Additional file 1.

Supplementary Information for

Identification of genomic regions for deep-water resistance in rice for efficient weed control with reduced herbicide use

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This PDF file includes:
Figs. S1 to S9.

Tables S1 to S6 are included in the **Additional file 2**.

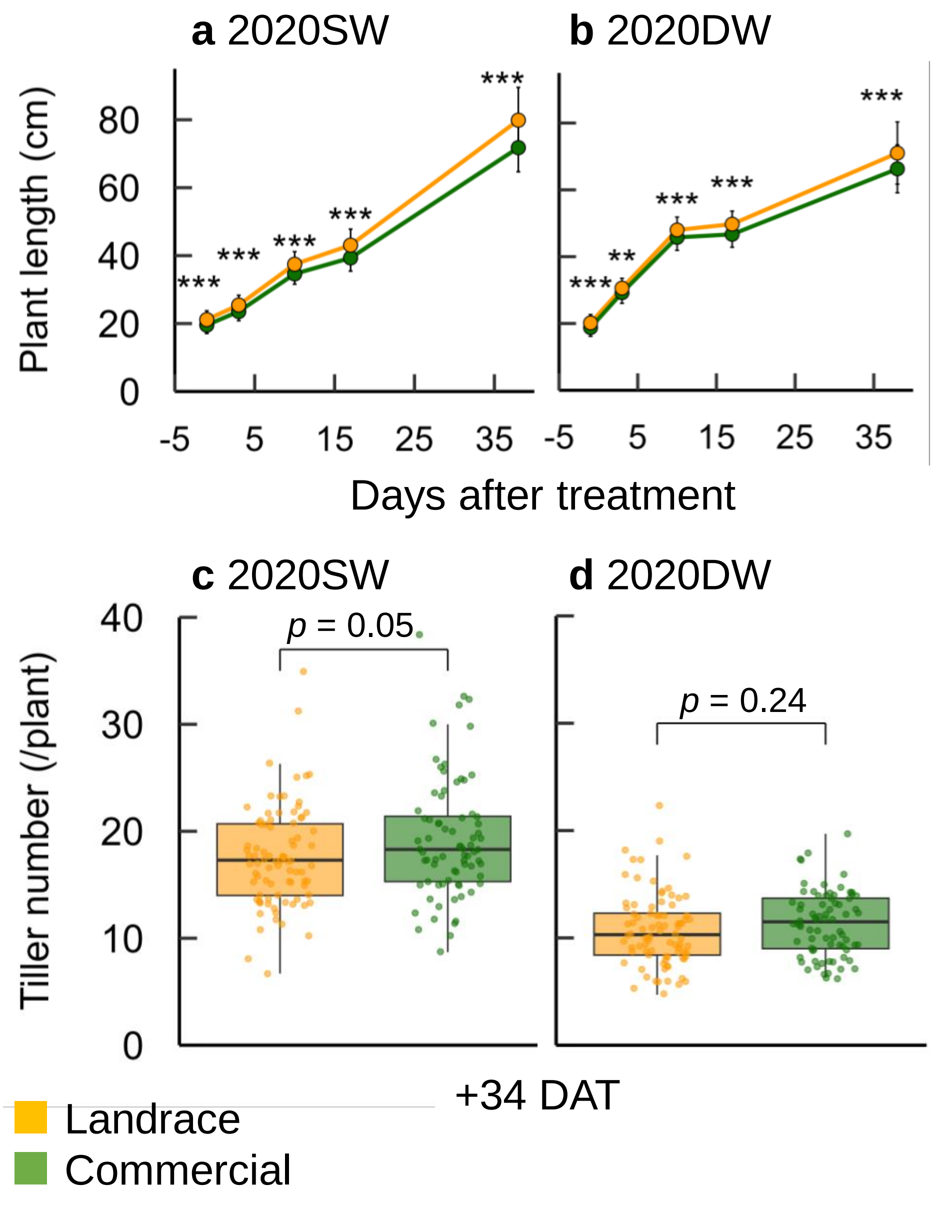

Figure S1.
Plant length (PL) and tiller number (TN) during the water treatments in 2020.

a,b: Changes of PL under shallow-water (SW) and deep-water (DW) of 165 temperate *japonica* varieties.

c,d: Changes of TN under SW and DW of 165 temperate *japonica* varieties.

