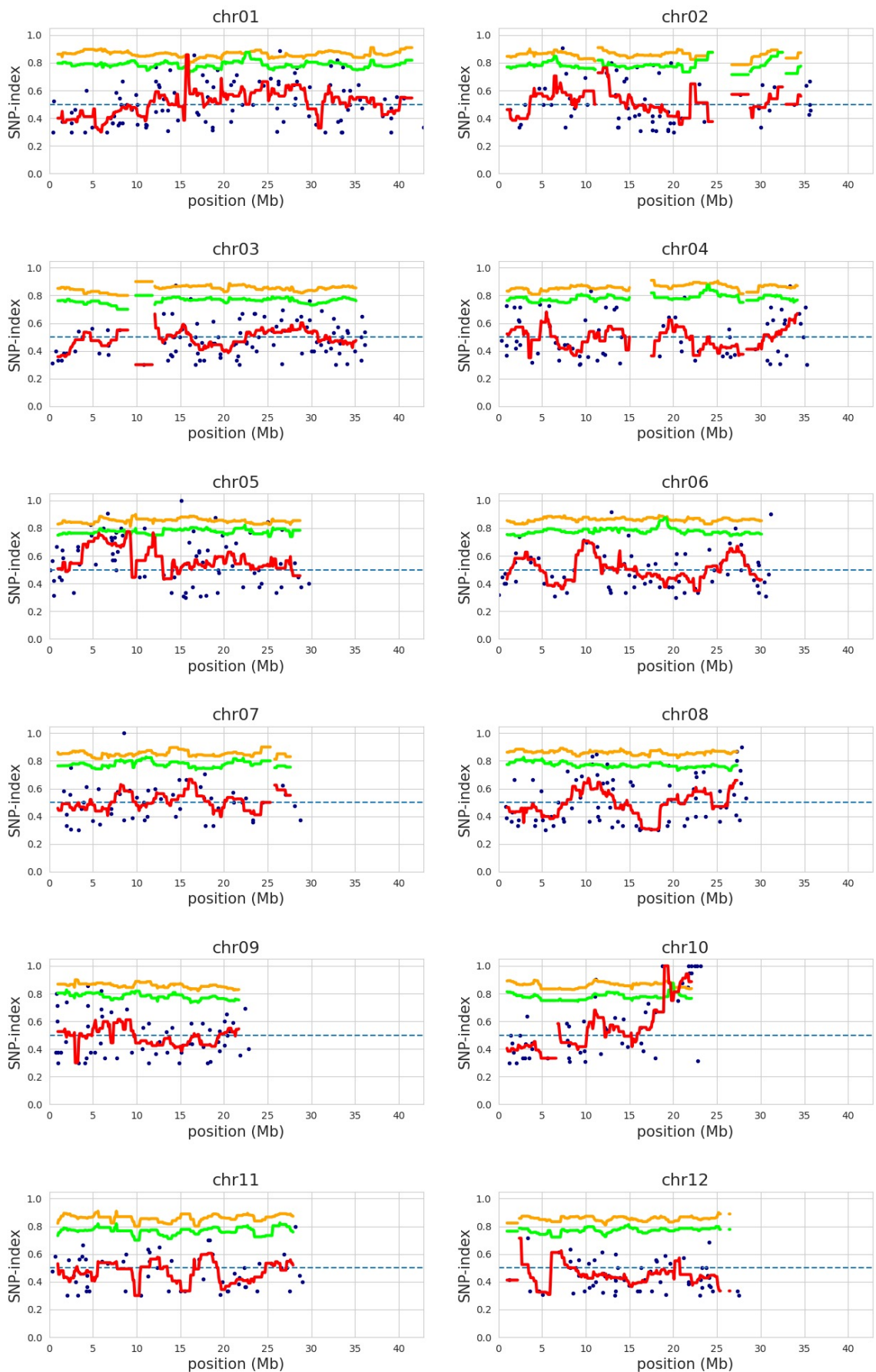
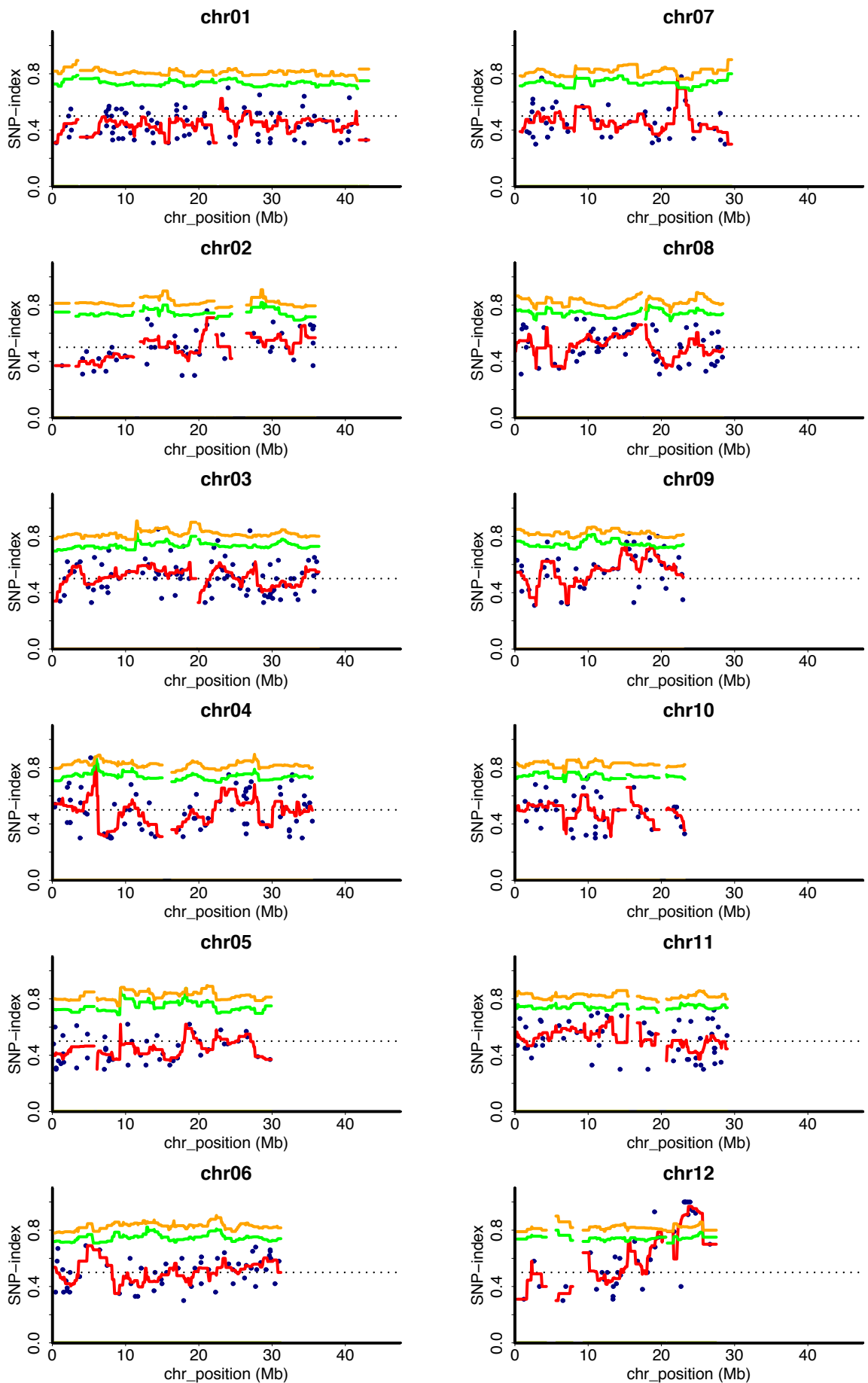


