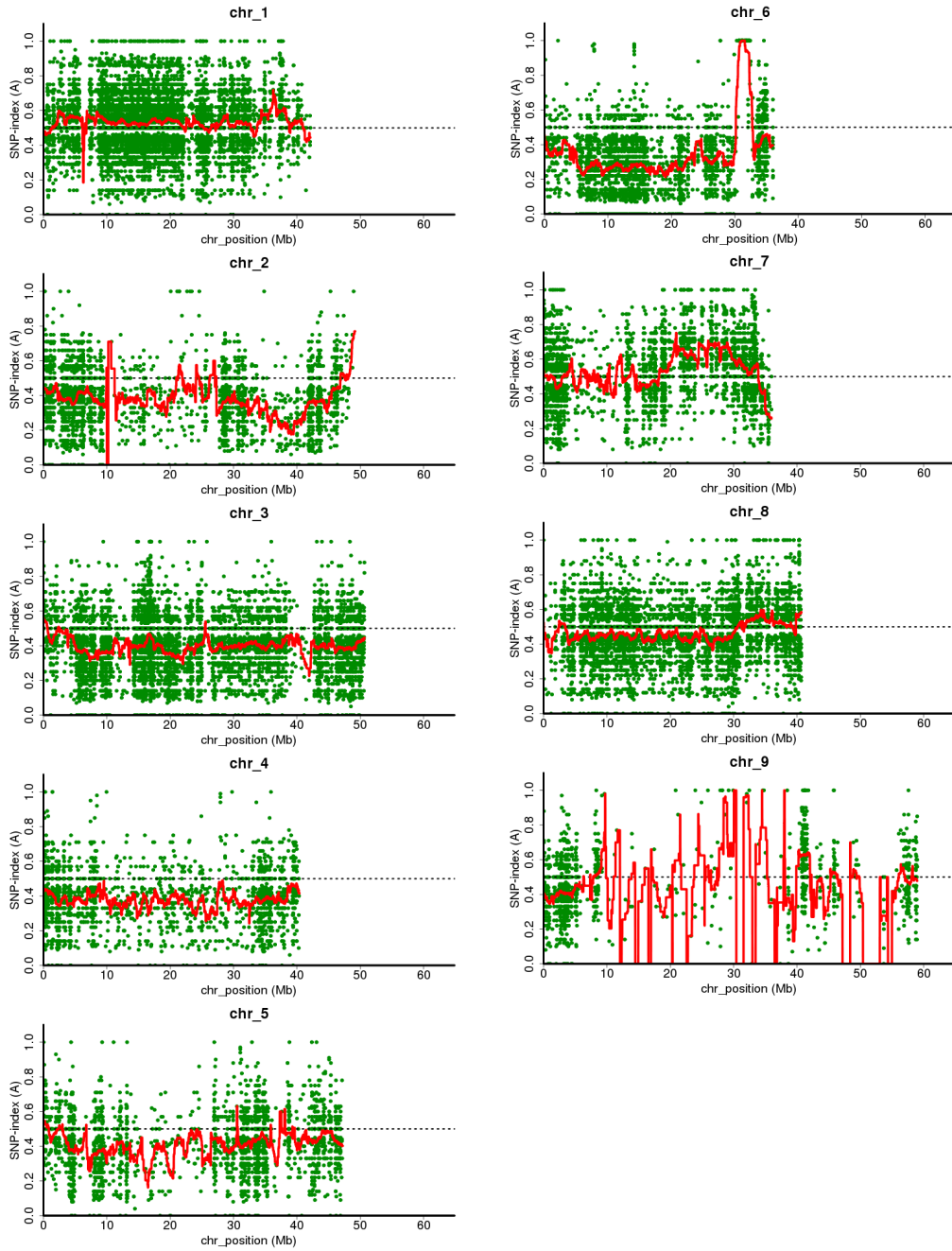


Supplemental Figure 1.

