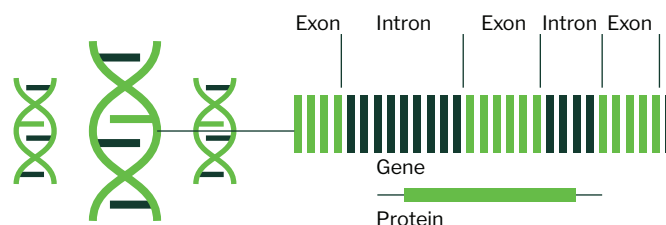


Signios Bio's advanced whole exome sequencing solutions

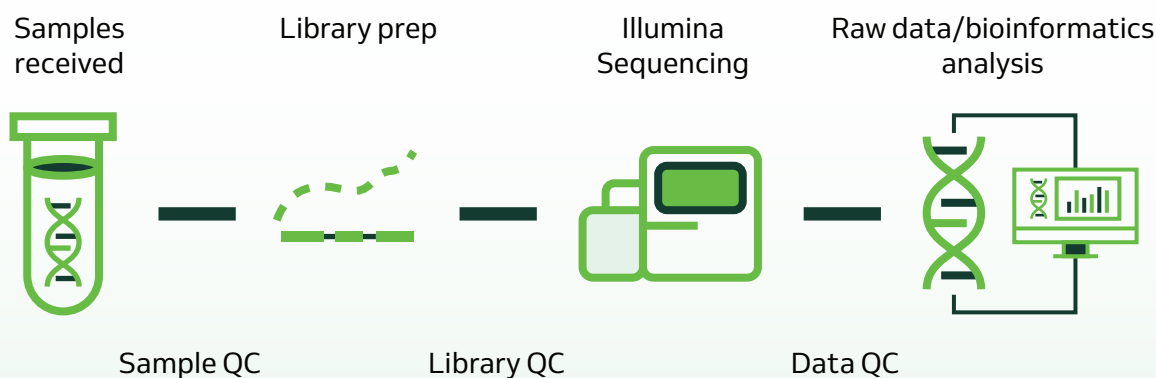
Whole exome sequencing (WES) is a targeted approach that sequences the protein-coding regions of the genome, known as exons. Although the exome comprises only about 1.5% of the human genome, it contains approximately 85% of known disease-causing variants, making WES a highly cost-effective and powerful tool for identifying these mutations. WES offers distinct advantages over whole genome sequencing by providing more focused coverage of the coding regions. It is particularly beneficial for research in areas like population genetics, the study of genetic diseases, oncology and pharmacogenomics.



Key advantages of Signios Bio's whole exome services

- **Cost-effective with swift turnaround:** Benefit from our affordable and rapid project completion capabilities.
- **Versatile read lengths:** Tailor your sequencing with options such as PE100, PE150, or customizable read lengths.
- **Optimized probe design:** Ensure precise and efficient sequencing with enhanced target capture.
- **Comprehensive coverage:** Achieve thorough analysis with extensive genetic variant detection.
- **Higher sequencing depth:** Enhance variant calling accuracy and sensitivity with deeper sequencing.
- **Accelerated research:** Reduce data analysis time and obtain faster results with a targeted sequencing approach.

Signios Bio's workflow is designed to seamlessly accommodate various types of input samples