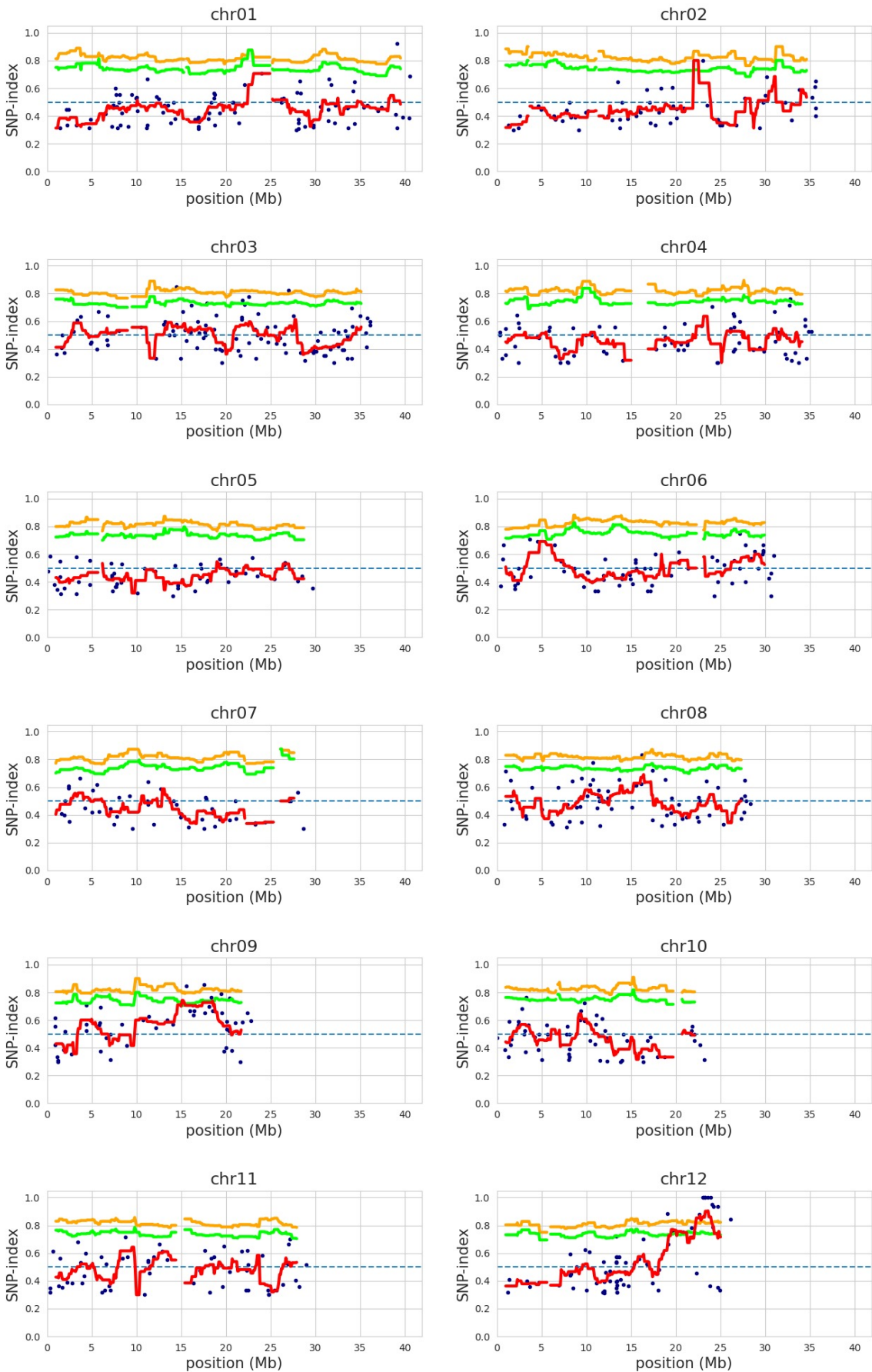
Supplemental Figure S1 (A) MutMap plot of Hit1917-pl from MutMap v1.4.5. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).