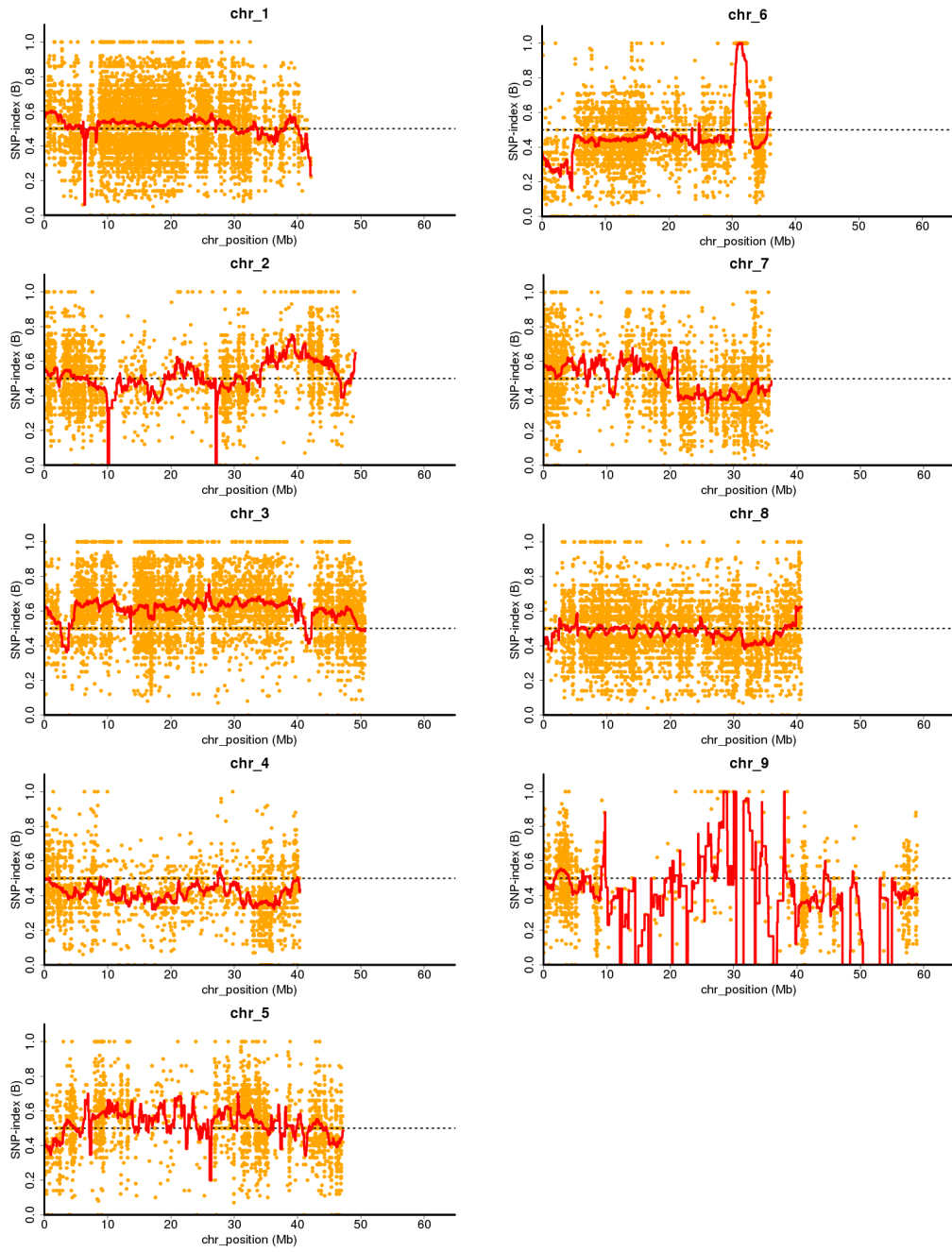
SNP-index and Δ (SNP-index) plots for nine chromosomes of the Y-bulk and S-bulk.

(A) SNP-index plot of the Y-bulk, (B) SNP-index plot of the S-bulk and (C) Δ (SNP-index of Y-bulk – S-bulk) plot of nine chromosomes with statistical confidence intervals under the null hypothesis of no QTLs (green, $P < 0.05$). Red lines indicate the sliding window average of a 1 Mb interval with 10 kb increment for the SNP-index and Δ (SNP-index).

