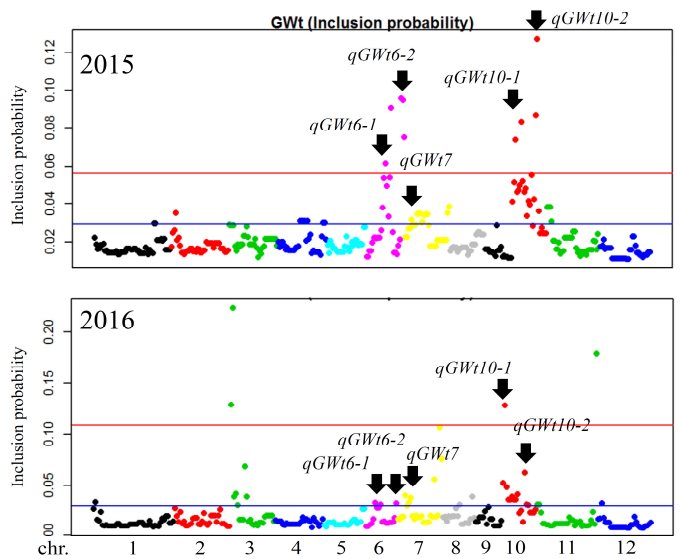
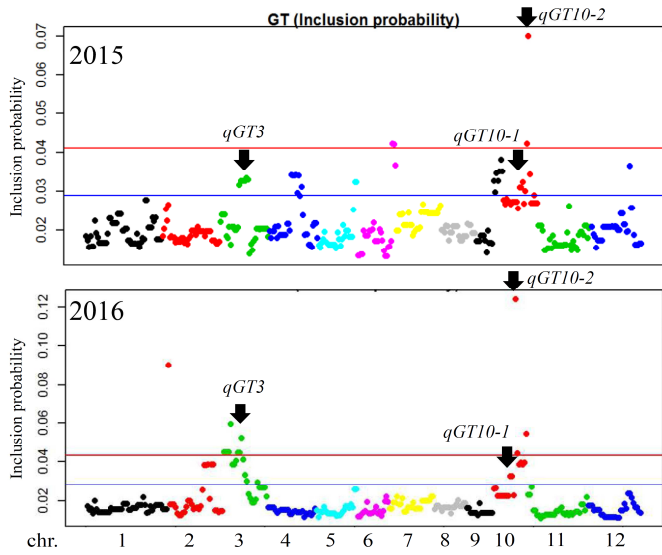
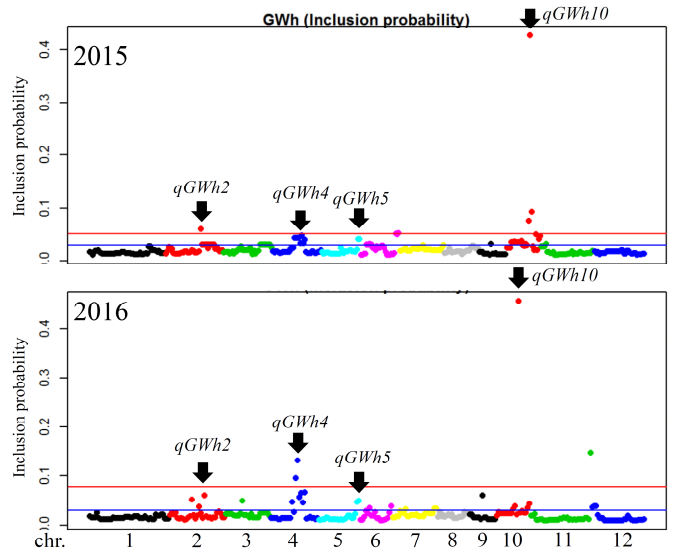
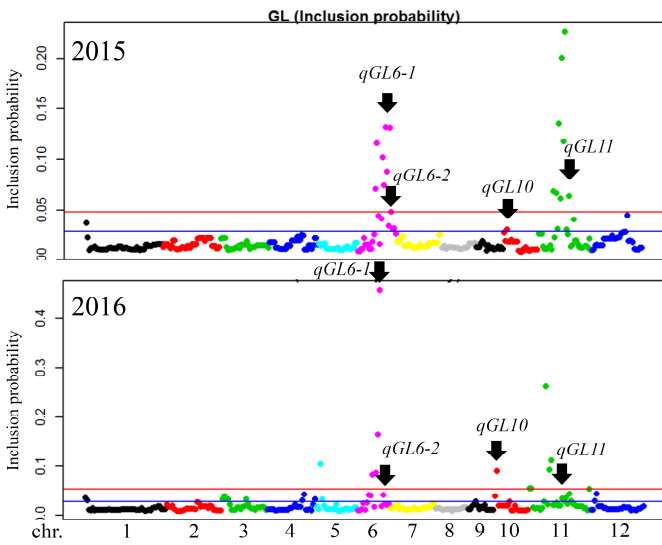
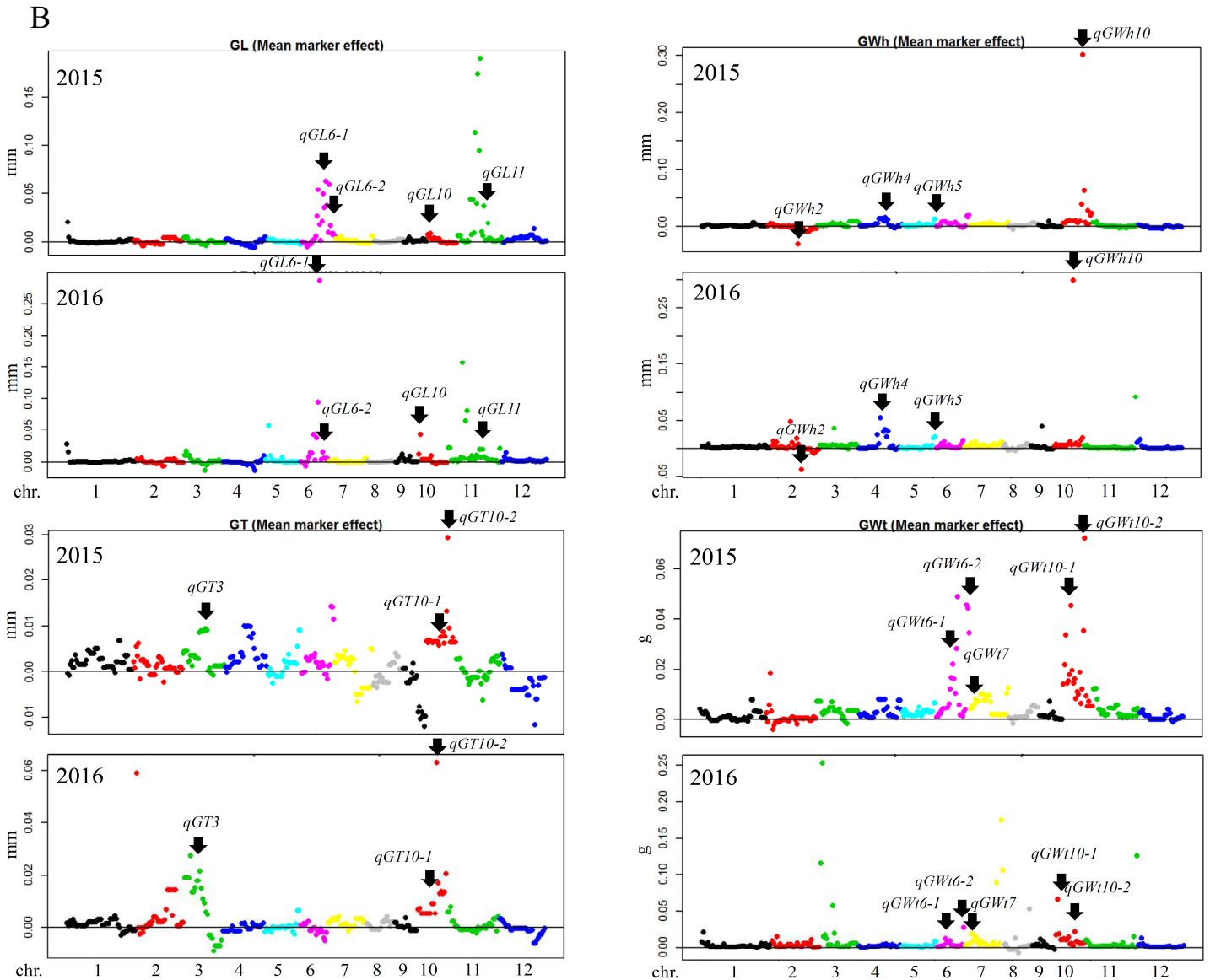


Supplemental Fig. 1. Histograms of days to heading (DTH) in the RIL population derived from Koshihikari/Yamadanishiki in 2013 (A) and 2014 (B). The blue, red, and yellow bars represent the early-flowering lines (eRILs;  $n = 88$ ), late-flowering lines (IRILs;  $n = 92$ ), and residual lines (rRILs;  $n = 10$ ), respectively.