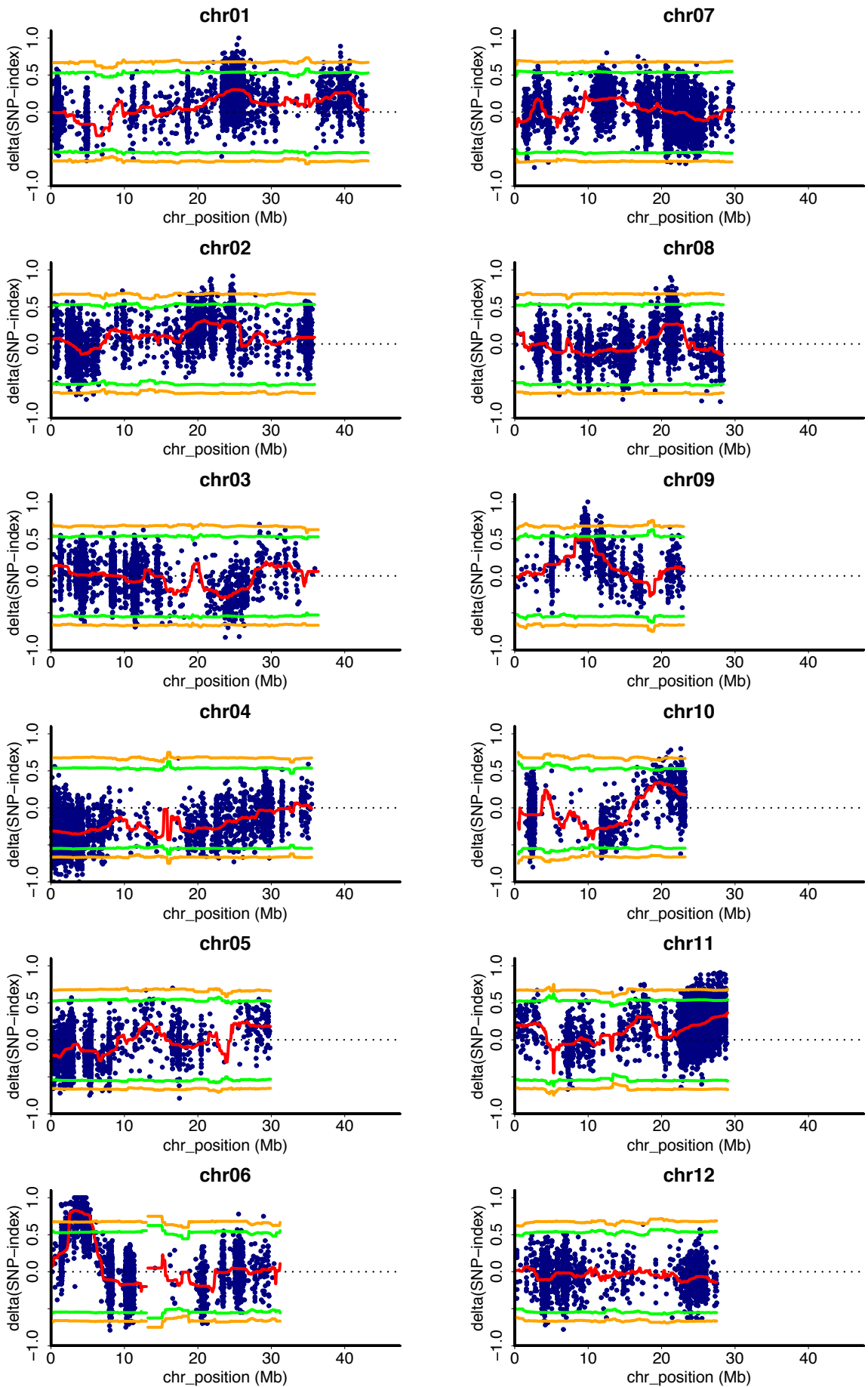
Supplemental Figure S1 (B) MutMap plot of Hit1917-pl from MutMap v2.3.2. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).



Supplemental Figure S1 (C) MutMap plot of Hit1917-sd from MutMap v1.4.5. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).