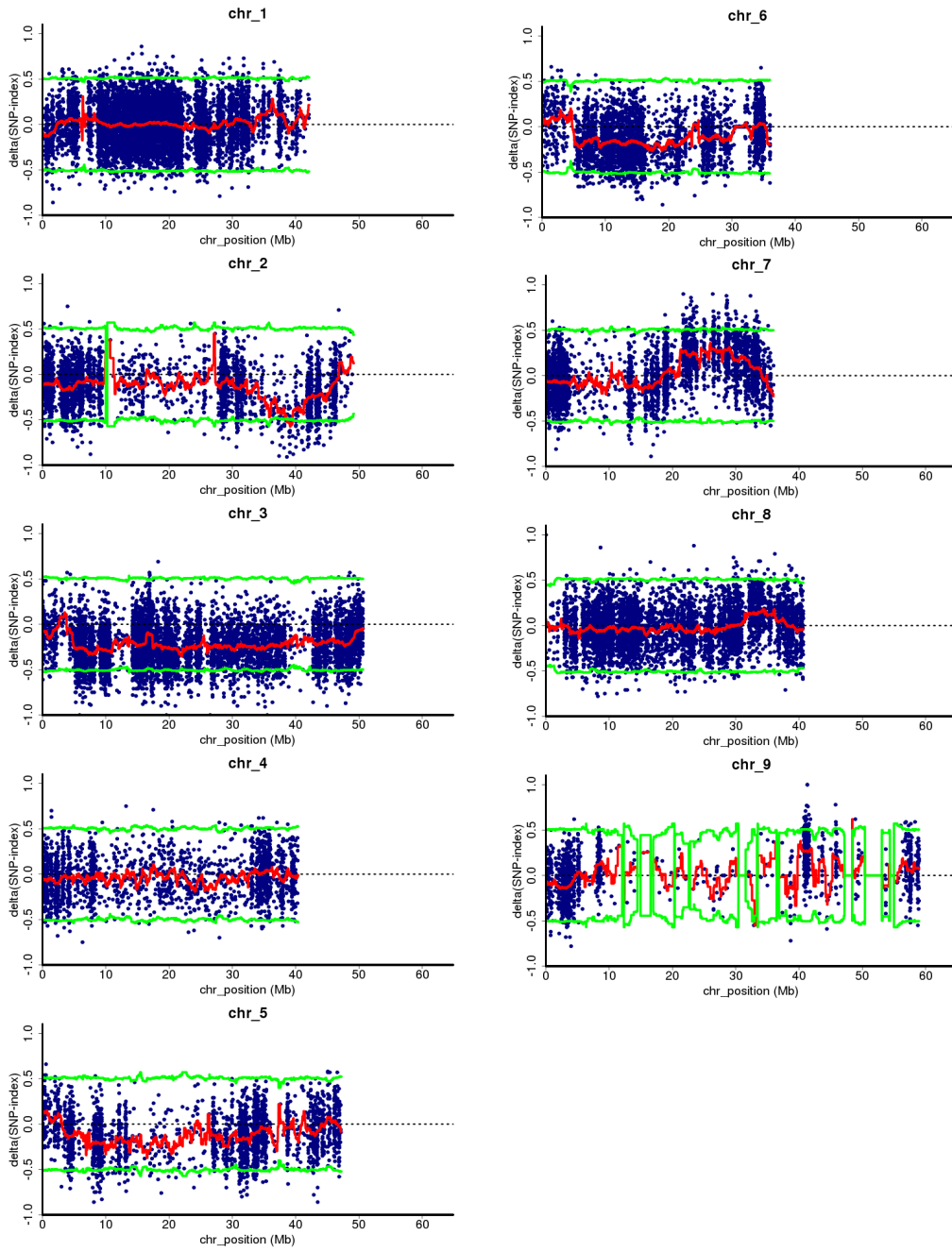
A



B



C

