

The title of the manuscript: Fine dissection of limber pine resistance to *Cronartium ribicola* using targeted sequencing of the NLR family

The authors: Jun-Jun Liu, Anna W. Schoettle, Richard A. Snieszko, Holly Williams, Arezoo Zamany, Benjamin Rancourt

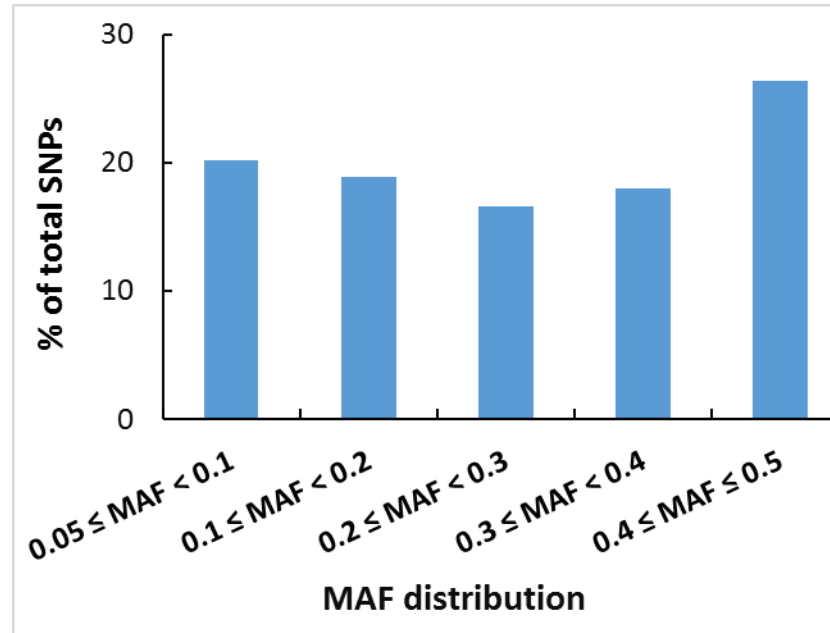


Figure S1: Distribution of minor allele frequency (MAF) of SNP loci detected in limber pine resistant gene analogs (RGAs).

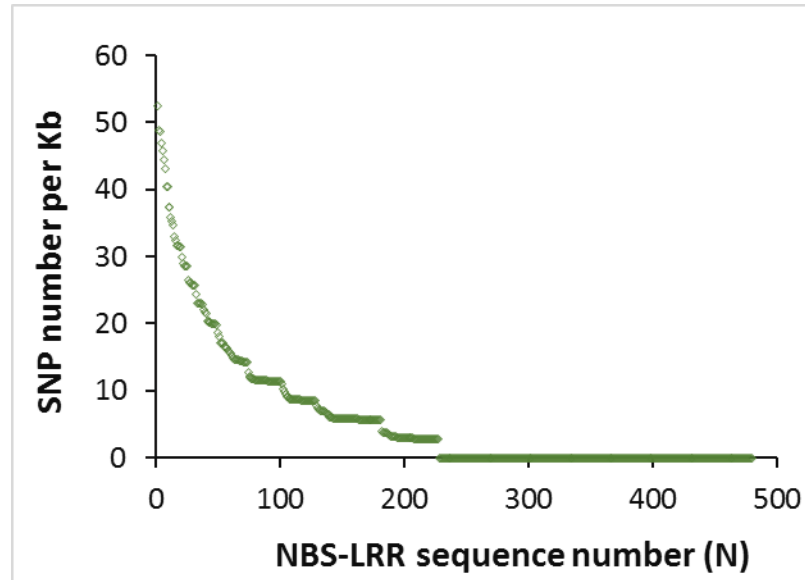


Figure S2: SNP frequencies of limber pine resistance gene analogs (RGAs).