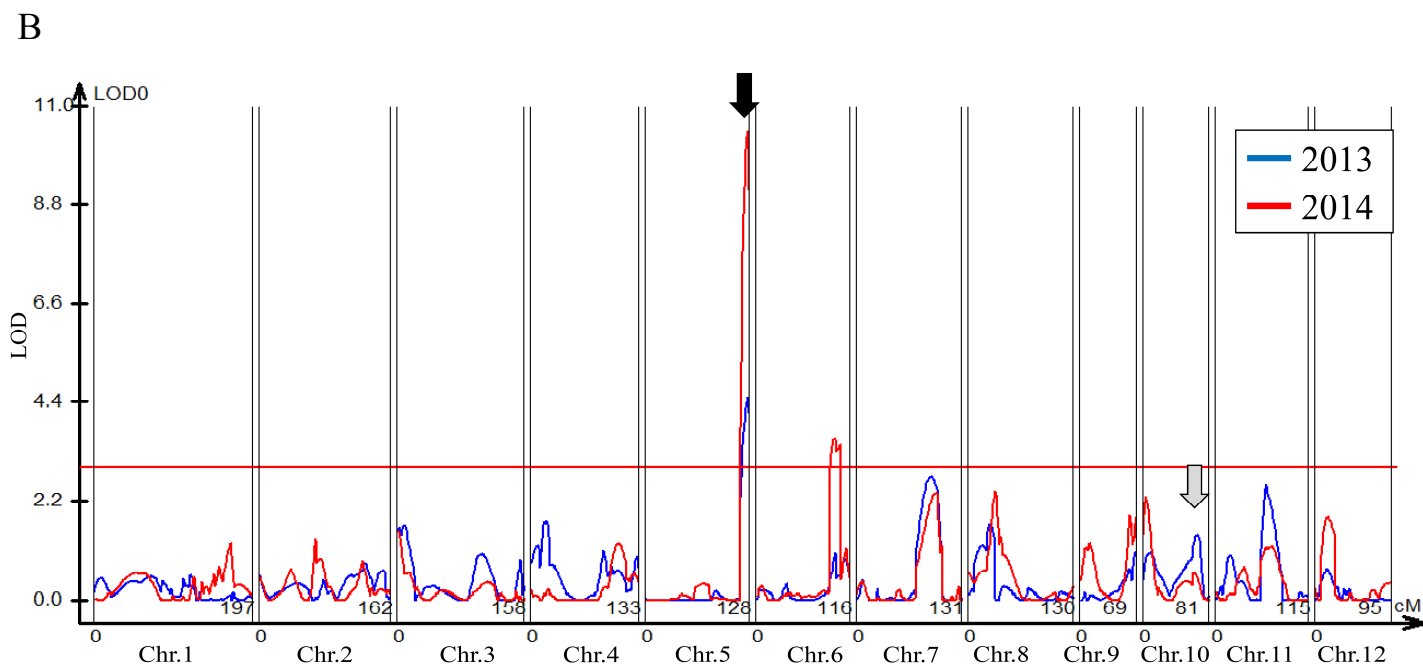
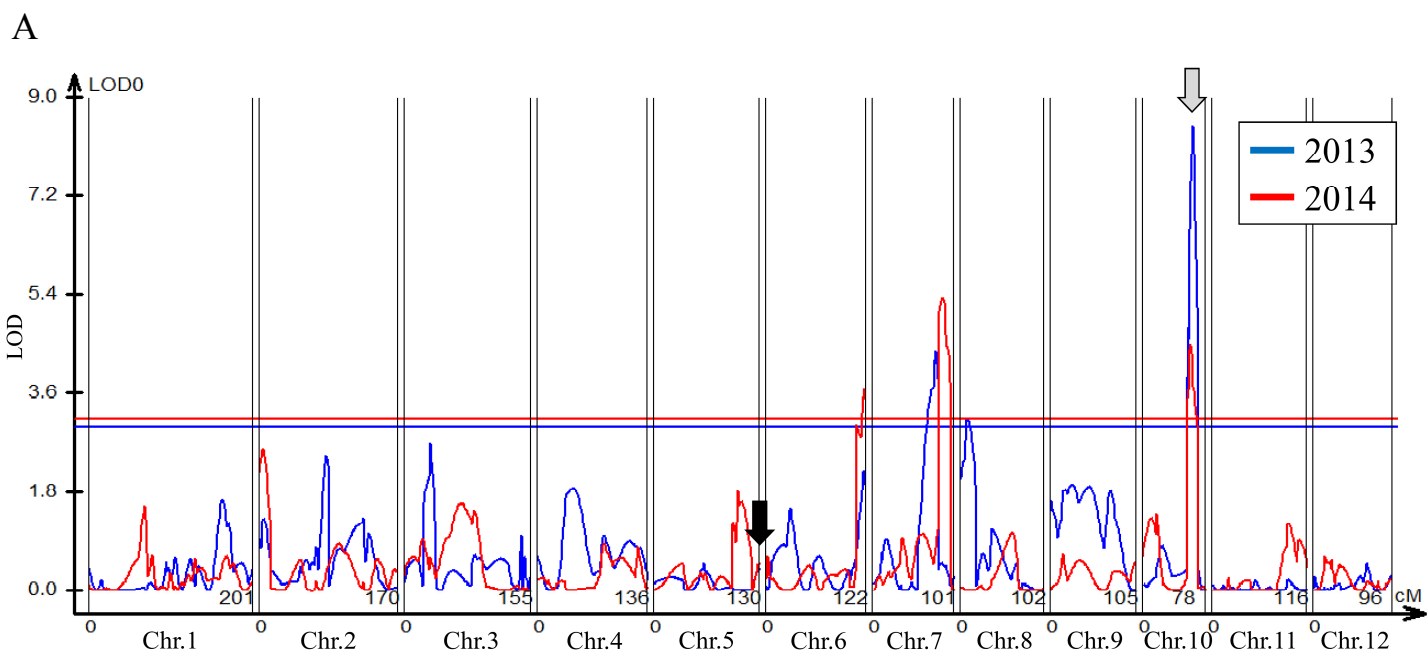
A



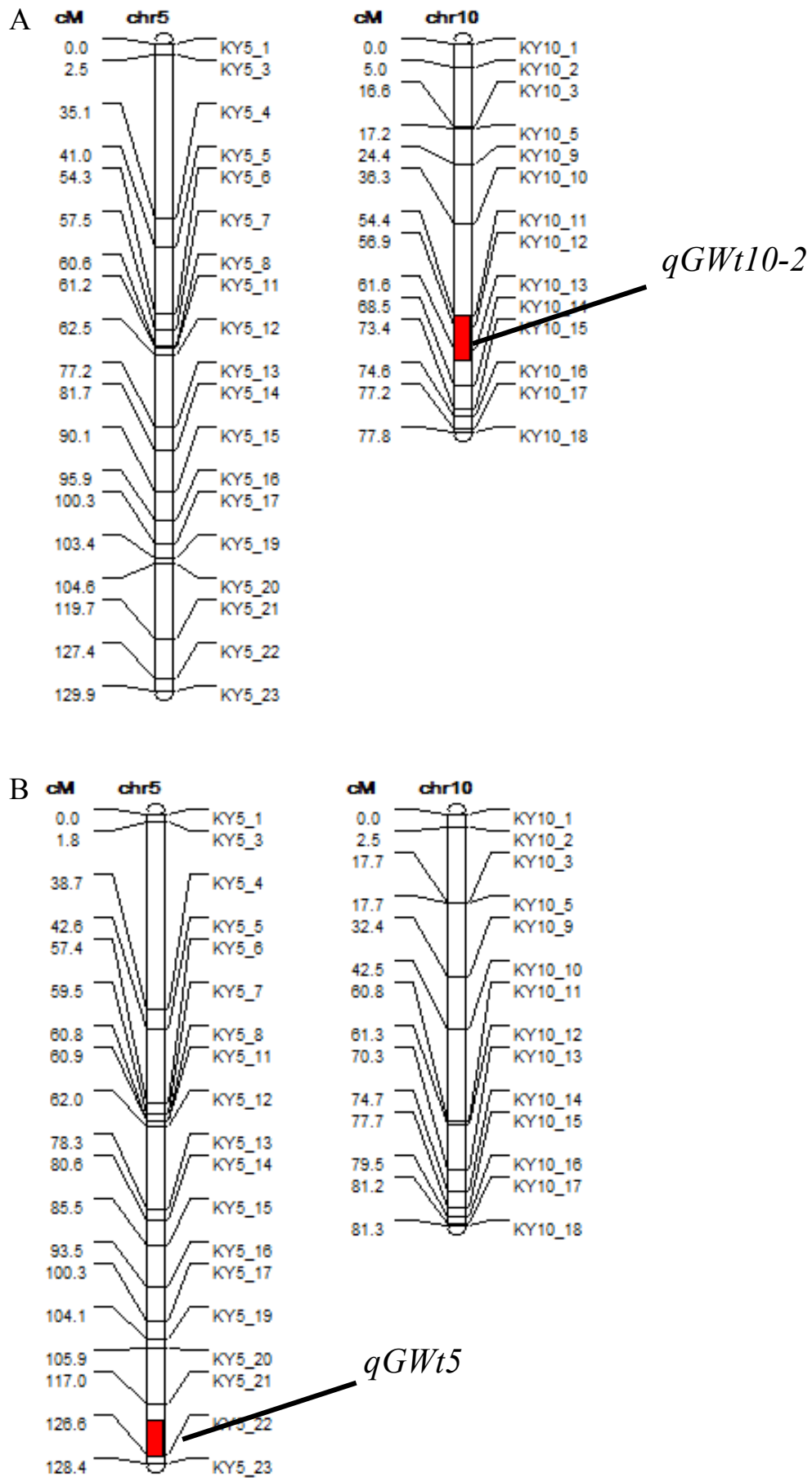
Supplemental Fig. 2. continued.



Supplemental Fig. 2. Inclusion probability (A) and marker effect (B) for four grain traits: grain length (GL), grain width (GWh), grain thickness (GT), and 100-grain weight (GWT). (A) Inclusion probabilities were calculated by a variable selection method with BayesC model for each marker from 2015 (upper panels in each pair) and 2016 (lower panels). Blue and red lines indicate the 0.05 and 0.01 significance levels, respectively. (B) Marker effect was estimated using a BayesC model with the Yamadanishiki CSSLs in the Koshihikari genetic background from 2015 (upper panels) and 2016 (lower panels). Dots above and below the zero lines represent traits whose values increased or decreased in the Yamadanishiki allele, respectively.



Supplemental Fig. 3. Logarithm of odds (LOD) curves for the QTL analysis for GWt in the eRILs (A) and IRILs (B). The blue and red lines represent data from 2013 and 2014, respectively. Black and gray arrows indicate *qGWt5* and *qGWt10-2*, respectively.



Supplemental Fig. 4. Linkage maps for chromosomes 5 and 10 of the eRILs (A) and IRILs (B). The red sections indicate the locations of the QTLs.