PACBIO CERTIFIED
SERVICE PROVIDER

WEBSITE SUPPORT GUIDE
APPLICATION MESSAGING

PACBIO®

APPLICATIONS OF SMRT® SEQUENCING

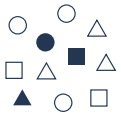
PacBio® Single Molecule, Real-Time (SMRT) Sequencing technology consistently produces some of the longest average read lengths available in the industry. With long reads, the high consensus accuracy (>99.999%, Q50), uniform coverage, and simultaneous epigenetic detection - SMRT Sequencing delivers valuable insights that previously have been unavailable to the scientific community.

The flexibility of the PacBio platform allows you to get the benefits of long-read sequencing across these applications:

WHOLE GENOME SEQUENCING

RNA SEQ

TARGETED SEQ



COMPLEX POPULATIONS

EPIGENETICS

WHOLE GENOME SEQUENCING FOR *DE NOVO* ASSEMBLY

Whole genome sequencing for *de novo* assembly using SMRT Sequencing is now the gold-standard for generating contiguous, highly accurate reference genomes across all species. With megabase-size contig N50s, consensus accuracies >99%, and tools for phasing haplotypes, PacBio assemblies capture undetected SNPs, fully intact genes, and regulatory regions embedded in complex structures that fragmented draft genomes often miss. Learn more about whole genome sequencing at pacb.com/wgs

WHOLE GENOME SEQUENCING FOR STRUCTURAL VARIANT CALLING

SMRT Sequencing enables structural variant discovery using low-coverage, long-read whole genome sequencing which has shown that any individual diploid human genome contains upwards of ~20,000 unique structural variants (defined as >50 bp in length), and another ~400,000 indel variants (ranging in length from 1 bp to 49 bp). Over 80% of these variants are currently not detected using standard short-read sequencing methods. Learn more about structural variant calling at pacb.com/sv

RNA SEQUENCING

The PacBio Isoform Sequence (Iso-Seq®) method allows sequencing of transcript isoforms in their entirety, with no assembly required by leveraging the long reads to deliver a single, highly accurate sequence for each transcript isoform, from the 5′ end to the poly-A tail. Learn more about RNA sequencing at pacb.com/iso-seq

TARGETED SEQUENCING

PacBio targeted sequencing application supports both amplicon sequencing as well as probe-based capture using DNA oligo hybridization. The long reads and the low sequence context bias allows you to characterize targeted regions of interest irrespective of their genetic complexity – including structural variations, rare SNPs, indels, copy number variation, microsatellites and extended conserved regions. Learn more about targeted sequencing at pacb.com/target

COMPLEX POPULATIONS

Bacteria, viruses, and cancer cells are often found in complex populations which contain many unique and evolving genomes. These variants allow for rapid evolution in response to environmental conditions, immune pressures, or drug treatments. Distinguishing co-existing variants can require complex assembly, making the identification of closely related individuals within a mixture extremely challenging. SMRT Sequencing provides the long reads, single-molecule resolution, and uniform coverage needed for the comprehensive characterization of heterogeneous samples and the identification of complex variation. Learn more about complex populations at pacb.com/pop

EPIGENETICS

SMRT Sequencing directly detects DNA modifications by measuring variation in the polymerase kinetics of DNA base incorporation during sequencing. With high throughput, long reads, and the sensitivity to detect epigenetic modification without amplification or chemical conversions you are able to assess DNA modifications in bacterial and eukaryotic genomes. Learn more about epigenetics at pacb.com/epigenetics

Like the application icons above and want to use them on your website?
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