

FIGURE S2 Quantitative trait locus (QTL) for flag leaf width was detected on chromosome 4 among hybrid populations derived from a Takanari × Akenohoshi cross. (A) QTL detected for flag leaf size and heading date among F₂ population of a Takanari × Akenohoshi cross. Triangles and squares indicate nearest markers to QTLs. (B) Genotype of recombinant fixed lines containing either Akenohoshi or Takanari fragment around 32 Mb on chromosome 4 in almost the same background (F₄ line_10-7-58-16-1 and -5). Plants with Akenohoshi fragment (31.2-35.0 Mb) on chromosome 4 have wider flag leaf and greater yield.

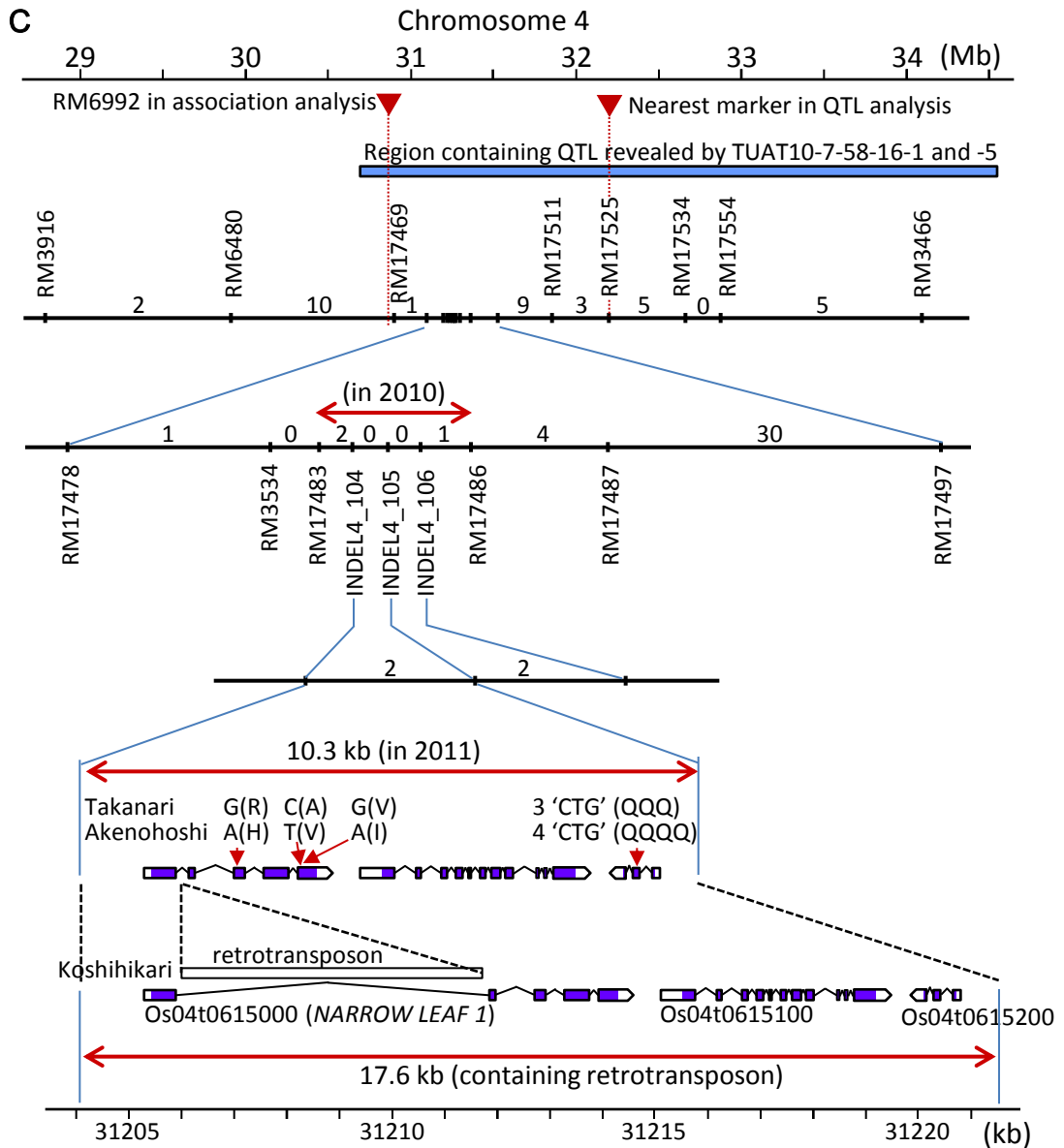


FIGURE S2 (continued)

(C) QTL for flag leaf width on chromosome 4 found among 77 recombinant fixed lines whose background was the same as that of F₄ line_10-7-58-16-1 or F₄ line_10-7-58-16-5. Numbers on lines indicate recombination frequency between neighboring markers observed among 77 lines. QTL was located within a 10.3-kb region containing three ORFs, where three nonsynonymous nucleotide substitutions and one deletion of a three-nucleotide repeat were present. Nucleotide positions at the bottom are based on Nipponbare genome (IRGSP-1.0).

