



PacBio Third Generation Sequencing Services

Avance Biosciences now offers long-read sequencing with the PacBio Vega system, expanding our capabilities alongside Illumina, AVITI™, and Sanger platforms. PacBio's HiFi technology delivers highly accurate, long reads without the need for PCR amplification, making it ideal for whole genome sequencing and detailed analysis of plasmids, viral genomes, and viral vectors. Its ability to sequence through GC-rich regions and complex secondary structures, areas where PCR-based methods like short-read and Sanger sequencing often struggle, makes it a powerful tool for resolving difficult sequences with precision.

Our Expertise

Avance Biosciences has been a pioneer in regulated next-generation sequencing (NGS) since introducing the Illumina MiSeq platform to our GMP lab in 2013. We have since delivered numerous method development, validation, and testing projects under CGMP and GLP standards, earning a reputation for excellence in compliant NGS applications.

Today, our capabilities include short-read platforms like Illumina and AVITI™, long-read technologies such as Oxford Nanopore and PacBio HiFi, and advanced single-cell platforms like 10x Genomics and Mission Bio. This broad portfolio allows us to support sequencing needs across all phases of drug development, cell and gene therapy, and biologics manufacturing.

Services Offered for CMC Support

Methods	Applications
Identity Testing	Full-length sequencing of plasmids, viral vectors, viral genomes, mRNA vaccines and therapeutics, and sgRNA+mRNA complexes
Purity Testing (Genetic)	Detection of sequence variants, contaminants, or unintended DNA species in plasmids, viral vectors, mRNA vaccines and therapeutics, and sgRNA+mRNA complexes
Structural Characterization	Verification of the structural integrity of viral vectors, AAV genomes, mRNA vaccines and therapeutics, and circular DNAs (e.g., minicircles) and RNAs (circRNAs)
Integration Site Analysis	Mapping the genomic location(s) and verifying the integrity of transgene integration in engineered cell lines or gene-edited cells
Whole Genome Sequencing	Comprehensive sequencing of engineered cell lines and allogeneic therapeutic cells

Services Offered for Preclinical and Clinical Studies

Application Area	Platform Capability (Detailed Explanation)
Variant Calling	Detection of single nucleotide variants (SNVs), insertions and deletions (indels), structural variants (SVs) such as large insertions, deletions, duplications, inversions, and translocations. Supports phasing (determining which variants are on the same chromosome) and direct detection of DNA methylation (an epigenetic modification affecting gene regulation).
Targeted Sequencing	Deep sequencing of specific genomic regions using gene panels, hybrid capture, or amplicon-based enrichment to analyze plasmids, transgenes, or therapeutic target loci.
Transcriptomics	Comprehensive analysis of full-length mRNA transcripts to resolve isoforms (different mRNA variants produced from the same gene) and single-cell RNA sequencing to study gene expression patterns at the individual cell level.
Epigenetics	Direct measurement of DNA methylation patterns across the genome without requiring bisulfite conversion, enabling analysis of gene regulation, potential biomarkers, and the effect of epigenetic therapies.
Metagenomics / Microbiome	High-resolution profiling of complex microbial communities present in clinical samples, biological materials, or production environments. Also supports detection of adventitious microbial agents (unintended microbial contamination).
Cancer Genomics	Detection of fusion genes (abnormal joining of two separate genes), comprehensive epigenetic profiling, identification of complex structural variants, and cancer-specific circRNA biomarkers frequently involved in cancer development and therapeutic resistance.
Rare Disease and Complex Variant Studies	Phasing of disease-associated variants (determining whether multiple pathogenic variants are inherited on the same or different chromosomes) and detection of repeat expansions (abnormally long repetitive DNA sequences linked to rare diseases).

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