

# Sequencing 100 whole plant genomes in 100 days

Nanopore long sequencing reads simplify genome assembly and enable the comprehensive, genome-wide analysis of structural variants



*Schatz et al. sequenced 100 tomato genomes in 100 days, using the high-throughput PromethION™, to elucidate the role of structural variation in the development of key agricultural and phenotypic traits*

# Impact

This research provided a thorough characterisation of the structural variant (SV) landscape in a genetically diverse range of tomato genomes. Such insight offers the potential to enrich for desired agricultural traits using targeted genome editing.

# Results

**The high-throughput PromethION platform enabled the team to sequence, assemble, and analyse complete genomes at a scale never seen before, at a fraction of the cost of short-read sequencing.**

**12–16**

tomato genomes sequenced per week

**1 Tb**

of sequencing data generated per week

**25–45k**

SVs detected per sample; many missed with short reads

**10x**

greater contig N50 lengths compared to original reference genome

**83 kbp**

tandem duplication in *EJ2*; associated with higher fruit yields

## HOW?

100 tomato samples were selected to capture the most inter-species genetic diversity<sup>1</sup>. Genomic DNA was fragmented to 30 kbp, sequenced on PromethION, assembled, and analysed for genome-wide SVs.

**Kit** Oxford Nanopore Ligation Sequencing Kit

Available here: [store.nanoporetech.com/ligation-sequencing-kit.html](https://store.nanoporetech.com/ligation-sequencing-kit.html)

**Device** PromethION

**Tools** Custom analysis pipeline, including:  
– NGMLR (alignment and SV detection)  
– Canu (assembly and SV detection)  
– Miniasm, wtdbg2, RaGOO (assembly alternatives)

Find out more about analysis pipelines available here: [community.nanoporetech.com/knowledge/bioinformatics](https://community.nanoporetech.com/knowledge/bioinformatics)

Find out more at: [nanoporetech.com/applications/whole-genome-sequencing](https://nanoporetech.com/applications/whole-genome-sequencing)

### Presentation

M. Schatz. 100 genomes in 100 days: The structural variant landscape in tomato genomes. Available at: <https://nanoporetech.com/resource-centre/michael-schatz-100-genomes-100-days-structural-variant-landscape-tomato-genomes> [Accessed 7 May 2019]

### Publication

1. F. Sedlazeck et al. SVCollector: Optimized sample selection for validating and long-read resequencing of structural variants. BioRxiv (2018). DOI: <https://doi.org/10.1101/342386>



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