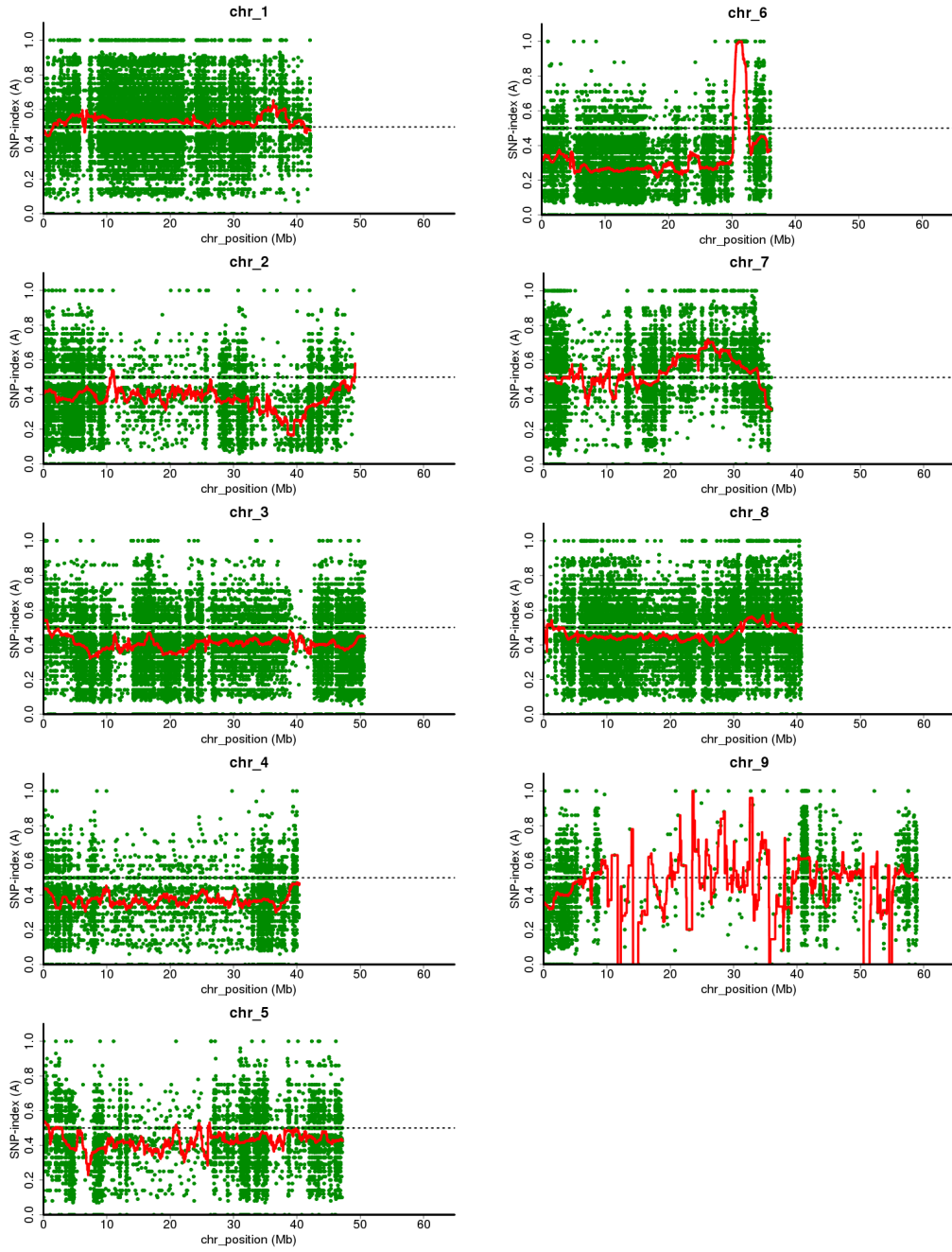


Supplemental Figure 2.

