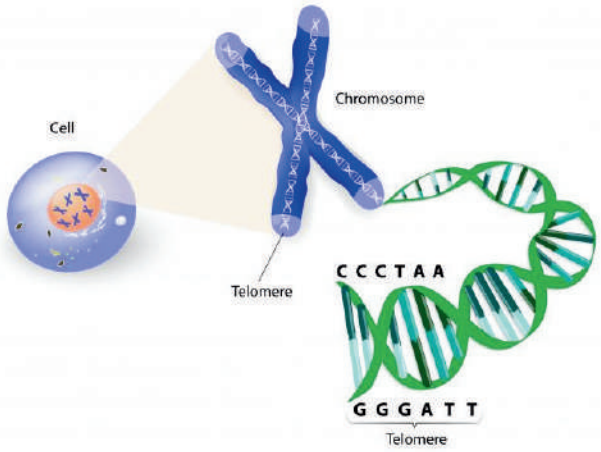
Genotypic
genomics simplified

Telomere-to-Telomere Sequencing

Unlocking the Genomic Mysteries

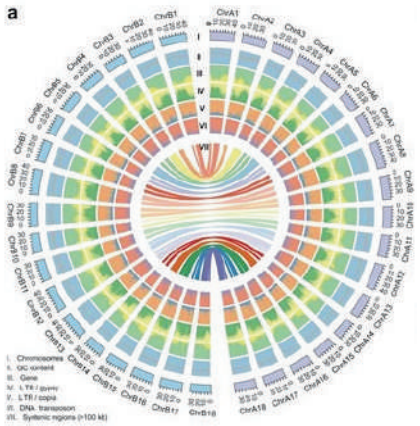


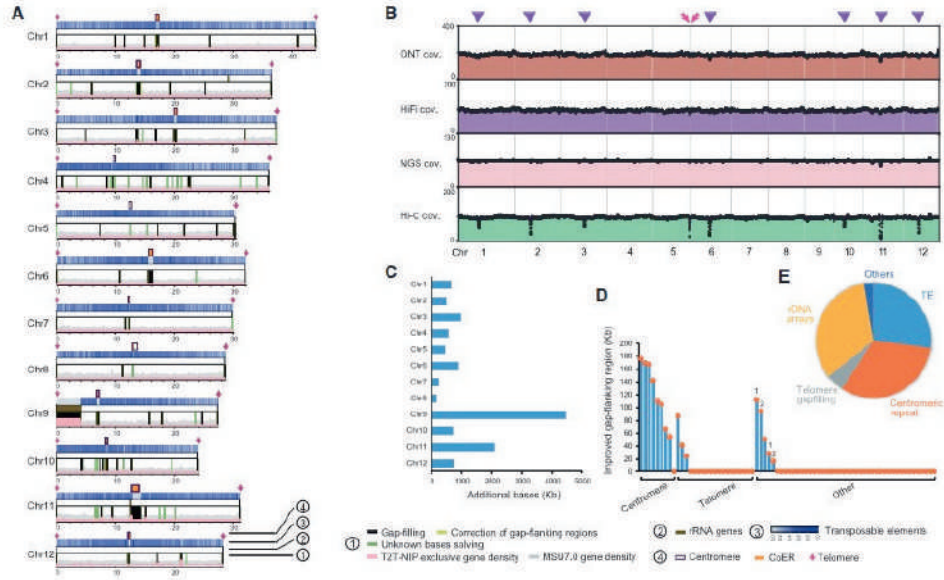
Assembly of High quality genomes:

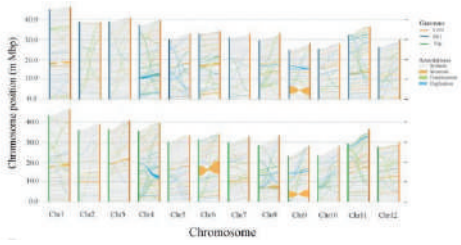
Sequencing and assembly of high quality gapless genomes is of at most importance for the advancement of multiple aspects of basic biology as well as medical and agricultural applications. Complete haplotype resolved genome assemblies require data from multiple platforms and high end computational requirements. Nanopore sequencing enables sequencing of ultra long reads of the genome as well helps to resolve chromosome conformation through Pore-C sequencing. With the combined data from long reads, ultra long read and Pore-C data, Nanopore sequencing data has the potential to assemble the complete genome. Telomere to telomere genomes not only improve our understanding of the genomic elements but also modifications of the genomes are better resolved. This resolution provides better insights into their role in health and disease.

Advantages of Nanopore Long read Technology

- High quality gap free assemblies for genomes
- Resolution of repeats for CentC-rich and CentC-poor centromeres
- Information of clusters of paralogous genes
- Resolution of Transposable elements and segmental duplications
- Resolution of structural Variations and Complex Genomic Regions
- Telomere Biology and Aging
- Better understanding of genomic regions and association to diseases.
- Improved molecular breeding and gene characterization in plants







Sequencing coverage and assembly validation of the T2T-NIP. Uniform whole-genome coverage of mapped HiFi, ONT, Hi-C, and Illumina reads is shown with primary alignments.

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