

Long reads reveal small scale genome structural variations in Allo-tetraploid Canola

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Exploring the dark matter of the rapeseed genome

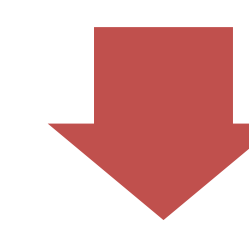
Introduction

Genomic structural variation (SV) in the form of insertions, deletions or translocations have been shown to contribute to multiple important traits in oilseed rape (*Brassica napus*), such as disease resistance and flowering time. However, effective detection of gene-sized SV events is limited by the read length of second-generation sequencing technologies.

Recent advances in long-read sequencing based on Oxford Nanopore technologies provide new opportunities to greatly expand our understanding of the influence of gene scale SV on key phenotypic traits. Here we identified widespread gene scale SV in the rapeseed genome. We also discovered genomic rearrangements associated with flowering time and disease resistance in the rapeseed genome.

Outline of the study

Genome-wide identification of small intra-genic SV



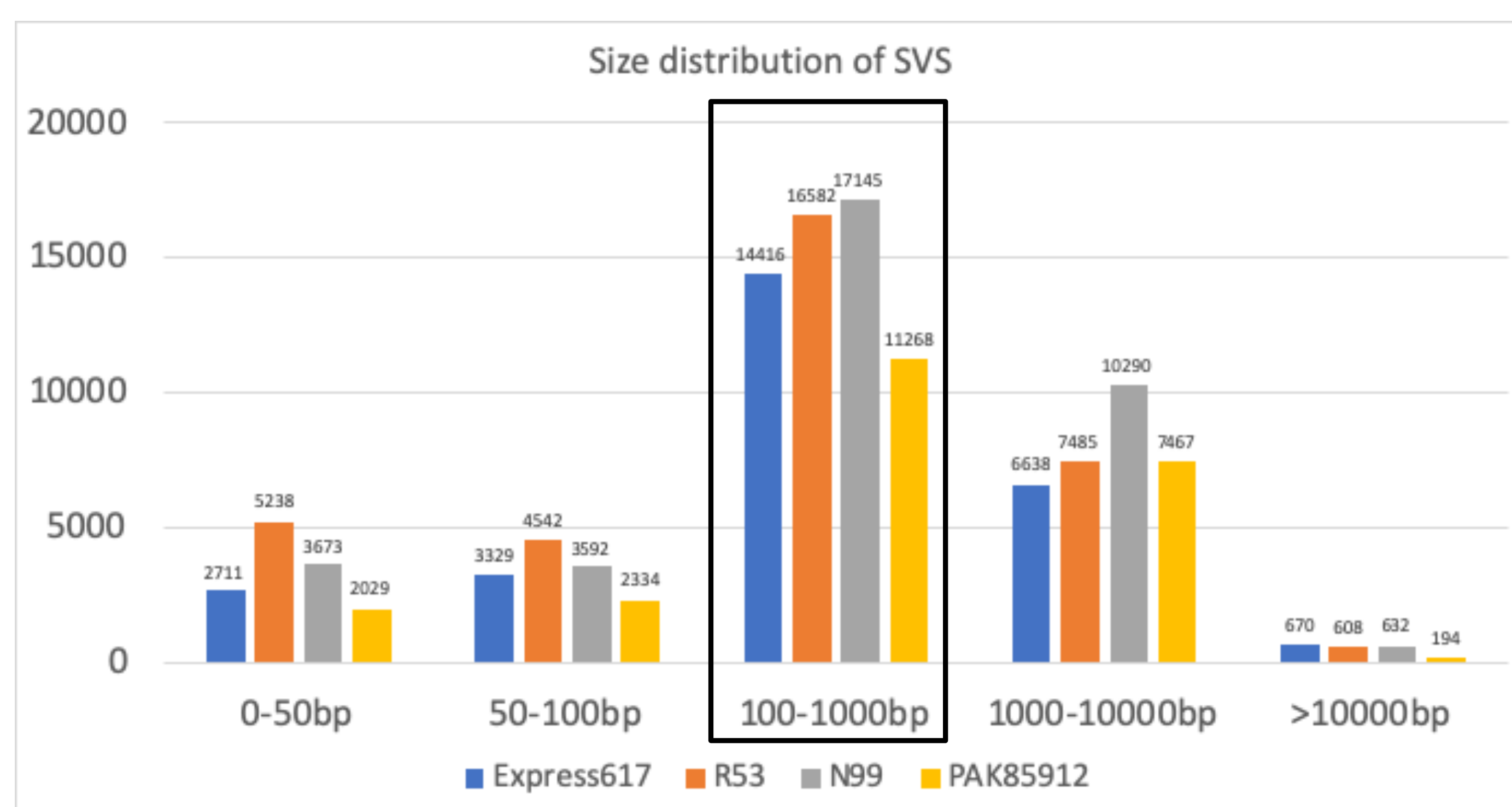
SV associated with eco-geographical adaptations



