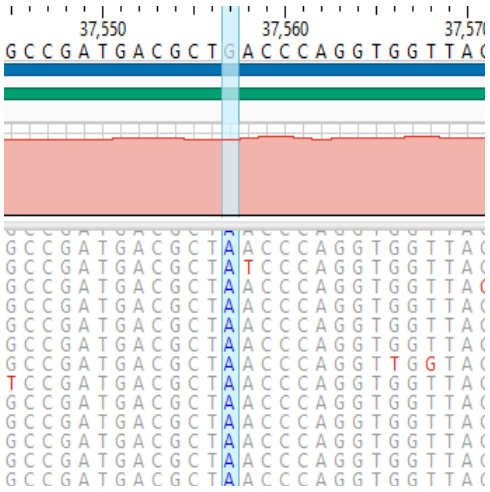
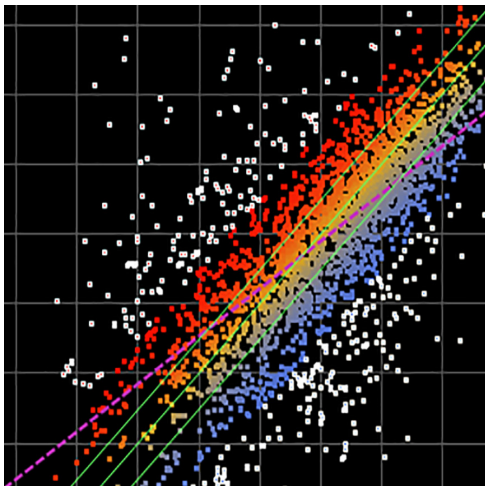
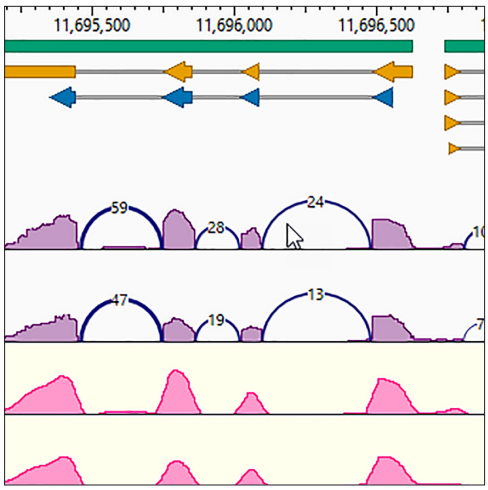
DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

LASERGENE GENOMICS

Accurate, intuitive software for NGS workflows







RESEQUENCING AND GENOTYPING

- Support for all major NGS technologies, including PacBio HiFi and ONT long-read data
- Reference-guided assemblies of any size
- Cancer genomics
- Viral genome analysis, including support for ARTIC network protocols
- Copy number variation (CNV) calculation
- Comprehensive variant analysis
- SNP to structure workflow for modeling impact of mutations on protein structure
- Comparison of data sets in VCF format

METAGENOMICS

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

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

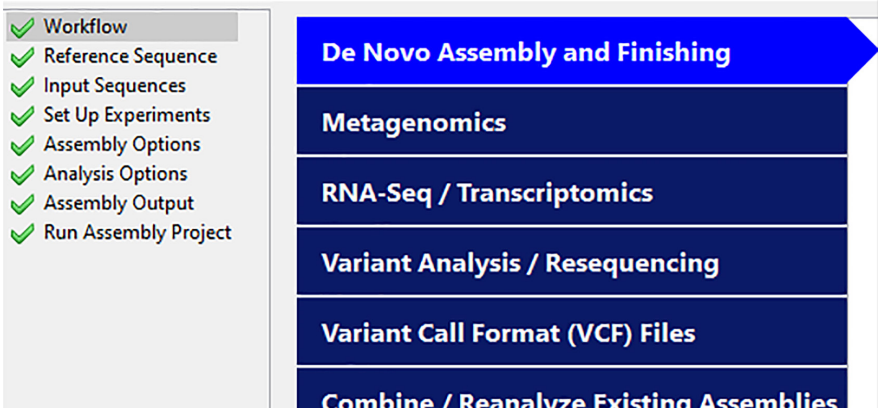
TRANSCRIPTOME ANALYSIS

- *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

DNASTAR

Quick setup for complex genomic sequencing projects

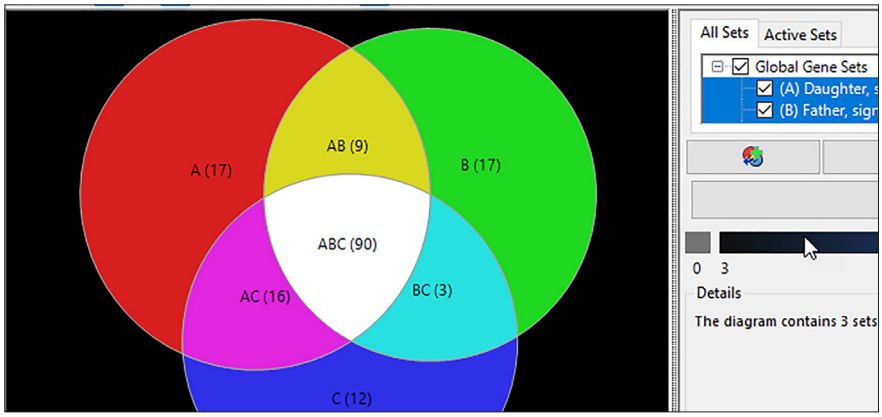
Lasergene Genomics includes SeqMan NGen, our revolutionary assembler that enables you to set up your entire genomic sequencing project in mere minutes and automates tasks that typically require extensive manual intervention.



Workflow categories in the SeqMan NGen project setup wizard.

Automated pipeline from raw data to advanced analysis

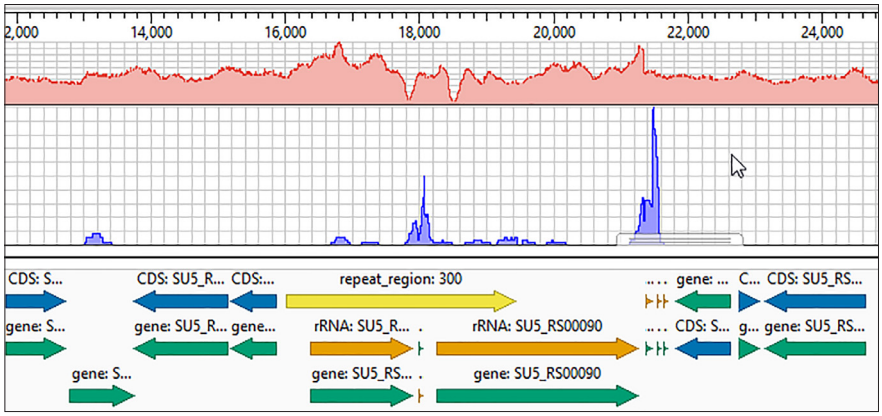
Our automated pipeline does the heavy lifting for you, including organizing replicates, incorporating BED and VCF files, and automatic detection and annotation of variants. Your finished project is delivered ready for you to view and analyze the results.



Venn diagram in ArrayStar, comparing variants from 3 individuals.

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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