Data are represented as mean ± SD (n = 3) of either landraces (yellow) or commercials (green). Differences between landraces and commercials were analyzed by Welch's t-test (*: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$).

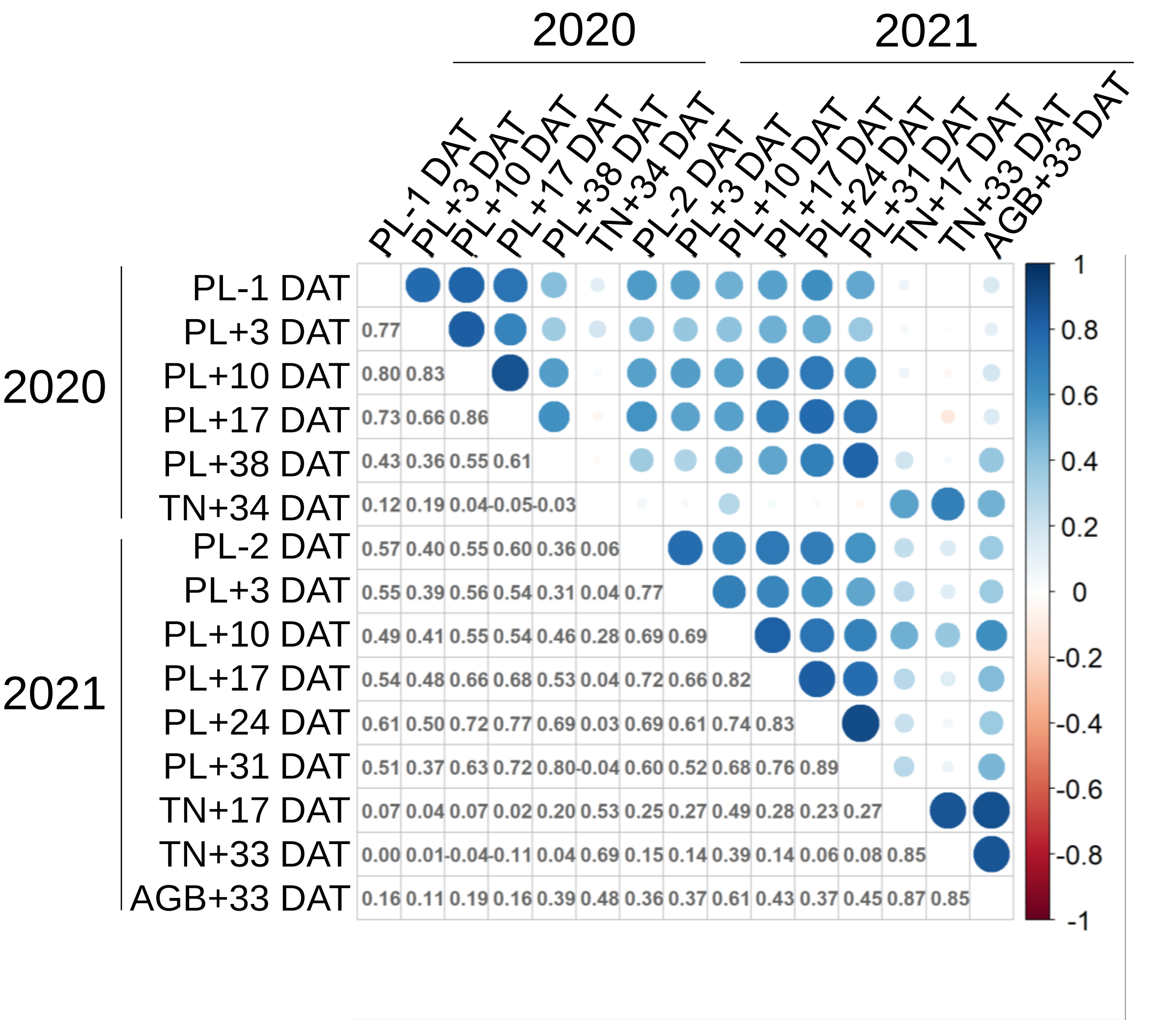

Figure S2.
Pearson's correlation matrix for the traits under deep-water (DW) between 2020 and 2021.
The traits that analyzed are plant length (PL), tiller number (TN), and above-ground biomass (AGB). Numbers on the lower triangular matrix indicate correlation between traits. The size of circle indicates the strength of correlation and blue indicates positive correlation (r = 1). DAT: days after treatment.