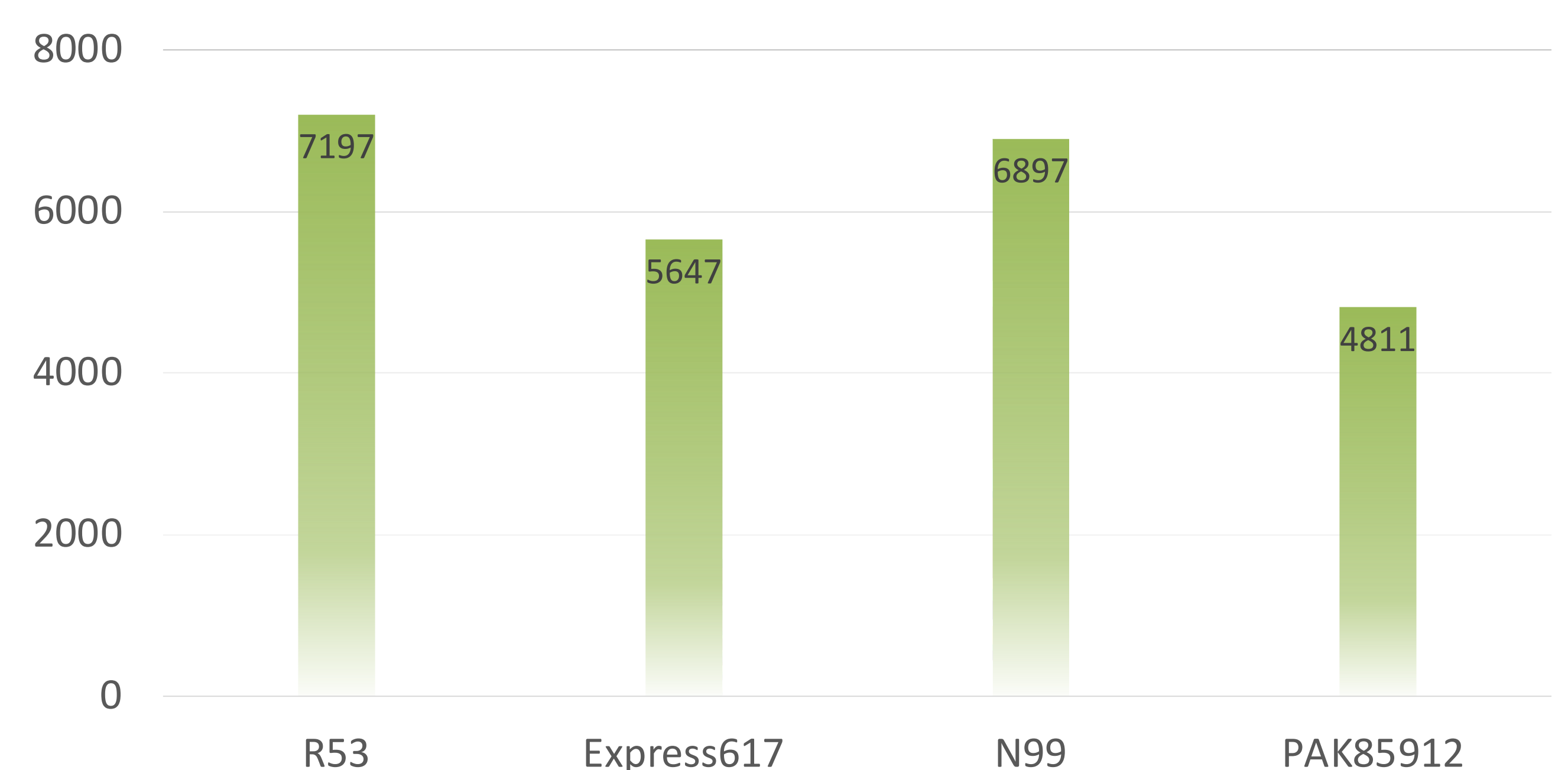
SV contributing to disease resistance

Genome-wide identification of small intra-genic SV

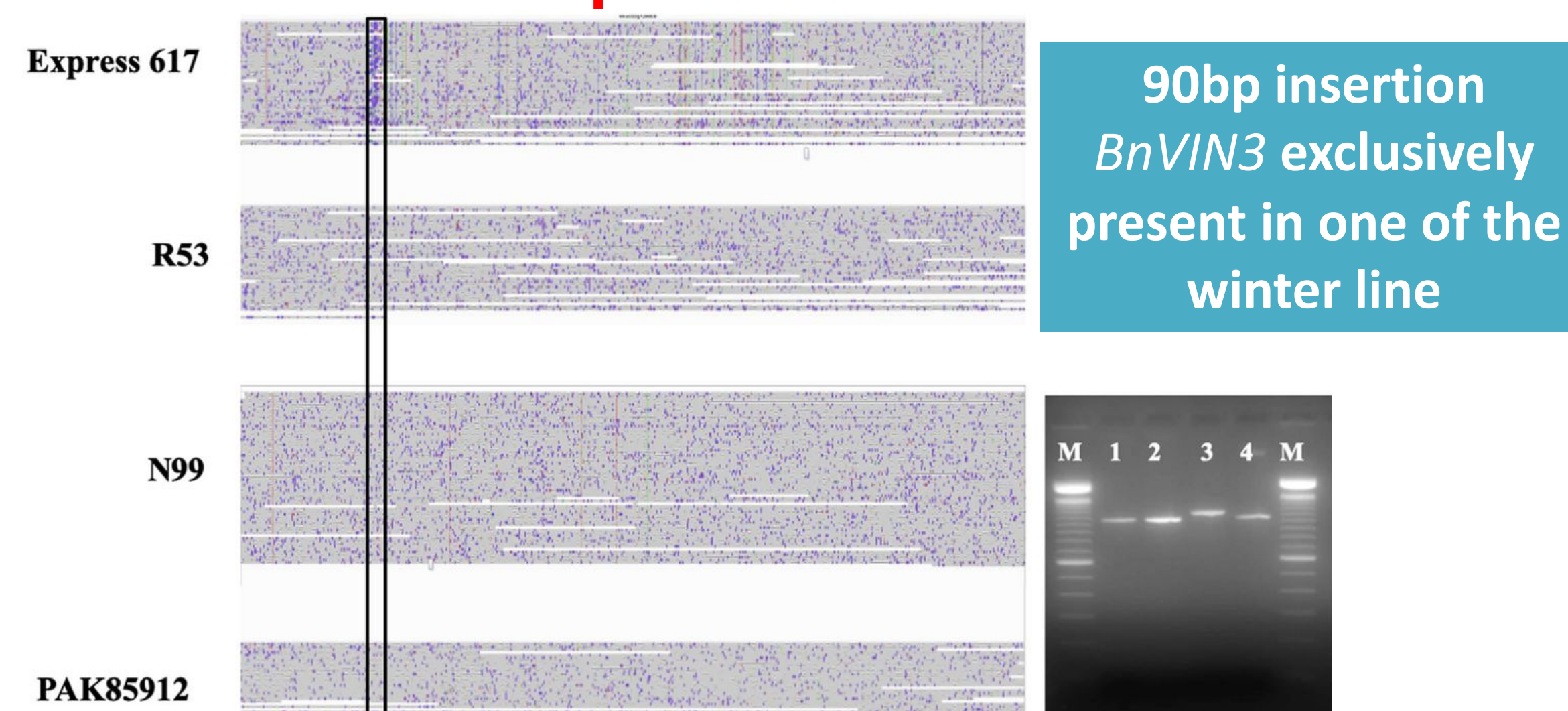
Most SVs range from 100-1000bp



Nearly 5-8% genes were found to contain SV



SV associated with eco-geographical adaptations



SV associated with disease resistance



Conclusion

Our results suggest that simple reference-based resequencing and alignment with long reads can uncover a new dimension of genetic and genomic diversity associated with important traits in crop plants. Particularly in polyploid plants, this may lead to discovery of previously unknown levels of functional diversity of major interest for breeding and crop adaptation.