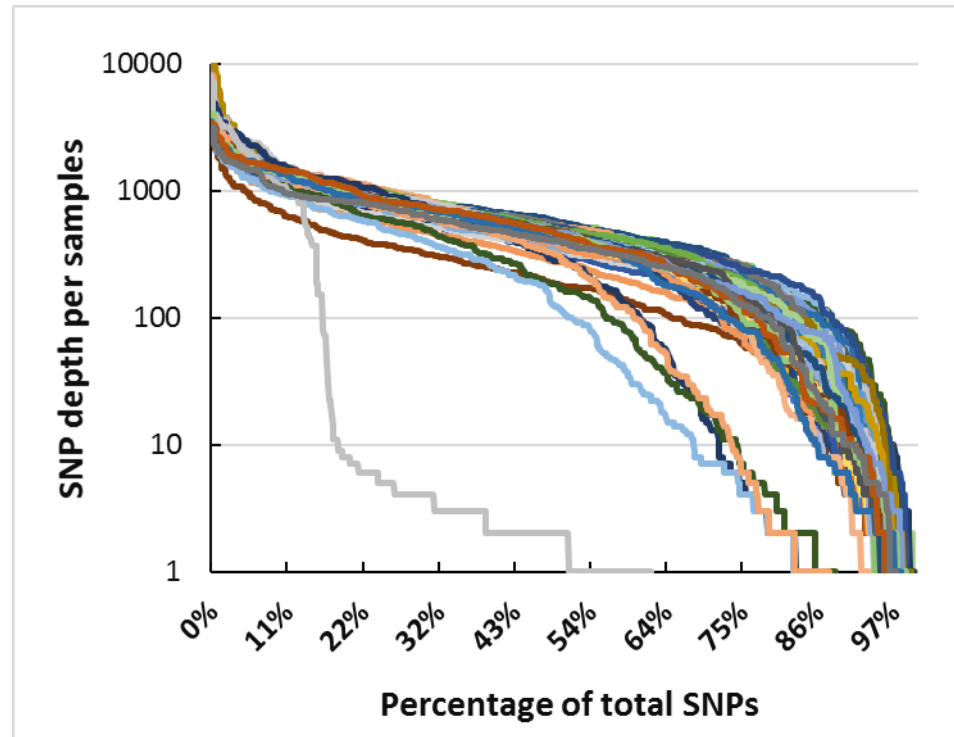


Figure S3: Sequencing depth of SNP loci in individual samples. The percentages of total SNPs (x-axis) have a coverage of a certain depth (y-axis). SNP depth was assessed in each individual of seed family LJ-112. The plot displays data for SNPs (967) with $MAF \geq 0.3$ and about 70% of them have a minimum depth at 10 x in all samples except one.

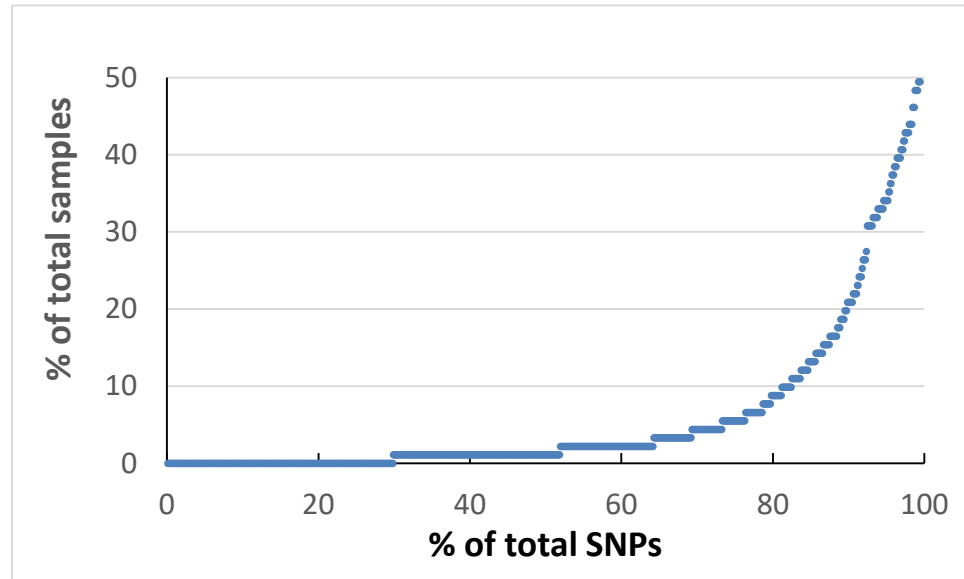
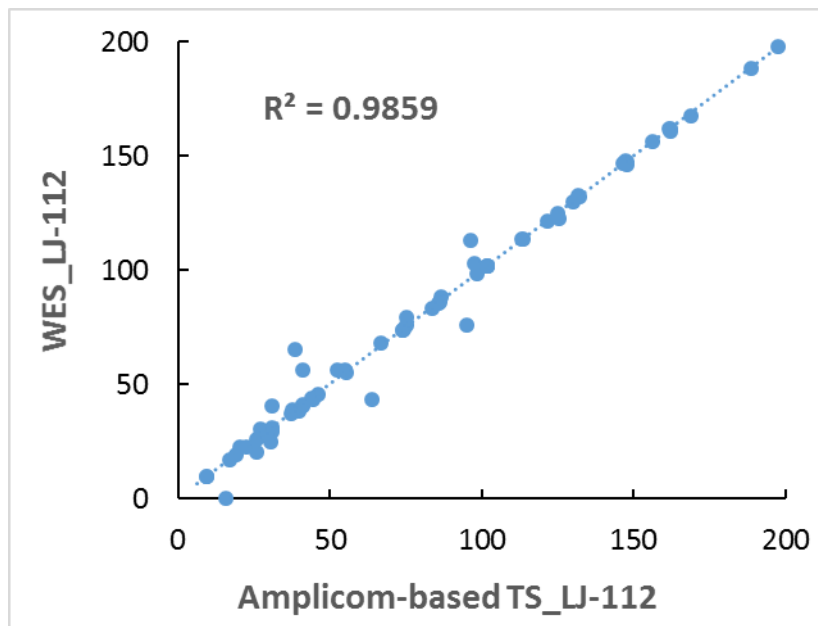