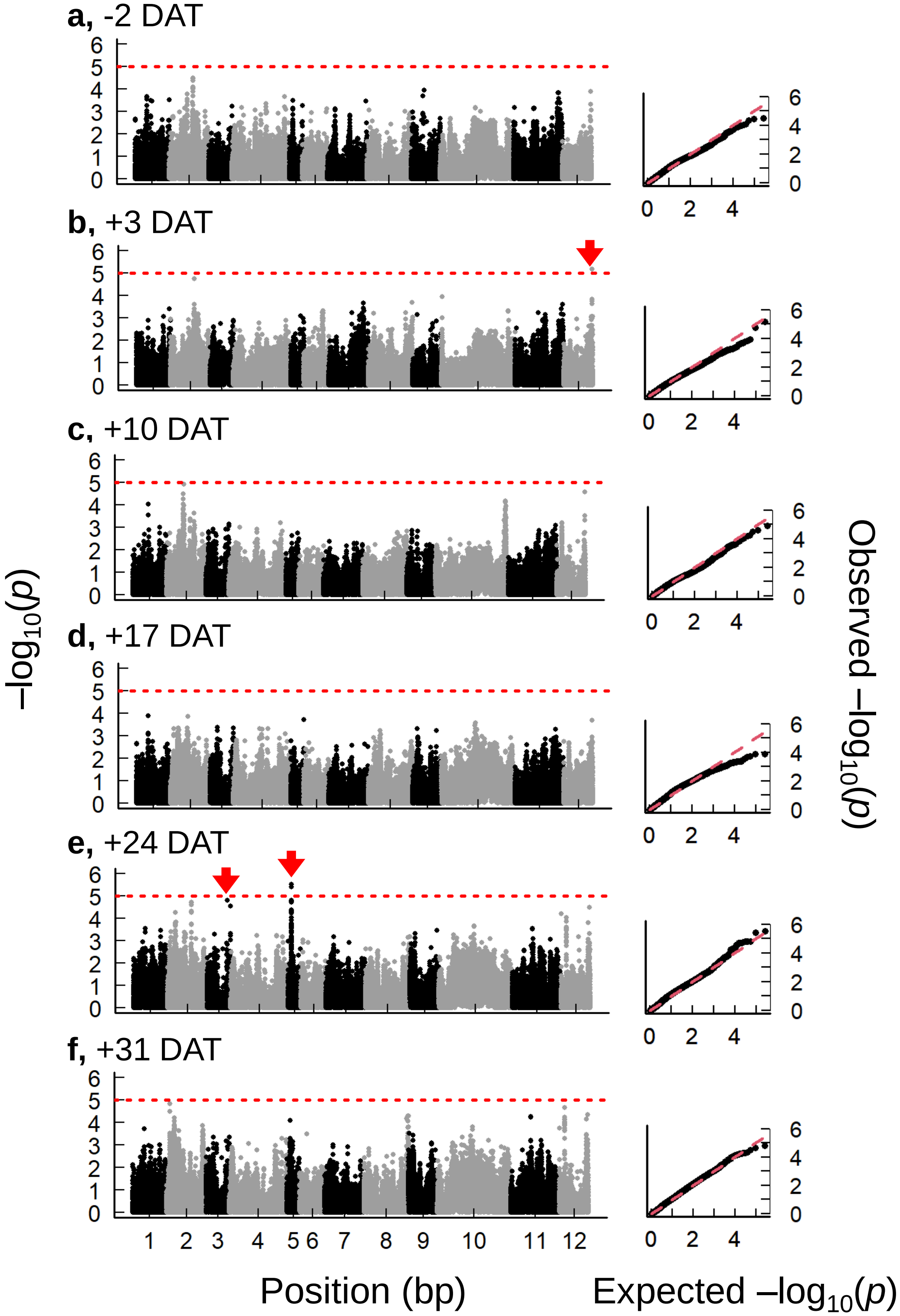

Figure S3.
Manhattan plots and quantile-quantile (Q-Q) plots of plant length (PL) under deep-water (DW) in 2021.
(**a**) -2 days after treatment (DAT): (**b**) +3 DAT: (**c**) +10 DAT: (**d**) +17 DAT: (**e**) +24 DAT: (**f**) +31 DAT in 2021. The x-axis indicates the SNPs or indels that physically mapped on each chromosome. The red arrows indicate the candidate region. The red dashed lines indicate the threshold lines ($-\log_{10}(p) = 5$) set in this study.