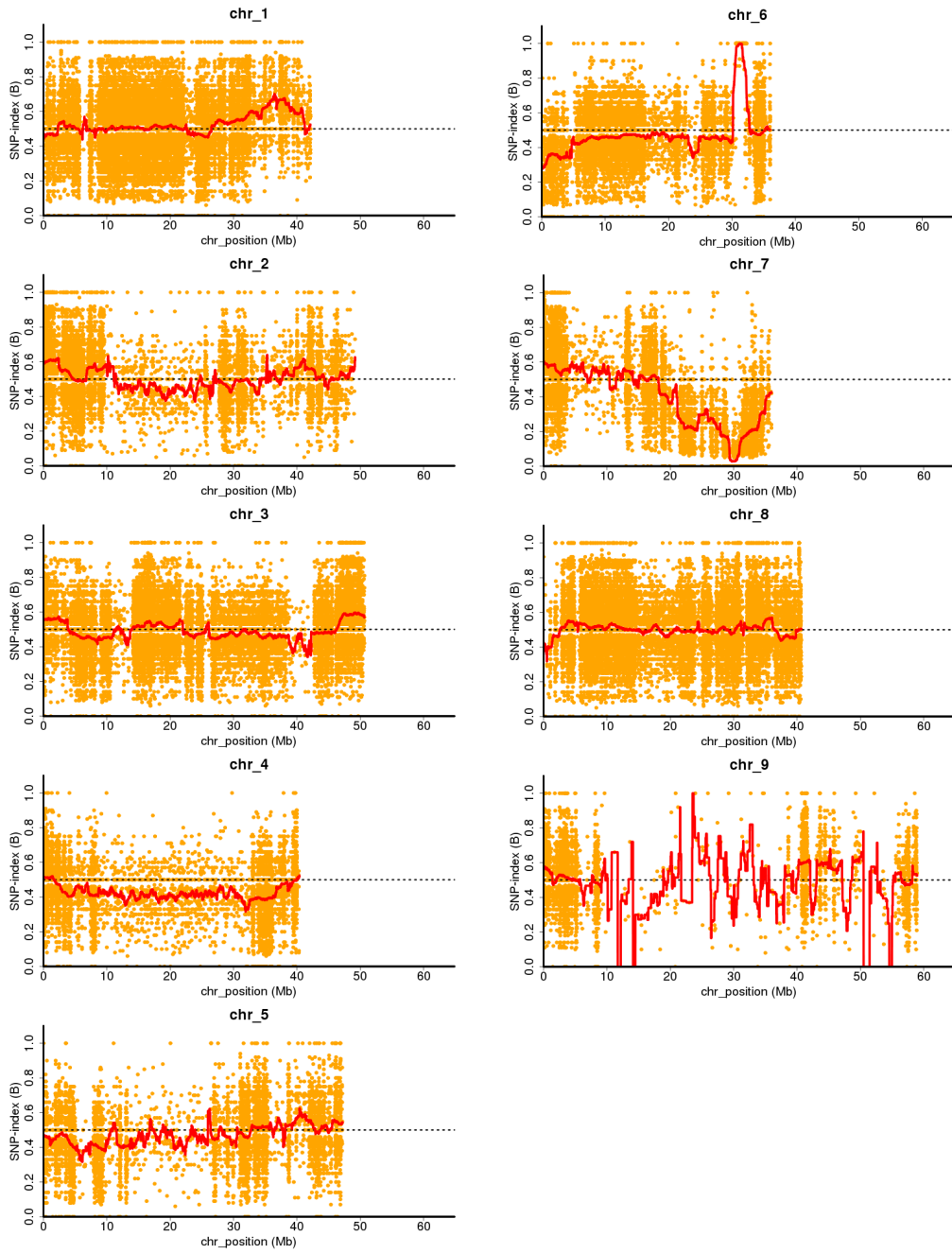
SNP-index and Δ (SNP-index) plots for nine chromosomes of the Y-bulk and the L-bulk.

(A) SNP-index plot of the Y-bulk, (B) SNP-index plot of the L-bulk and (C) Δ (SNP-index of Y-bulk – L-bulk) plot of nine chromosomes with statistical confidence intervals under the null hypothesis of no QTLs (green, $P < 0.05$). Red lines indicate the sliding window average of a 1 Mb interval with 10 kb increment for the SNP-index and Δ (SNP-index).