Figure S4: The extent of missing data for 967 SNP loci in 96 individual samples of seed family LJ-112. Individual samples with missing data were calculated as a percentage of the total (y-axis) and plotted across the cumulative total SNPs (x-axis). Over 80% of total SNPs showed missing data in less than 10% of total individual samples.

(a)



(b)

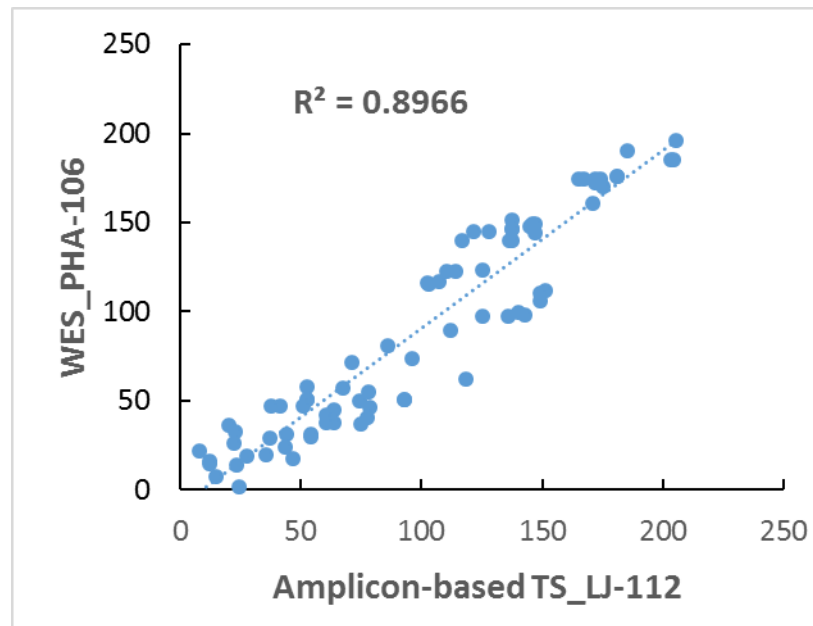


Figure S5: Correlation of SNP positions of the same NLR gene mapped on the same linkage groups (LGs) by both Fluidigm amplicon-based targeted-seq (TS) and whole exome-seq (WES). (a) Comparison of TS and WES in seed family LJ-112; (b) comparison of TS and WES between seed families LJ-112 and PHA-106.