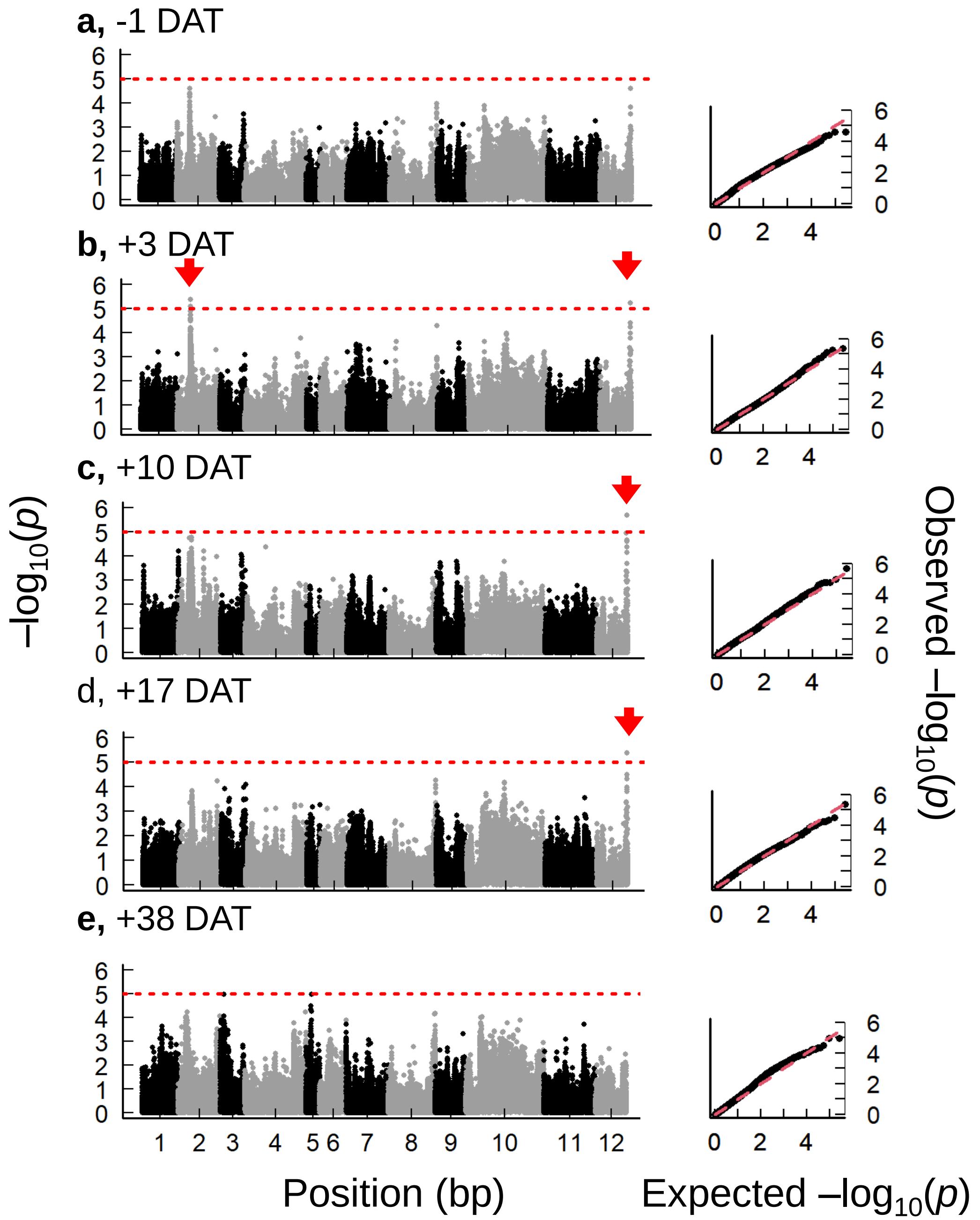

Figure S4.

Manhattan plots and quantile-quantile (Q-Q) plots of plant length (PL) under shallow-water (SW) in 2020.

(**a**) -1 days after treatment (DAT): (**b**) +3 DAT: (**c**) +10 DAT: (**d**) +17 DAT: (**e**) +38 DAT.

