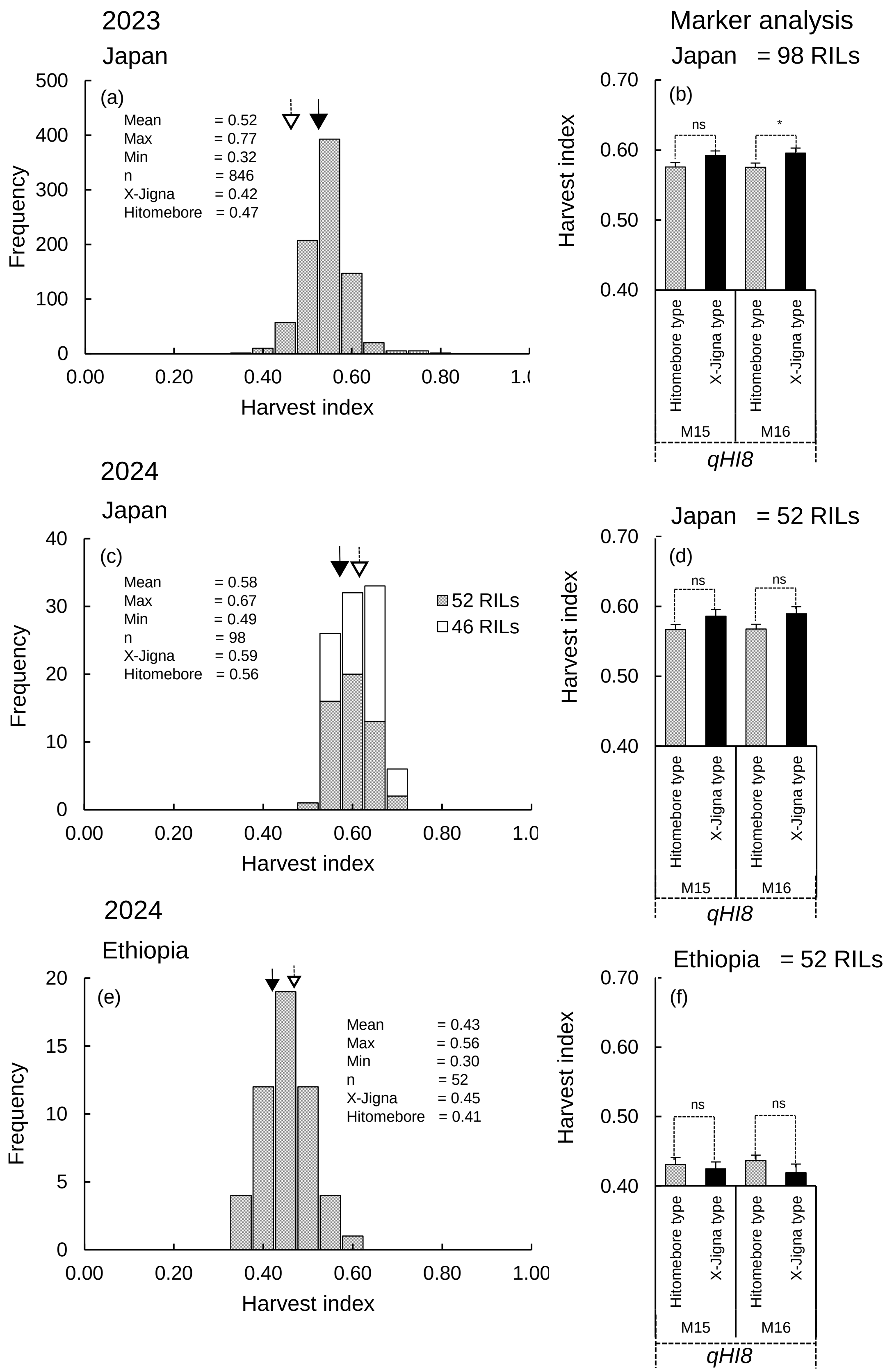
Supplementary Fig. S18. Histograms of rice RILs developed from ‘X-Jigna’ and ‘Hitomebore’ for panicle length (cm) in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = ‘Hitomebore’, *, **, *** and ns refers significant level at p<0.05, p<0.01, p<0.001 and non-significant respectively, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical to the RILs in Ethiopia