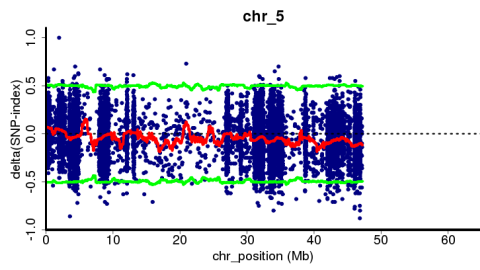
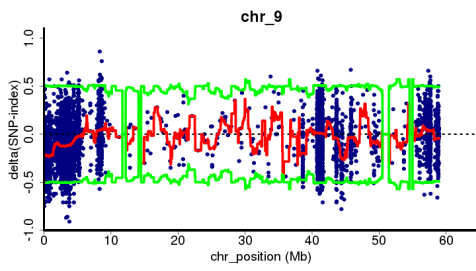
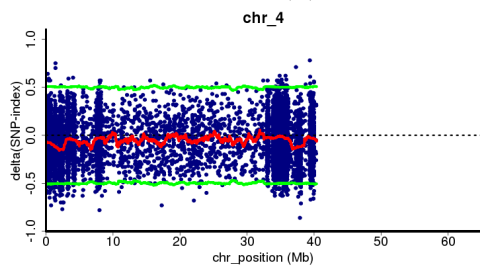
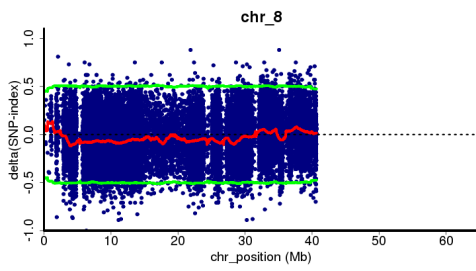
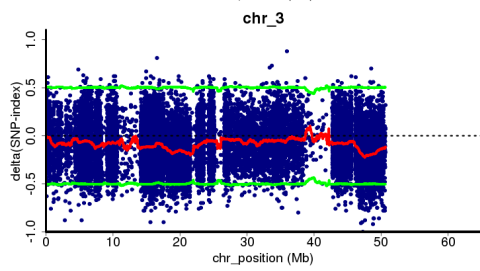
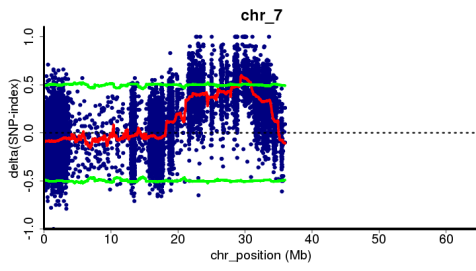
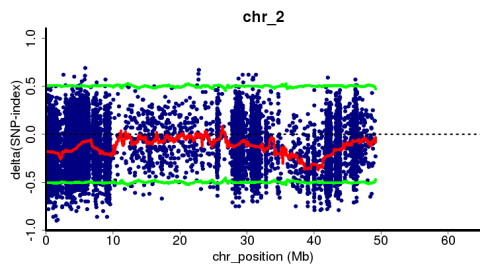
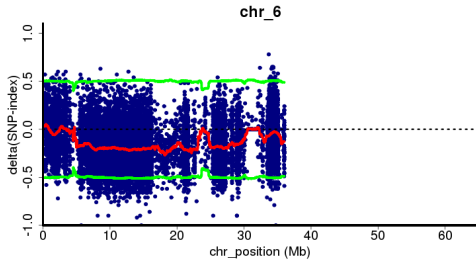
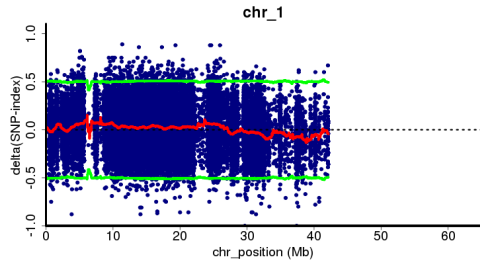
A



