

Unlocking genomic potential: *de novo* genome assembly and annotation with PacBio long-read sequencing

Comprehensive genome sequencing and annotation are fundamental to understanding the biology of any organism. While short-read sequencing technologies have revolutionized genomics, they struggle to resolve complex genomic regions and repetitive elements, leading to fragmented assemblies and incomplete annotations. PacBio long-read sequencing technology overcomes these limitations, enabling the generation of highly contiguous and accurate *de novo* genome assemblies, even for complex genomes.

Signios Bio offers a streamlined and comprehensive solution for *de novo* genome assembly and annotation. Leveraging our expertise in high molecular weight DNA and RNA, long-read sequencing, and bioinformatics pipelines we can partner with you to generate a reference-quality genome for use in your biological research.

A seamless workflow for complete genome understanding



Benefits of our integrated approach

- **Reference-quality genome assembly:** Obtain a highly contiguous and accurate genome assembly, exceeding the quality of short-read based assemblies.
- **Comprehensive genome annotation:** Achieve complete and accurate gene models, including identification of isoforms, alternative splicing, and gene fusion events, including identification of isoforms and alternative splicing, crucial for downstream functional studies.
- **Streamlined workflow:** Benefit from a single, integrated solution provider for all your genome sequencing and annotation needs, saving time and resources.
- **Expert support:** Our team of experienced scientists and bioinformaticians provides expert guidance and support throughout the entire project as collaborators and not just data providers.

Genome assembly and annotation analysis solutions

Our dedicated team of bioinformaticians employs a robust pipeline for:

- **Genome assembly:** Generating a high-quality, contiguous genome assembly with minimal errors.
- **Genome annotation:** Identifying and annotating genes, coding sequences, regulatory elements, and repetitive regions using both *ab initio* and evidence-based approaches, including mapping Iso-seq data for accurate gene models.
- **Comparative genomics:** Providing insights into genome evolution and species-specific features.

Specifications for genome assembly and annotation projects

Genome Assembly		Genome Annotation	
Input DNA	≧5µg	Input RNA	≧600ng
DNA size distribution	50% >30kb	RNA quality	RIN≧7
Coverage	10 to 15-fold per haplotype	Coverage	5-10 million reads per sample
SMRT Cells	1 per 3Gb of genome	SMRT Cells	1 per 4-8 tissues

Signios Bio: your research partner for de novo genome assembly and annotation

Our integrated PacBio long-read sequencing service for *de novo* genome assembly and annotation empowers researchers with a powerful tool to unlock the full potential of their genomic data. Our comprehensive solution delivers a high-quality, annotated genome ready for immediate use in downstream analyses, accelerating your research and driving impactful discoveries. Contact us today to discuss how we can help you decipher the complexities of your target genome.



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