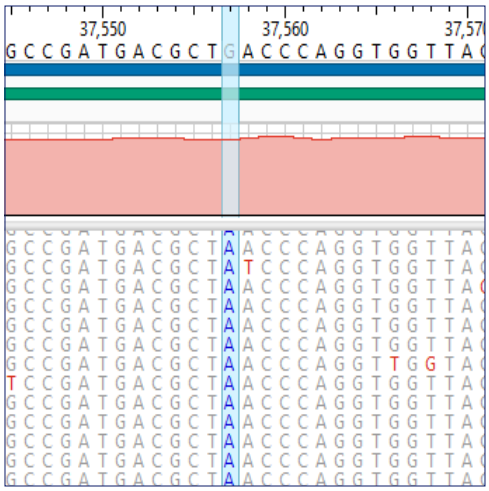
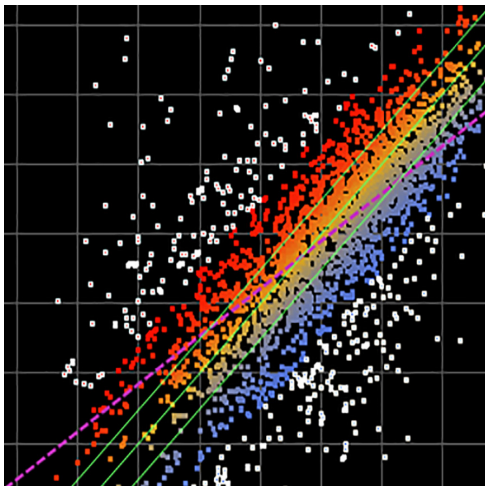
DNASTAR

LASERGENE

LASERGENE GENOMICS

Accurate, intuitive software for sequencing data analysis





RESEQUENCING AND GENOTYPING

- Support for all major sequencing technologies
- Comprehensive multi-sample variant analysis, variant filtering and variant set comparison
- Identification of maternal/paternal haplotypes in long-read data up to human genome size
- Viral genome analysis, including ARTIC
- Copy number variation (CNV) calculation
- SNP to structure workflow for modeling impact of mutations on protein structure

GENOME ASSEMBLY AND EDITING

- *De novo* genome assembly and contig editing
- Hybrid *de novo* assembly with closely related reference for contig ordering and scaffolding
- Gap closure for genomic alignments

METAGENOMICS

- Alignment of metagenomic sequencing data to biome genomes and gene databases
- *De novo* assembly of novel sequences

TRANSCRIPTOME ANALYSIS

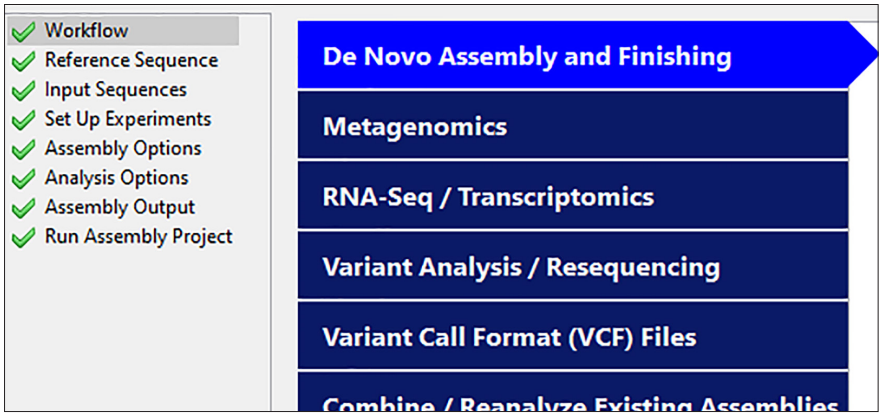
- *De novo* transcriptome assembly with auto-mRNA annotation
- RNA-Seq gene expression analysis with EdgeR or DESeq2 generates PCA and Volcano plots
- ChIP-Seq peak detection
- Microarray analysis
- miRNA discovery, quantification, and gene expression
- Combined analysis and visualization of gene expression data from multiple technologies

Comprehensive tools that are easy to learn and use

QUICK SETUP FOR GENOMIC SEQUENCING PROJECTS

Lasergene Genomics includes SeqMan NGen, our revolutionary assembler that enables you to set up your entire genomic sequencing project in mere minutes and automates tasks that typically require extensive manual intervention.