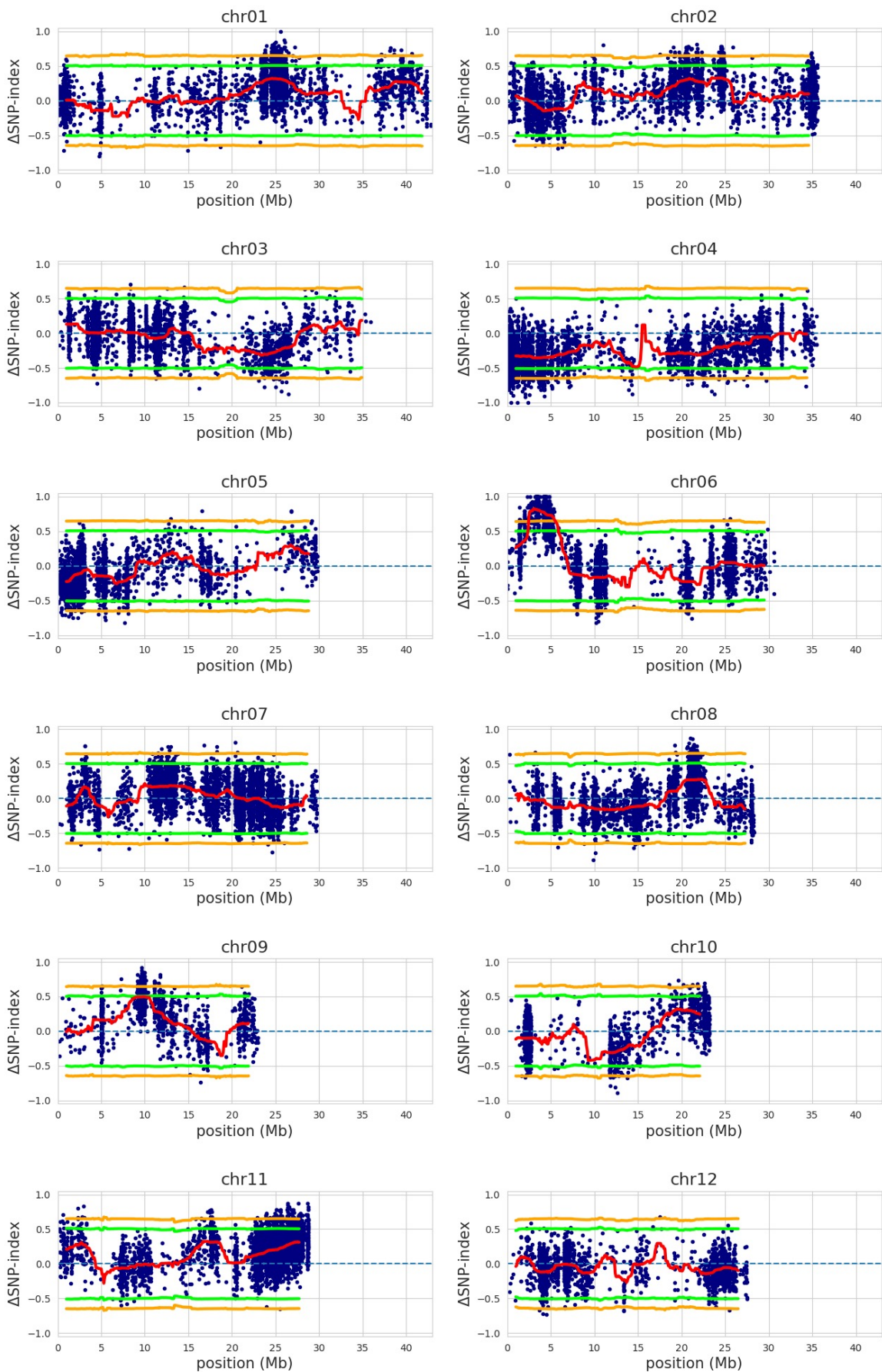


Supplemental Figure S1 (D) MutMap plot of Hit1917-sd from MutMap v2.3.2. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).