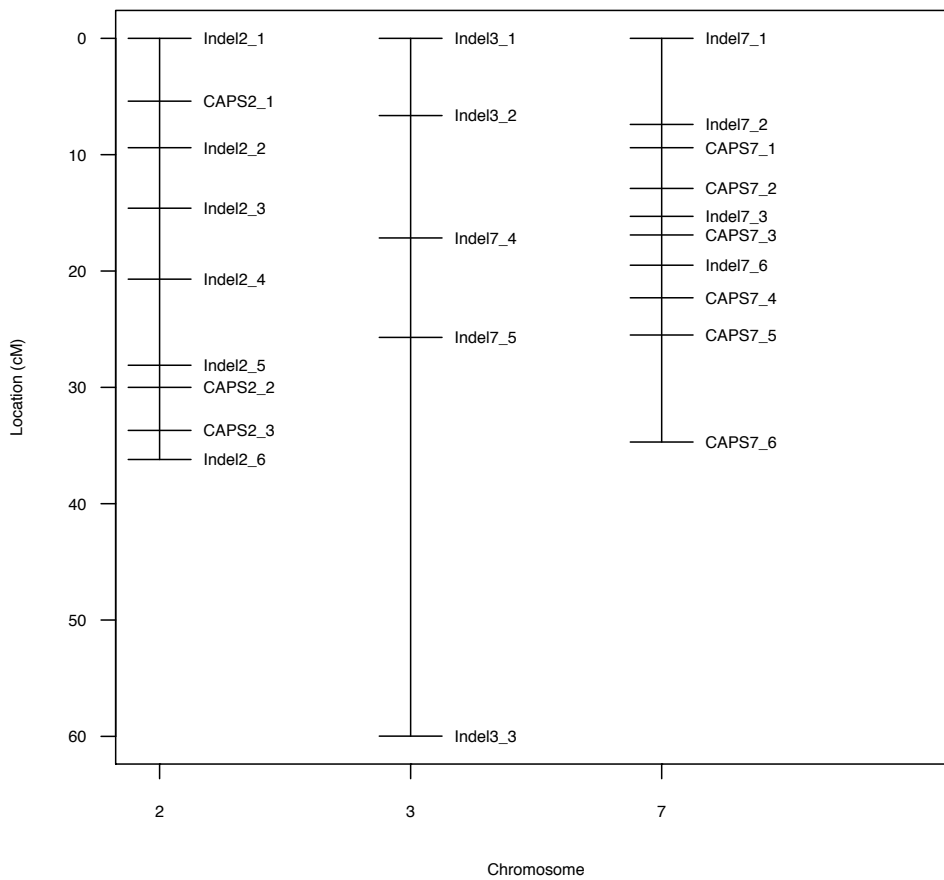
B



C

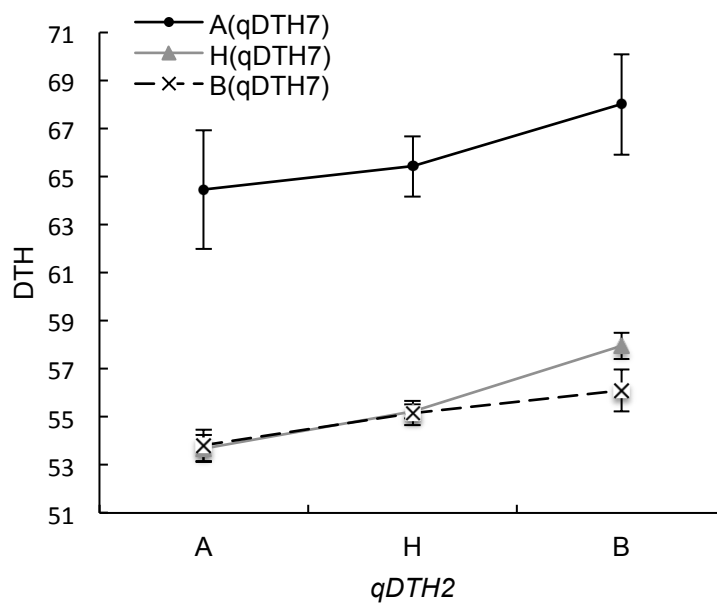


Genetic map



Supplemental Figure 3.

Genetic linkage map (chr.2, 3 and 7) of foxtail millet constructed based on an F_2 population of a cross between Shinanotsuhime and Yuikogane. The linkage group of chr.2 was constructed between 36.3 Mb and 41.8 Mb, chr.3 was constructed between 46.6 Mb and 50.5 Mb and chr.7 was constructed between 28.5 Mb and 31.5 Mb based on the physical map, respectively.



Supplemental Figure 4.

Effect plots showing the interaction between *qDTH2* and *qDTH7*. Line interaction plot of *qDTH2* (Indel2_3) and *qDTH7* (CAPS7_3) in the F₂ population. There are no significant interactions between *qDTH2* and *qDTH7*. The “A” allele is from Yuikogane, whereas the “B” allele is from Shinanotsuhime.