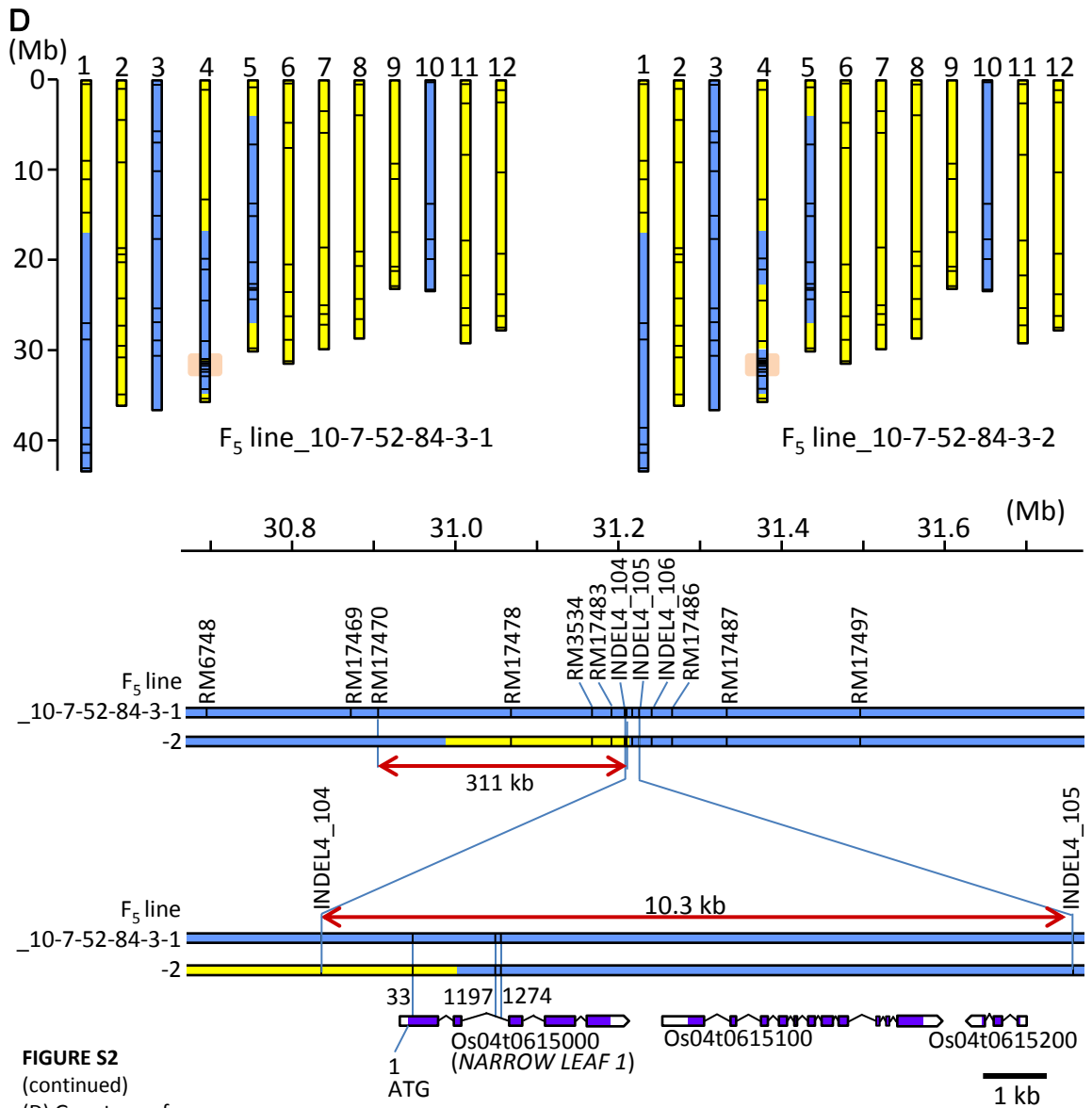


FIGURE S2

(continued)

(D) Genotype of recombinant fixed lines, F₅ line_10-7-52-84-3-1 and -2 containing Akenohoshi and Takanari fragment, respectively, upstream of *NAL1* in almost the same background. No significant differences in flag leaf size and yield-related traits were observed between plants with different promoters driving *NAL1*.