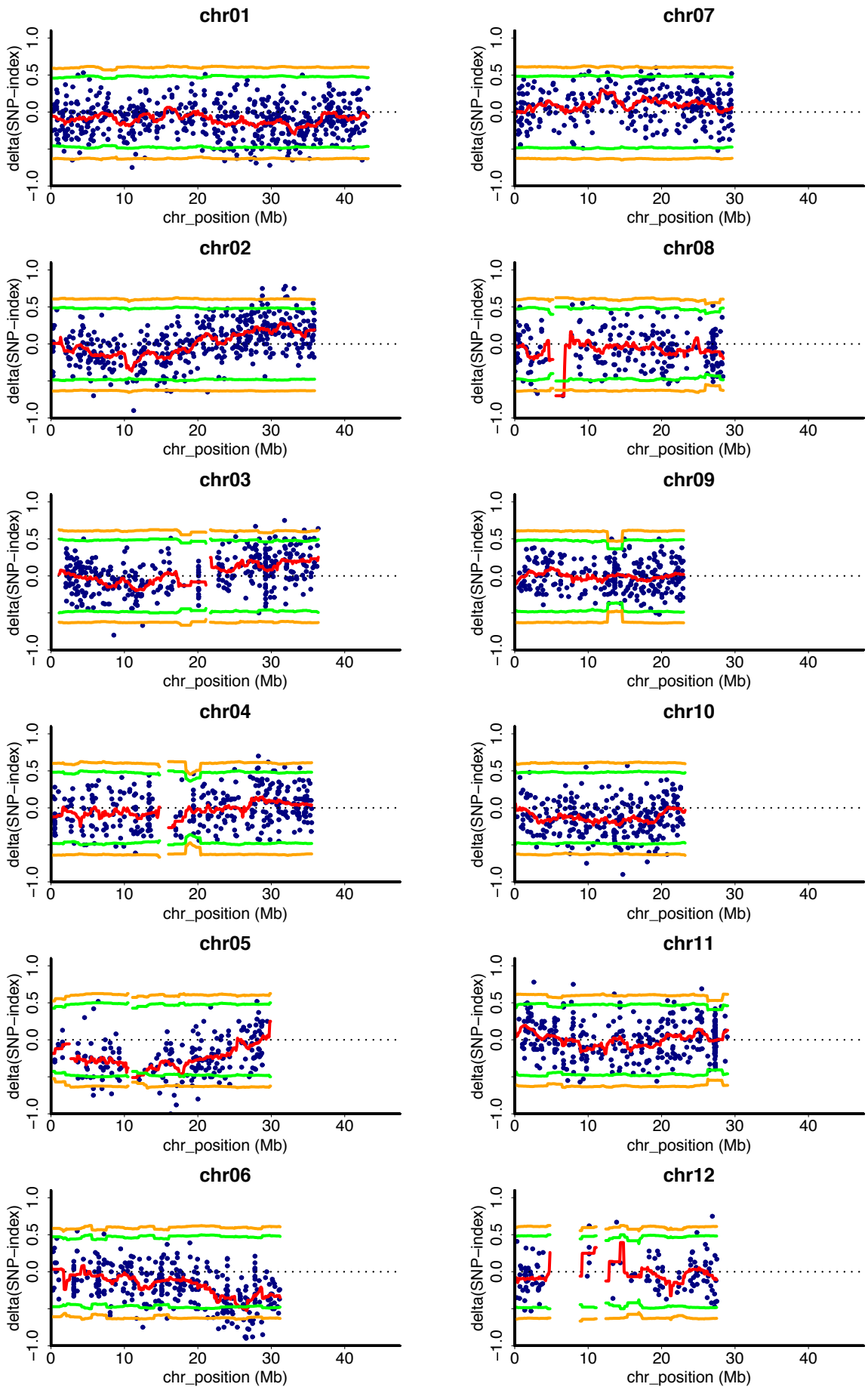
Supplemental Figure S1 (E) QTL-seq plot of RILs from QTL-seq v1.4.5.

The Δ SNP-index plot obtained by subtraction of the susceptible-bulk SNP-index from the resistance-bulk SNP-index for RILs obtained from a cross between Nortai and Hitomebore. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).

