

Gene presence-absence variation associates with quantitative *Verticillium longisporum* disease resistance in *Brassica napus*

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Supplementary Figures: S1 to S3

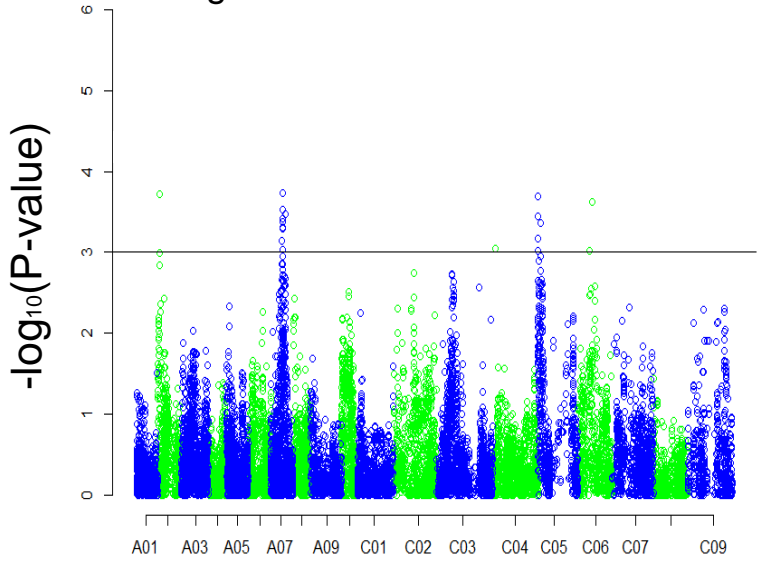
Supplementary Figure Legends

Supplementary Figure S1. Comparison of genome-anchored 60k Illumina Infinium array polymorphic marker data (a) (4 and 12 replicated samples) with genome-anchored Optical Mapping Bionano data for parental genotypes Express617 and R53 for a 3.4 Mbp section from the end of chromosome C01. Consecutively anchored failed calls (grey boxes) in (a) and missing optical mapping molecule alignment (no blue bars) in (b) indicate long-range deletions (absence) in Express617 or R53.

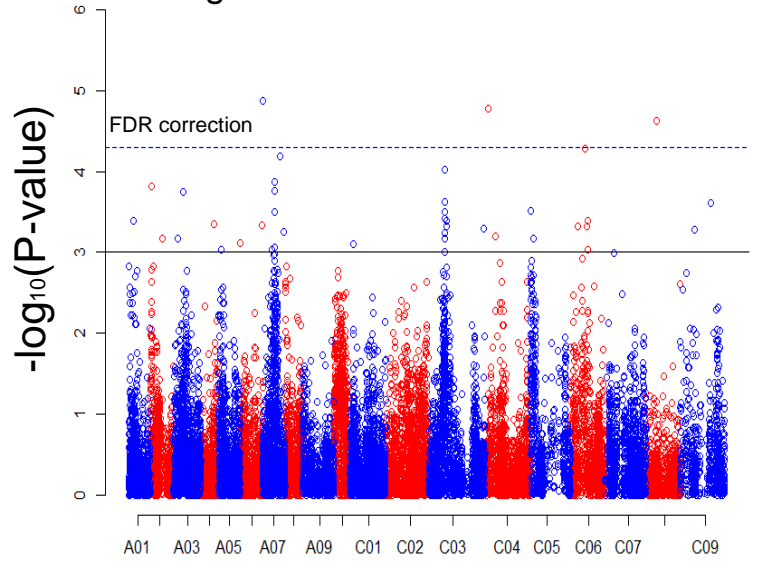
Supplementary Figure S2. GWAS for *V. longisporum* resistance in NAM population comparing SNP map with SNaP map.

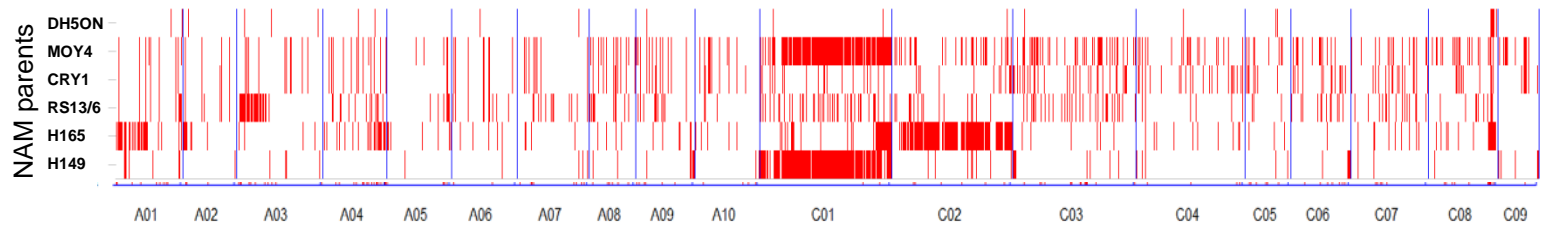
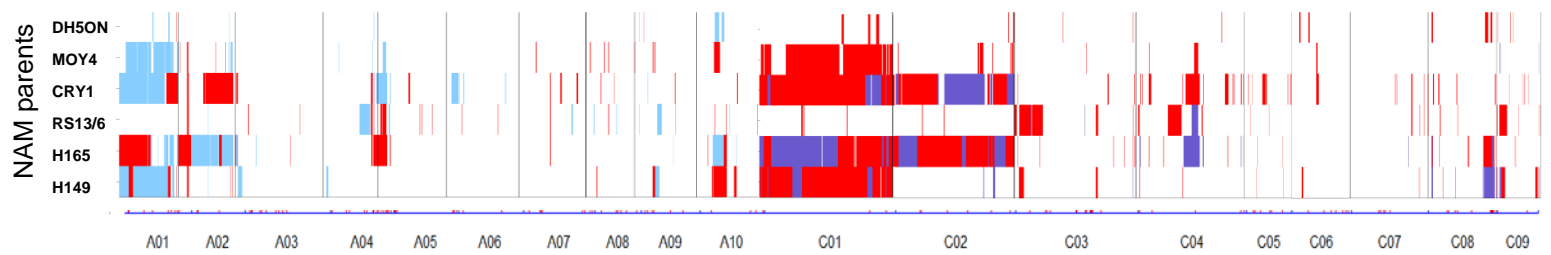
Supplementary Figure S3. Comparison of (a) failed SNaP calls in array genotyping data in red with (b) whole genome sequence coverage data analyses marking deleted regions (red), and homeologous exchanges with duplications in the A genome (light blue) and homeologous exchanges with duplications in the C genome (dark blue) for 6 NAM parental lines.

Using SNP markers



Using SNP and SNaP markers



a.**b.**

Legend:

| SNaP markers

