



# Assembling plant genomes to greater contiguity

Long-read, PCR-free nanopore sequencing simplifies large genome assembly, enabling resolution of even the highly repetitive regions prevalent in plant genomes.



*Steven Salzberg and colleagues used long nanopore reads in their hybrid assembly of the mega-genome of the giant sequoia, generating the largest scaffolds so far seen for any genome*

# Impact

The greater contiguity of this new giant sequoia genome assembly will enhance the study of its biology. This knowledge will support conservation and breeding efforts, helping to preserve this tree, the largest on Earth, for generations to come.

## Results

**The use of long-read sequencing data generated on the MinION™ device significantly improved the assembly of the giant sequoia genome, and facilitated the generation of the largest chromosome scaffold to date.**

**22x**

genome depth of coverage with nanopore reads

**8.2 Gb**

assembled genome size

**348 kb**

increase in N50 from addition of long nanopore reads

**985 Mb**

largest scaffolded chromosome

**30-fold**

reduction in contig number by including nanopore data

## HOW?

DNA was extracted from giant sequoia (*Sequoiadendron giganteum*) needle tissue, prepared for sequencing using a ligation-based method, and sequenced for 48 hours on 13 MinION Flow Cells. Hybrid assembly was then performed, with the incorporation of chromatin conformation capture data.

<b>Kit</b>	Oxford Nanopore Ligation Sequencing Kit <a href="https://store.nanoporetech.com/ligation-sequencing-kit.html">Available here: store.nanoporetech.com/ligation-sequencing-kit.html</a>
<b>Device</b>	MinION
<b>Tools</b>	MaSuRCA (assembly) Read more about the assembly method used in this study here: <a href="https://nanoporetech.com/resource-centre/sequencing-and-assembling-mega-genomes-mega-trees-giant-sequoia-and-coast-redwood-0">https://nanoporetech.com/resource-centre/sequencing-and-assembling-mega-genomes-mega-trees-giant-sequoia-and-coast-redwood-0</a> Find out more about analysis pipelines available here: <a href="https://community.nanoporetech.com/knowledge/bioinformatics">community.nanoporetech.com/knowledge/bioinformatics</a>

Find out more at: [nanoporetech.com/applications/plant-research](https://nanoporetech.com/applications/plant-research)

## References

S. Salzberg. Sequencing and assembling the mega-genomes of mega-trees: the giant sequoia and coast redwood genomes. Available at: <https://nanoporetech.com/resource-centre/sequencing-and-assembling-mega-genomes-mega-trees-giant-sequoia-and-coast-redwood-0> [Accessed: 20th December 2019]



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RS\_1053(EN)\_V1\_06Jan2020