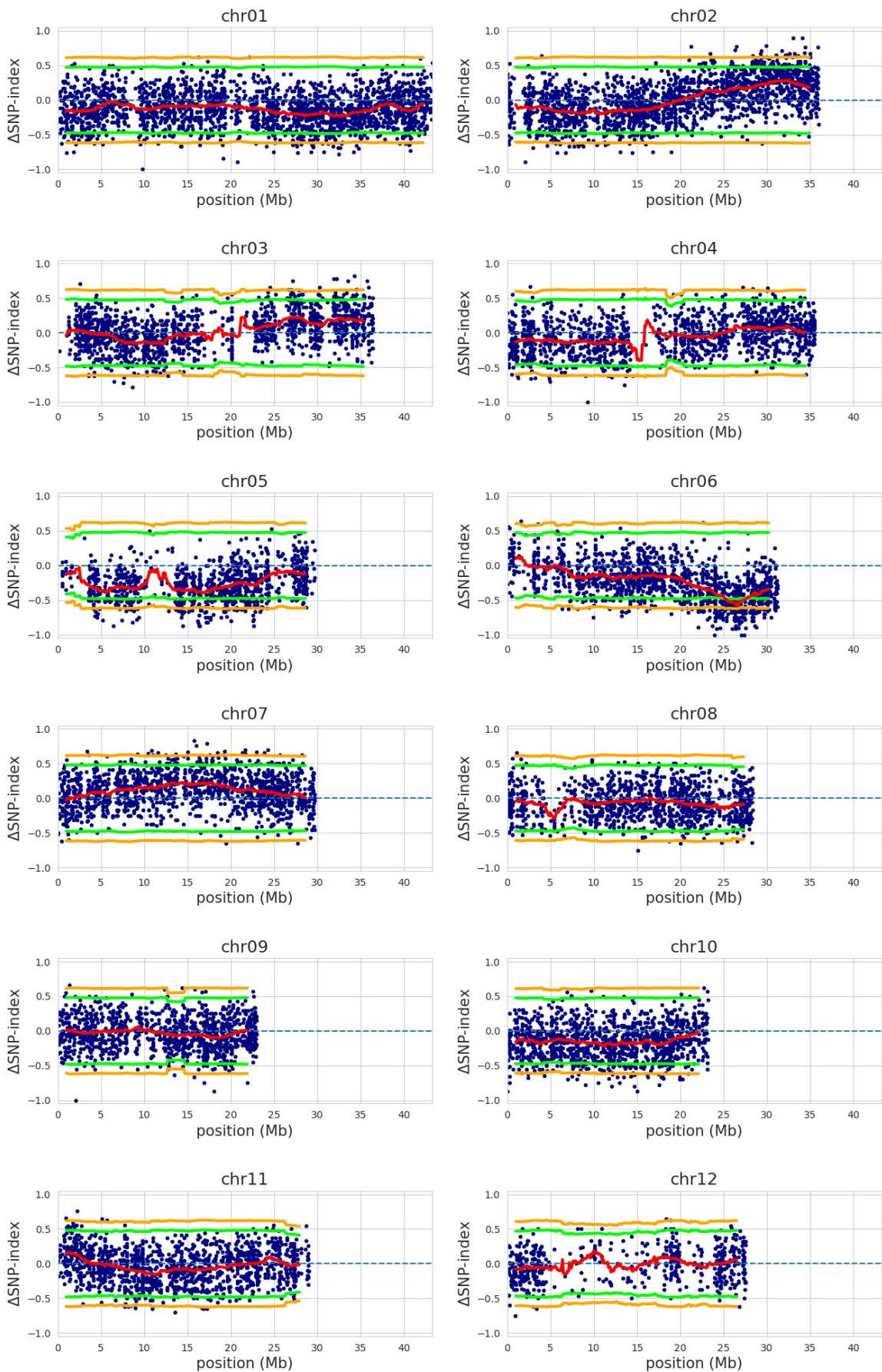


Supplemental Figure S1 (F) QTL-seq plot of RILs from QTL-seq v2.2.2.

The Δ SNP-index plot obtained by subtraction of the susceptible-bulk SNP-index from the resistance-bulk SNP-index for RILs obtained from a cross between Nortai and Hitomebore. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).



Supplemental Figure S1 (G) QTL-seq plot of F2 progeny from QTL-seq v1.4.5. The Δ SNP-index plot obtained by subtraction of Highest-bulk SNP-index from Lowest-bulk SNP-index for F2 progeny obtained from a cross between Hitomebore and WRC57. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).



Supplemental Figure S1 (H) QTL-seq plot of F2 progeny from QTL-seq v2.2.2. The Δ SNP-index plot obtained by subtraction of Highest-bulk SNP-index from Lowest-bulk SNP-index for F2 progeny obtained from a cross between Hitomebore and WRC57. Statistical confidence intervals under the null hypothesis of no QTL are shown (green: $P < 0.05$; yellow: $P < 0.01$).