The x-axis indicates the SNPs or indels that physically mapped on each chromosome. The red arrows indicate the candidate region. The red dashed lines indicate the threshold lines ($-\log_{10}(p) = 5$) set in this study.

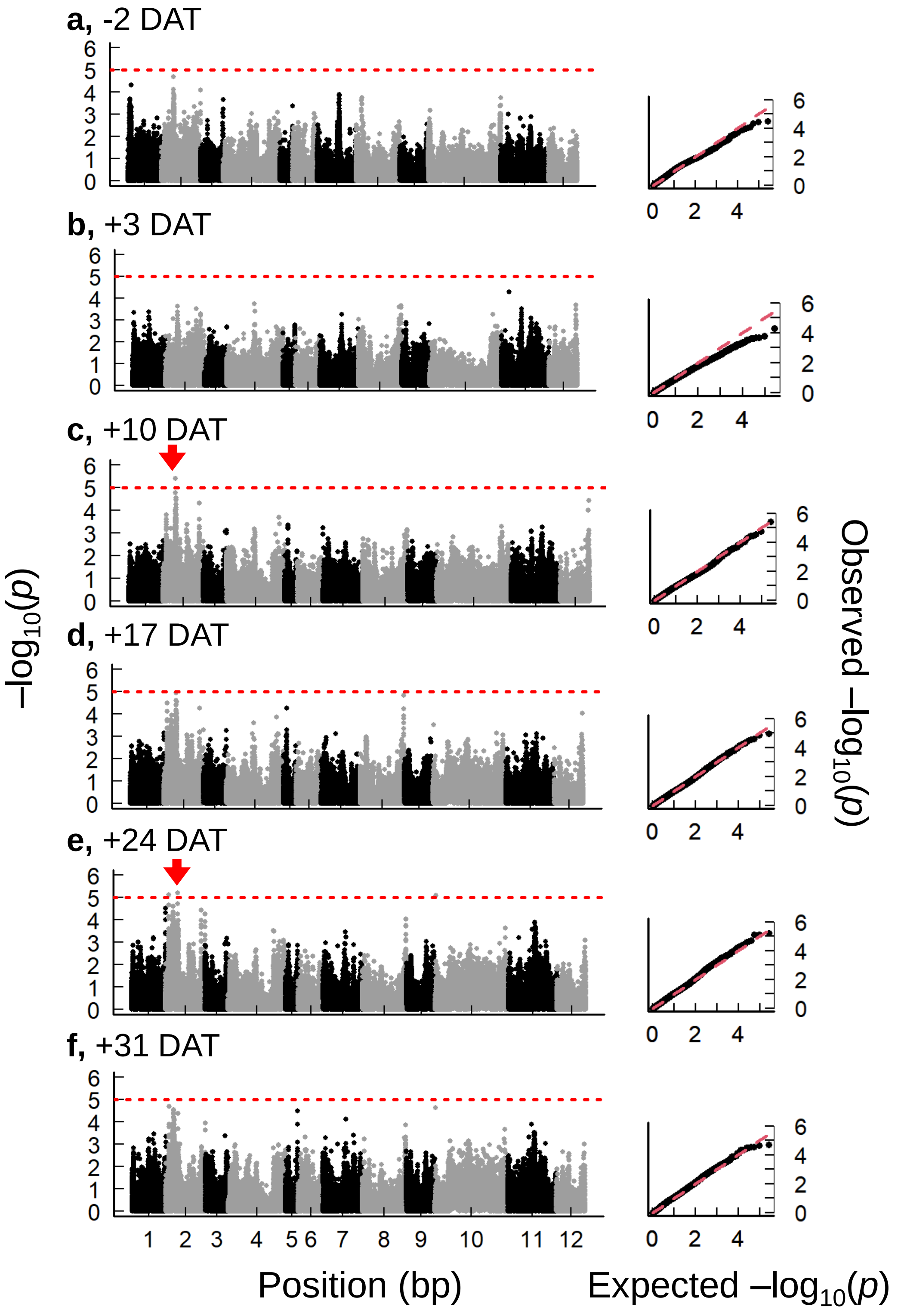

Figure S5.

Manhattan plots and quantile-quantile (Q-Q) plots of plant length (PL) under shallow-water (SW) in 2021.