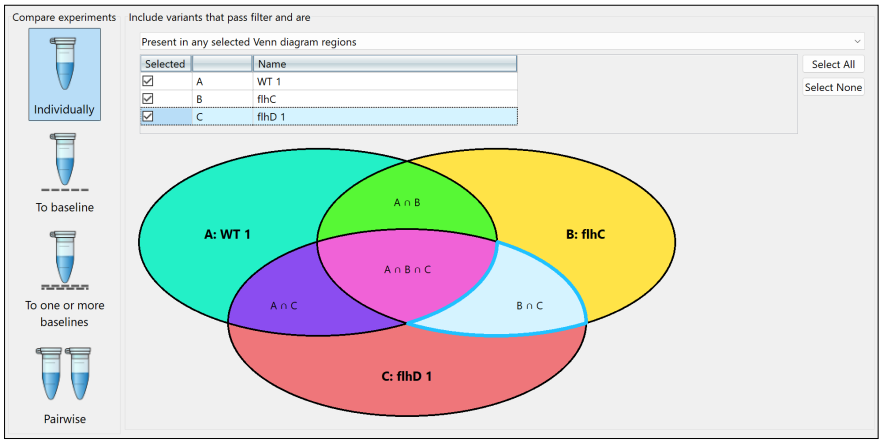
Lasergene Genomics supports PacBio CLR and HiFi, Oxford Nanopore Technologies (ONT), Illumina, Ion Torrent, and Sanger/ABI read technologies.



The simple SeqMan NGen wizard makes it easy to set up even the most complex projects. Start by choosing the workflow of interest from the Workflow screen.

AUTOMATED PIPELINE FROM RAW DATA TO ADVANCED ANALYSIS

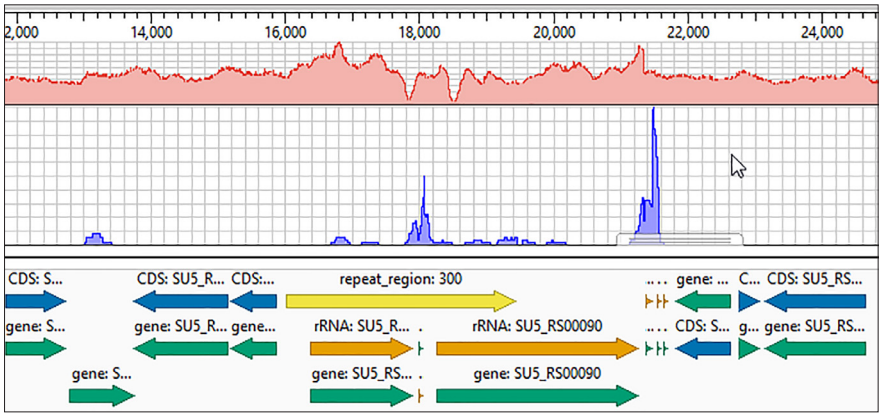
Our automated pipeline does the heavy lifting for you, including organizing replicates, incorporating BED and VCF files, and automatic detection and annotation of variants. Your finished project is delivered ready for you to view and analyze the results.



GenVision Pro provides numerous options for filtering variants and creating variants sets, including the selection of components from a Venn diagram.

INTEGRATED ACCESS TO DNASTAR CLOUD ASSEMBLIES

Our patented algorithms enable you to assemble and align your sequencing data with unsurpassed ease and speed, but if your project requires more computing power, we provide integrated access to our secure cloud computing resources, freeing up your local computer for other tasks.



Annotated genome showing coverage and split reads graphs in SeqMan Ultra.

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