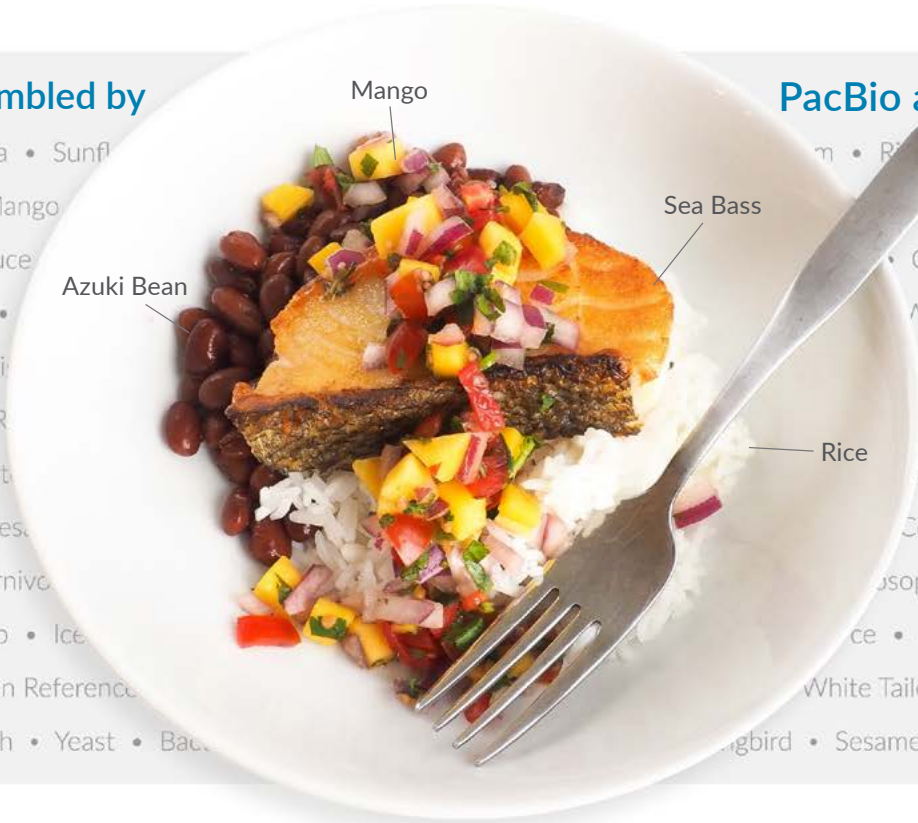


Transforming *De Novo* Assembly

Industry-leading reference-quality genome assembly services

Genomes assembled by

Goat • Azuki Beans • Cassava • Sunflower
 Bovine • Mustard Greens • Mango
 Sea Bass • Pea • Norway Spruce
 Cannabis • Maize • Aspen •
 Hawaiian Crow • Cabernet Sauvignon
 Human Twins • Silkworm • Rice
 Bean • Chinese Herb • White
 Quinoa • Hummingbird • Sesame
 Sugar Beet • Wild Potato • Carnivorous
 Cassava • Sunflower • Sheep • Ice
 Mustard Greens • Rice • Human Reference
 Pea • Norway Spruce • Spinach • Yeast • Bac



PacBio and DNAnexus

m • Rice • Arabidopsis • Sunflower
 Herb • White Tailed Deer • C
 Crab • Tobacco • Duroc PigS
 Wild Potato • Carnivorous Plan
 Sunflower • Sea Bass • Plan
 Mango • Human Reference • M
 Pea • Spinach • Yeast • Bac
 Cotton • Sugar Pine • Duroc P
 Asophila • Mosquito • Azuki Bea
 Pea • Arabidopsis • Mango • Bovin
 White Tailed Deer • Coffee • Sea Bass
 Hummingbird • Sesame • Crab • Tobacco • Cannab

De Novo Genome Assembly is Complex

De novo genome assembly is a complex task made more challenging by high levels of genetic diversity, repetitive elements, and duplicated genomic regions. Plant species are especially challenging because of their higher ploidy and high repeat content.

Recent advances in long-read sequencing have allowed researchers to improve the accuracy of assemblies through longer contiguous sequences, allowing reads to span repeat elements and unambiguously link neighboring sequences. The algorithms used to perform these assemblies can be difficult to tune for each species and require massive computational resources to weave these long-reads into a final, polished assembly.

Let us do the heavy lifting, so you can focus on advancing science. DNAnexus genome assembly services provide an easy path to reference-quality genomes.