(**a**) -2 days after treatment (DAT): (**b**) +3 DAT: (**c**) +10 DAT: (**d**) +17 DAT: (**e**) +24 DAT: (**f**) +31 DAT. The x-axis indicates the SNPs or indels that physically mapped on each chromosome. The red arrows indicate the candidate region. The red dashed lines indicate the threshold lines ($-\log_{10}(p) = 5$) set in this study.

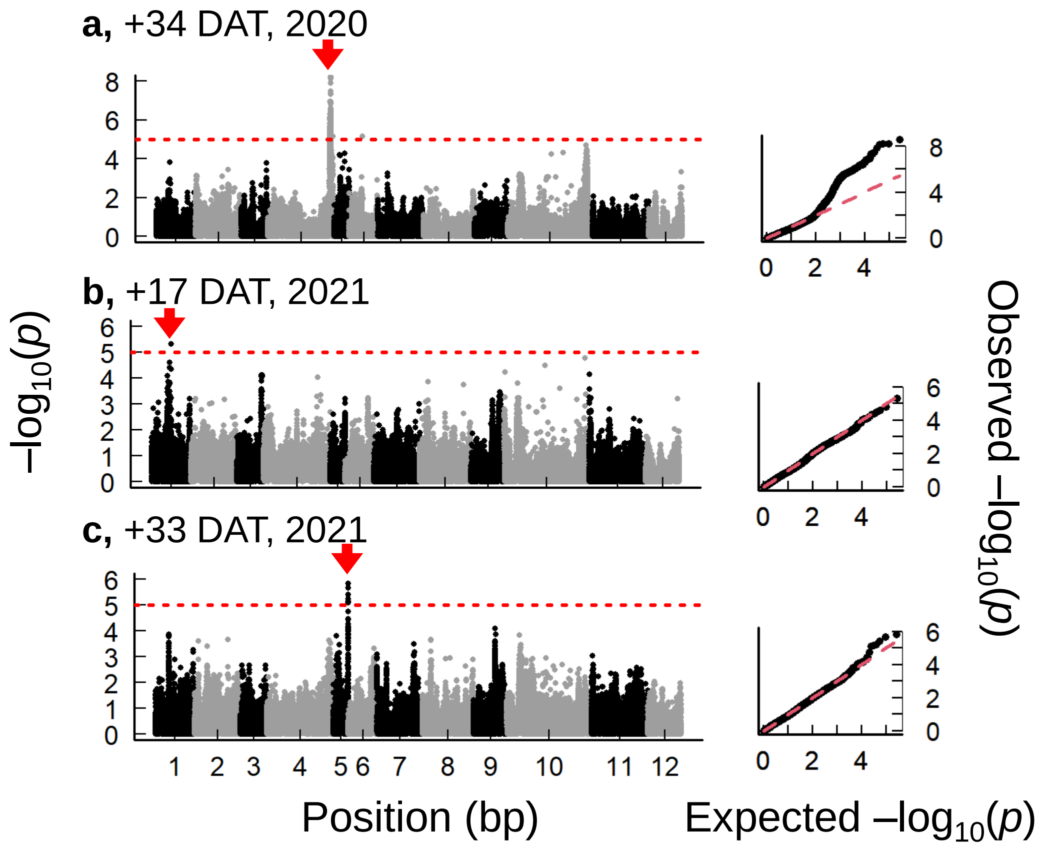

Figure S6.
Manhattan plots and quantile-quantile (Q-Q) plots of tiller number (TN) under shallow-water (SW).
(**a**) +34 days after treatment (DAT) in 2020: (**b**) +17 DAT in 2021: (**c**) +33 DAT in 2021.
The x-axis indicates the SNPs or indels that physically mapped on each chromosome. The red arrows indicates the candidate region. The red dashed lines indicate the threshold lines ($-\log_{10}(p) = 5$) set in this study.