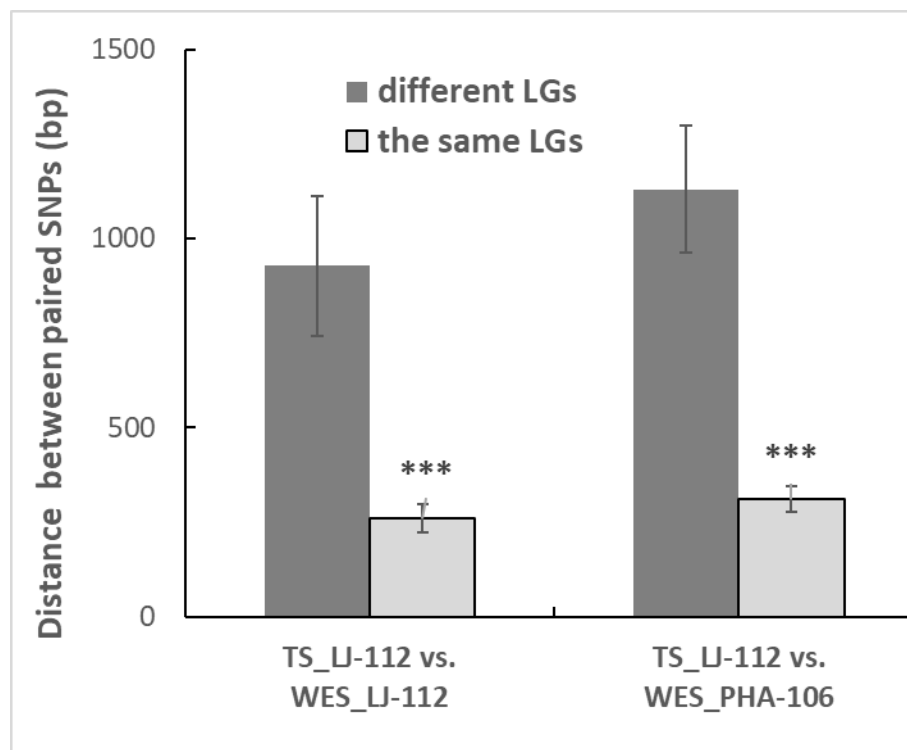
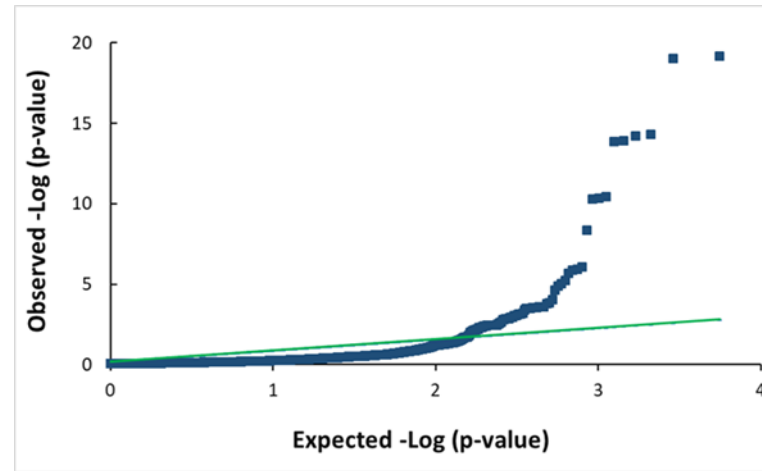


Figure S6: Physical distances (bp) of paired SNPs mapped by Fluidigm amplicon-bases targeted-seq (TS) and whole exome-seq (WES).

(a)



(b)

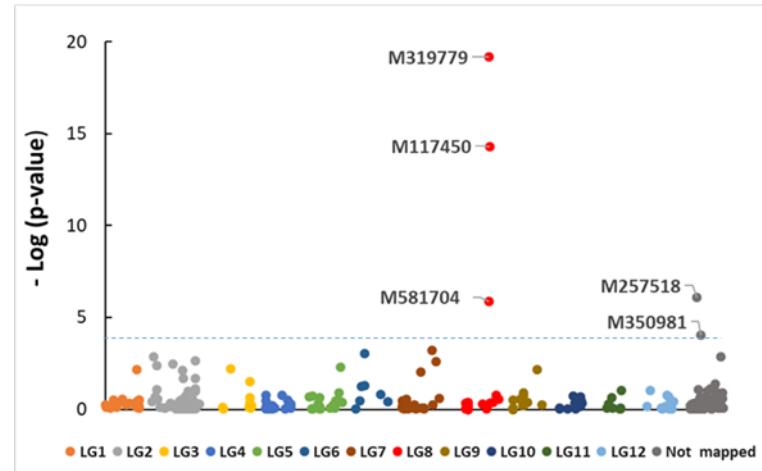


Figure S7: Identification of NLR alleles significantly associated with MGR-conferred phenotypes using extreme-phenotype genome-wide association study (XP-GWAS). (a) Quantile–quantile plot of the test statistic: 5,608 SNPs detected in 354 RGAs with coverage > 50 were subjected to association analysis. (b) Manhattan plot: top SNPs were selected for each genes and plotted against genetic maps of 12 linkage groups, and those genes not mapped so far were included as a separate group. Significant threshold value ($p = 1.69 \times 10^{-4}$) is presented by a horizontal dash line.