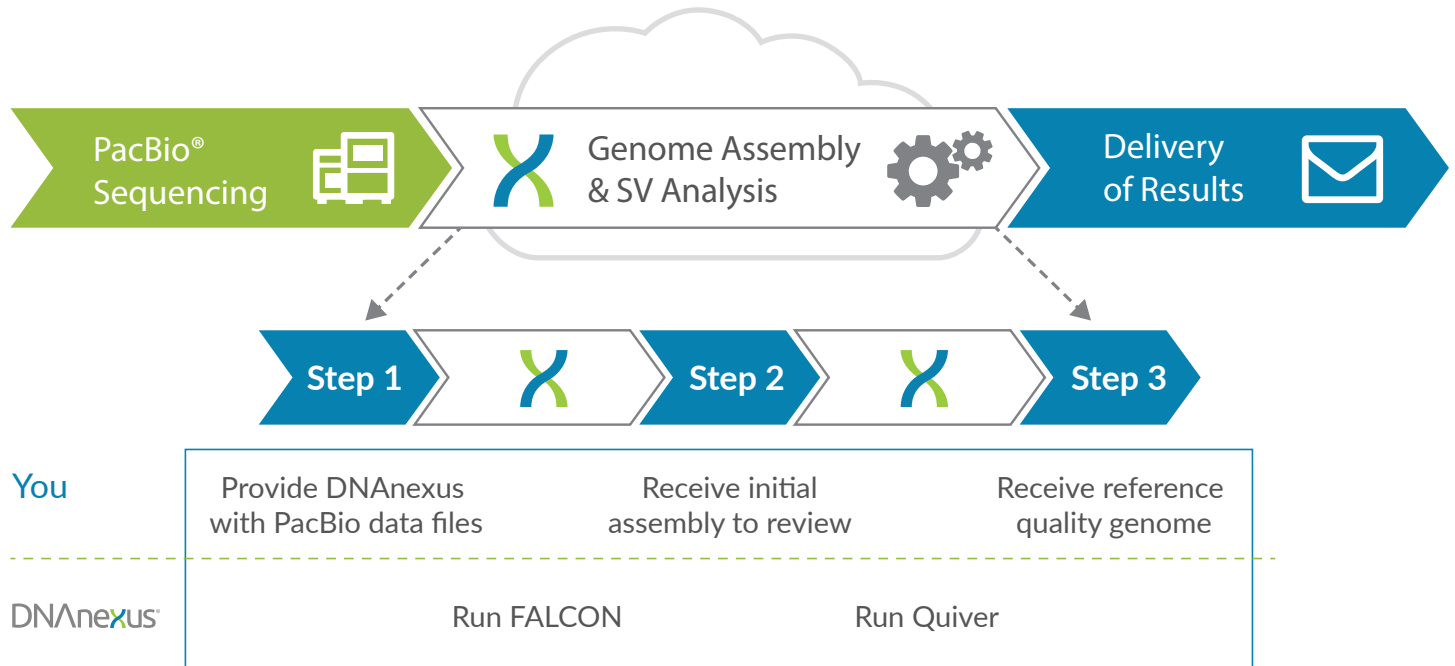
Let us be your bioinformatics partner!

DNAnexus Services make *De Novo* Assembly SIMPLE:

- Fast, accurate, and cost-efficient solution
- Expert bioinformatics support
- Secure delivery of results and quality metrics
- No need for complex local compute infrastructure, applications deployment, and support
- Easy utilization of additional bioinformatics tools (e.g., structural variant callers)

We Make the Complex Simple

Rapid reference-quality genome assembly services



CASE STUDY: Turnkey Tobacco Assembly

OBJECTIVE: Scientists need a reference-quality genome to gain a more comprehensive understanding of the genetics of tobacco, a key commercial crop.

CHALLENGES: The tobacco genome is large (comprised of 4.5 billion base pairs), tetraploid, and highly repetitive.

RESULTS: From data files to delivery, DNAnexus assembled the tobacco genome in 9 days, utilizing 160,000 core-hours of compute. This would have taken >6 weeks if performed by the customer.

Pangu Gene Company: Tianjin, China

“DNAnexus provided us with a turnkey solution for de novo genome assembly of the complex tobacco genome. Once we uploaded the raw PacBio reads to the DNAnexus Platform, a reference quality genome was delivered to us in 20% of the time it would have taken on a local HPC cluster.”

Yaoshou ZHANG, Vice President
Tianjin International Joint Academy of Biomedicine (TJAB)

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