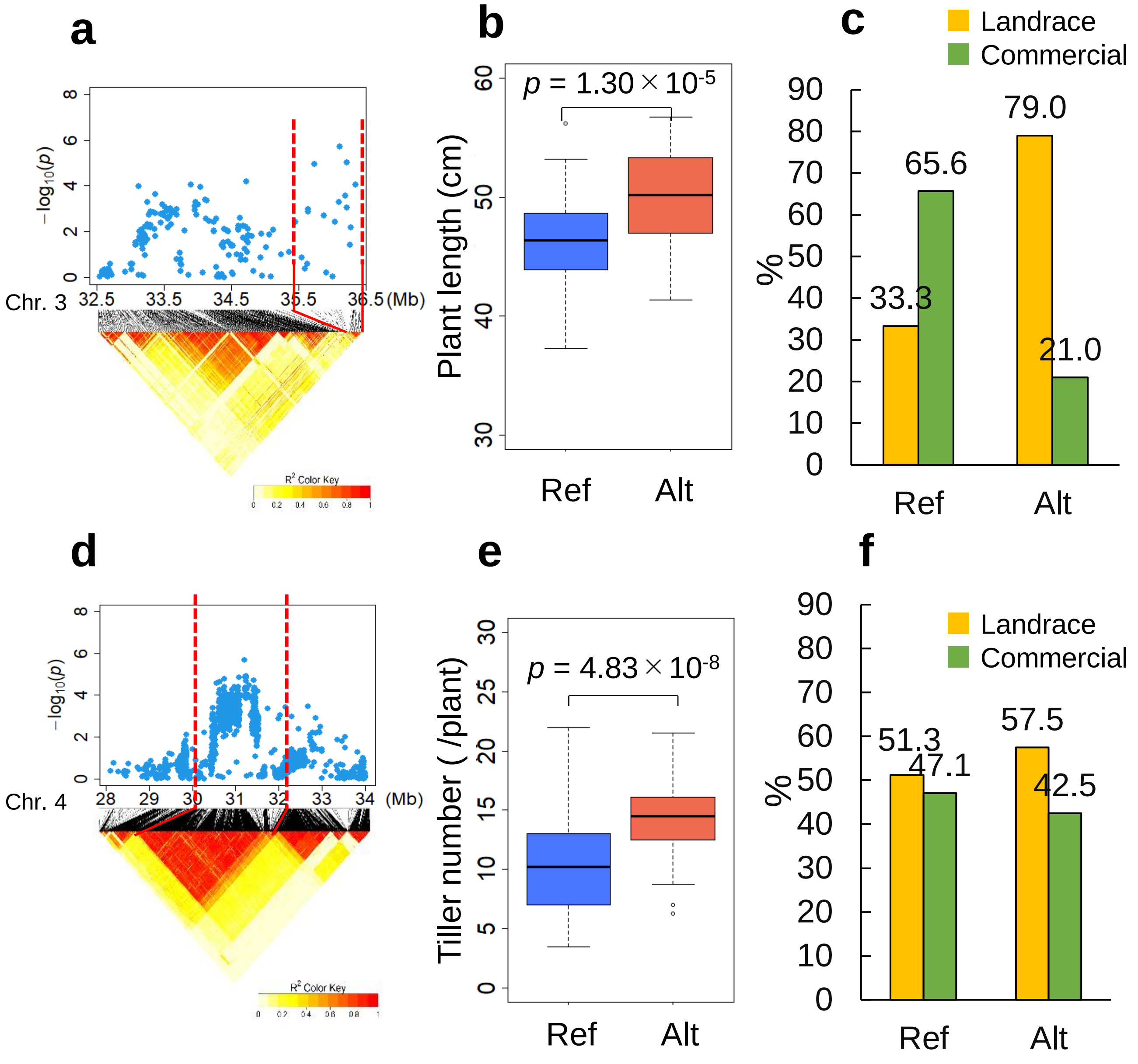

Figure S7.

Detailed analysis of *qPL3* and *qTN4*.

a,d: The enlarged view of the candidate region and LD heat block of *qPL3* (**a**) and *qTN4* (**d**).

b,e: Plant length at +10 days after treatment (DAT) for the indicated genotype of *LOC_Os03g64200* (**b**). TN for the indicated genotype of *LOC_Os04g52479* (**e**). Differences between varieties with reference genotype (ref; colored by blue) and alternative genotype (alt; colored by red) were analyzed by Welch's t-test.

c,f: The allele frequency between landraces (yellow) and commercials (green) at the peak of *qPL3* (**c**) and *qTN4* (**f**).