Technical guidelines for various sample types

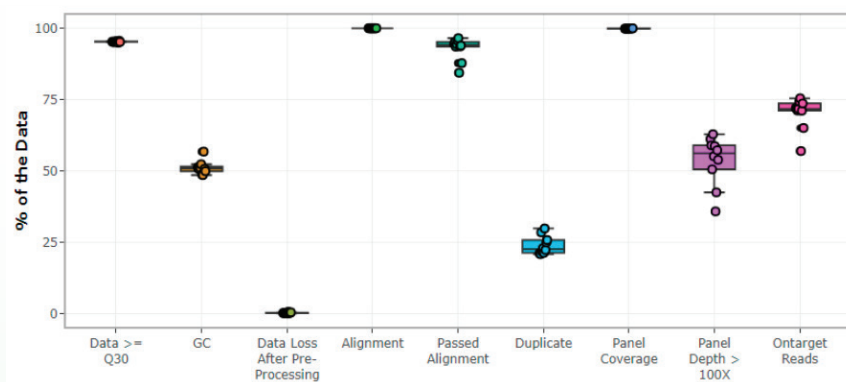
Sample type	Purified gDNA	Ideal: 1-3 µg gDNA Minimum: 250 ng gDNA and above (Qubit quantified) Concentration: 10-50 ng/µl (minimum 20 µl and above volumes)
	Cells	Recommended: 1e+6 cells frozen and pelleted
	Tissue	60 mg of fresh or frozen tissue or 20 mg of stabilized tissue
	Blood	gDNA: 0.5 - 1 mL cfDNA: minimum 10mL; 20mL recommended
	FFPE	5 slides with 10 µM thick tissues and surface area of 250 mm ²
	Curls	5 curls (10 µM thick)

WES bioinformatics analysis capabilities

Signios Bio's WES comprehensive bioinformatics solutions transform complex data into actionable insights, facilitating drug discovery and biomarker identification. Our advanced pipelines excel in analyzing germline, somatic, structural, and copy number variants.

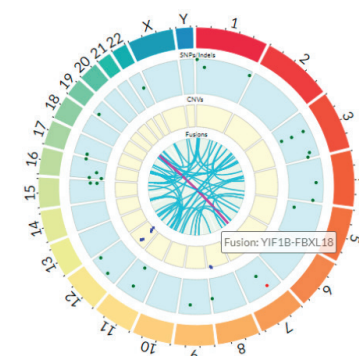
- Detailed data quality, alignment, and coverage statistics
- Distribution of base changes for SNVs
- Circos plots for SNPs, InDels, CNVs, and structural variant representation
- Lollipop plots for gene variant visualization
- Mutation signatures and tumor mutation burden

Detailed data quality, alignment and coverage stats

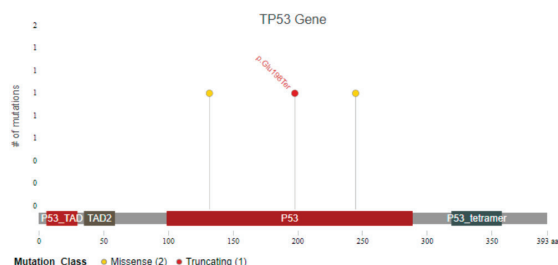




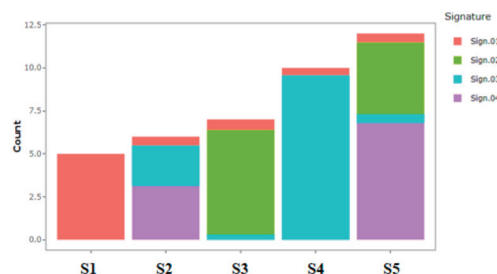
Distribution of base changes for SNVs



Circos plots for SNPs, Indels, CNVs and SV representation for selected genes



Lollipop plots showing variants for genes



Explore mutation signatures

Leverage Signios Bio's expertise for superior WES results

- Tailored experimental design and workflow optimization based on your research goals
- Experience in handling diverse sample types with options for low-input and degraded samples
- Comprehensive services from sample extraction to in-depth bioinformatics analysis
- Enhanced data interpretation through customized visualizations and publication-ready figures
- Access to a secure customer portal to track your project and view results
- 30-day sample and data storage
- Expert consultations for quality assurance
- Dedicated technical support for laboratory and bioinformatics inquiries

Contact us today for pricing and to begin planning your customized solution.

✉ info@signiosbio.com

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