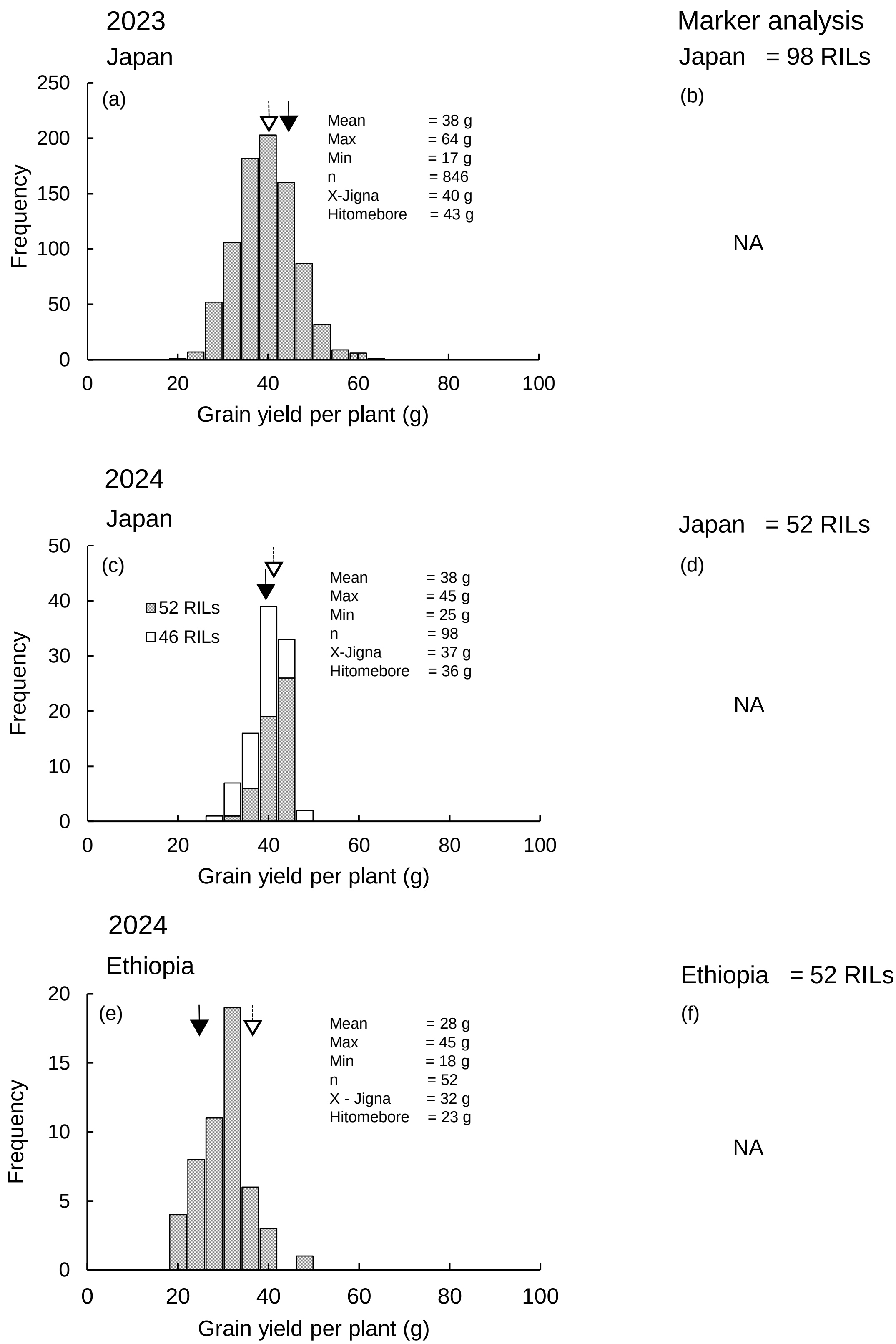
Supplementary Fig. S19. Histograms of rice RILs developed from ‘X-Jigna’ and ‘Hitomebore’ for biomass per plant (g) in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = ‘Hitomebore’, *, and ns refers significant level at p<0.05, and non-significant respectively, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical with the RILs in Ethiopia



Supplementary Fig. S20. Histograms of rice RILs developed from 'X-Jigna' and 'Hitomebore' for biomass per panicle (g) in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = 'Hitomebore', ns refers to non-significant, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical with the RILs in Ethiopia



Supplementary Fig. S21. Histograms of rice RILs developed from ‘X-Jigna’ and ‘Hitomebore’ for harvest index in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = ‘Hitomebore’, ns refers non-significant, (b), (d), and (f) are QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical to the RILs in Ethiopia



Supplementary Fig. S22. Histograms of rice RILs developed from ‘X-Jigna’ and ‘Hitomebore’ for grain yield per plant (g) in 2023 (a), and 2024 (c), Iwate, Japan, and, in 2024 (e), Fogera, Ethiopia, arrow heads indicate days to heading of parents: white = X-Jigna, black = ‘Hitomebore’, and NA = data not available for (b), (d), and (f) QTL-confirmation through InDel marker developed in the peak regions of the ΔSNP index in QTL-seq analysis, QTL-seq confirmation through InDel marker was conducted in Japan for 98 RILs (b) and 52 RILs (d), and Ethiopia for 52 RILs (f). The 52 RILs in Japan are identical to the RILs in Ethiopia