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CAACTAAATAGCTGACATCAGCATGGTATTAAATTTGGTACCTACGGAGTAGTATCATGTTTGATACCAGAGACACTAGCCAATTAATCC 180

CGTGTGGTTCCGGTGCACCGCGGCTTCTGAGAGGAGCTCGGGGAGGCATGTGTGGCTGCTGTTGTGGTGCCGACGGCGAGGGGCAAGTTC 270

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GATCGCCAATATCAACAAGCAGCTCATCTTCTCCATCGCGTGCCAAGGTTGAAGCGCCTCGATCGGTAGGTGGATCGCTCGCTGCTGAAG 450

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CCTTGCCATCGCCCTTCTCCAATAAGCGGCACACCTGCCTAGTCCCTCCTTCCTATCCATGTCTACCTTACACATTGTGTGCTCCGGCCA 630

GCTCGTGAGCCAGAACGAGCTGGCTGGAGCTTTGCTTCCGAGCCGAGCCGAACTCCACTTTTTGCTCATTTAGATAACGAGCCGAGTCAA 720

GCCAGCTCGTTATCTAAATGAGCTGGAGCGACATATACCCCTATCTGTATACTGAAGGTATCATATCCGATACTTAGGGTATCATACTGA 810

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TAAATATTTAAAATAAATCCAGCGTAGATGCTAAGGGAACTCGAGTCCTCCTATCCCGCTAGATCACCATTTAATTAAGGAGGAAGGGAG 1800

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Figure S8. continued

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                                                        M  S  M  V  V  Q  Q  E  Q  E  V  V    3960
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 *                                                                                           5130

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Figure S8. Nucleotide and amino acid sequences of 5.7 kb region of *OsGA20ox1*.
None of the nucleotide sequence had any mutation among the four varieties listed in Table S2.

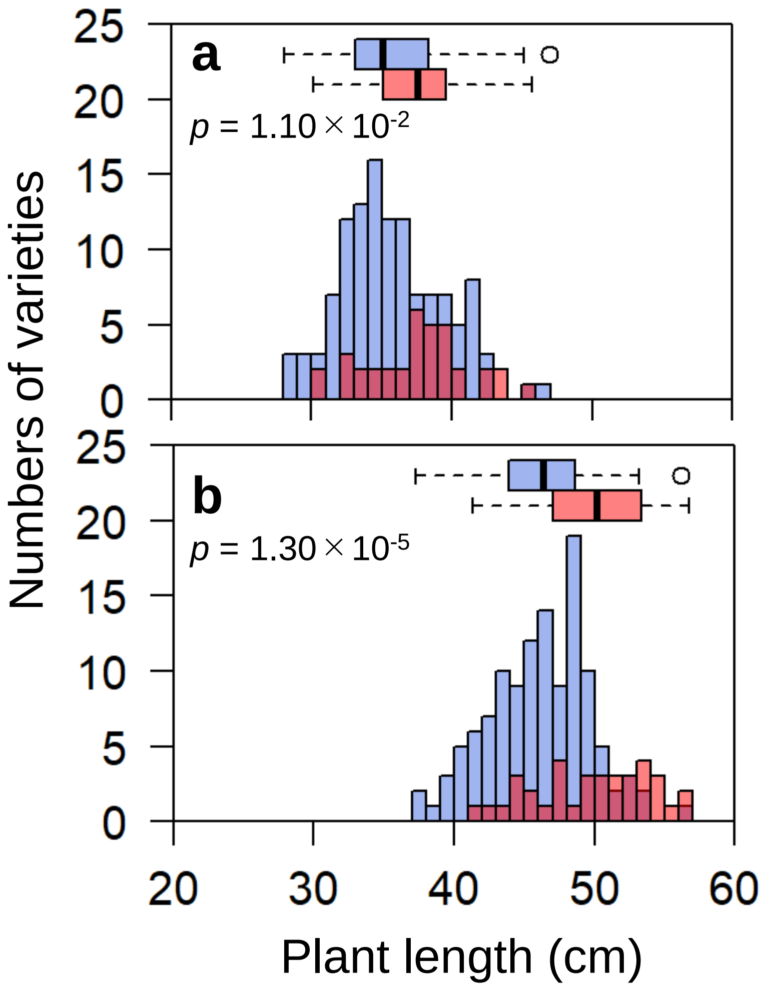

Figure S9.
Histogram of plant length (PL) at +10 days after treatment (DAT) in 2020.
(**a**) Data in shallow-water (SW). (**b**) Data in deep-water (DW).
Blue and red bars indicate the results of varieties with reference and alternative genotype of *qPL3*, respectively.