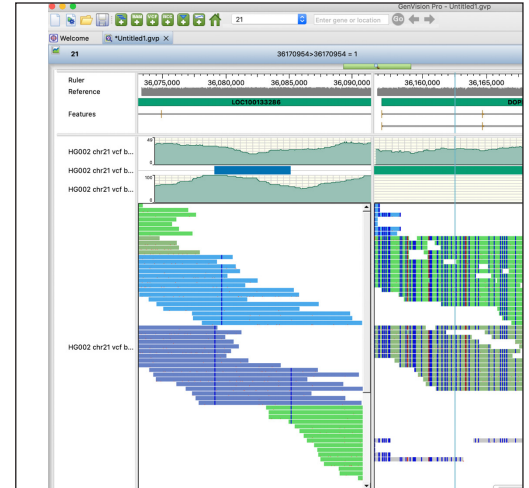
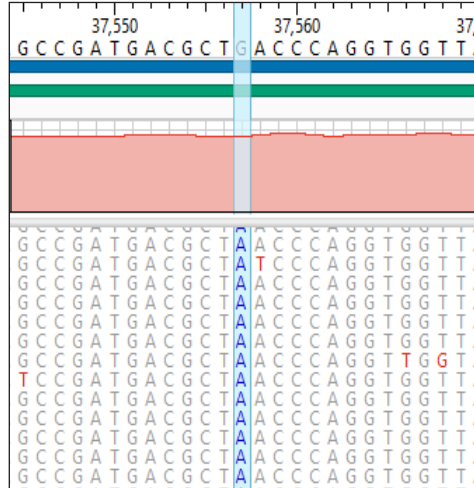
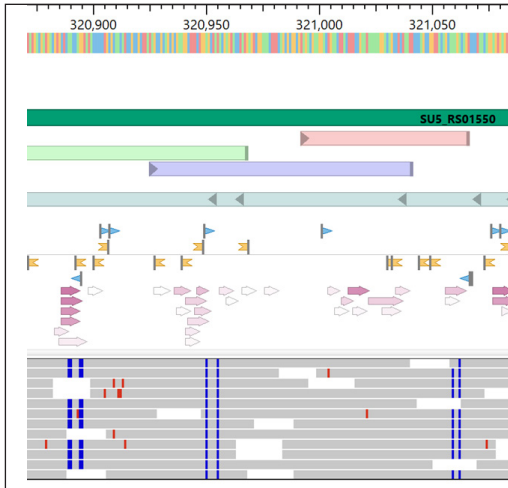


# LASERGENE GENOMICS

## Accurate, intuitive software for NGS workflows



### RESEQUENCING AND GENOTYPING

- Assemble Sanger, Illumina, Element, IonTorrent, PacBio and Oxford Nanopore reads
- Reference-guided assemblies of any size
- Cancer genomics (paired tumor/normal analysis)
- 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 with optional automated AUGUSTUS/Swiss-Prot annotation
- Hybrid *de novo* assembly with closely related reference for contig ordering and scaffolding
- Workflows for contig editing and gap closure

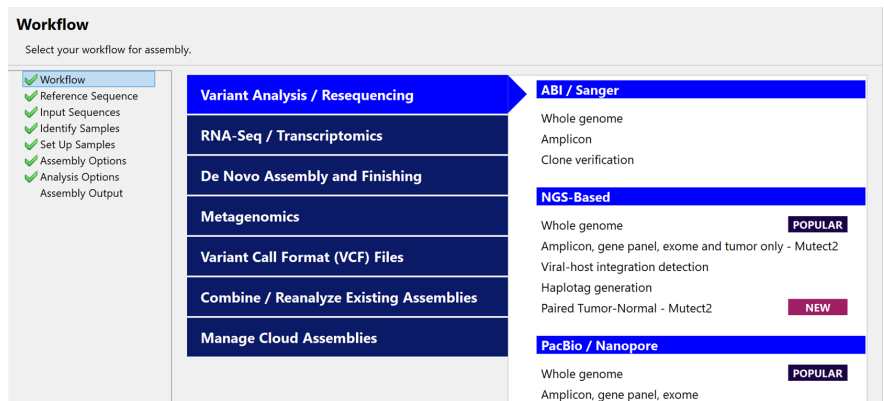
### TRANSCRIPTOME ANALYSIS

- *De novo* transcriptome assembly with auto-mRNA annotation
- PacBio Iso-seq alignment for detailed transcript/isoform analysis and discovery
- RNA-Seq gene expression analysis with EdgeR or DESeq2 generates PCA & Volcano plots
- ChIP-Seq peak detection & microarray analysis
- Combined analysis and visualization of gene expression data from multiple technologies
- Single-cell V(D)J antibody repertoire analysis

# 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.

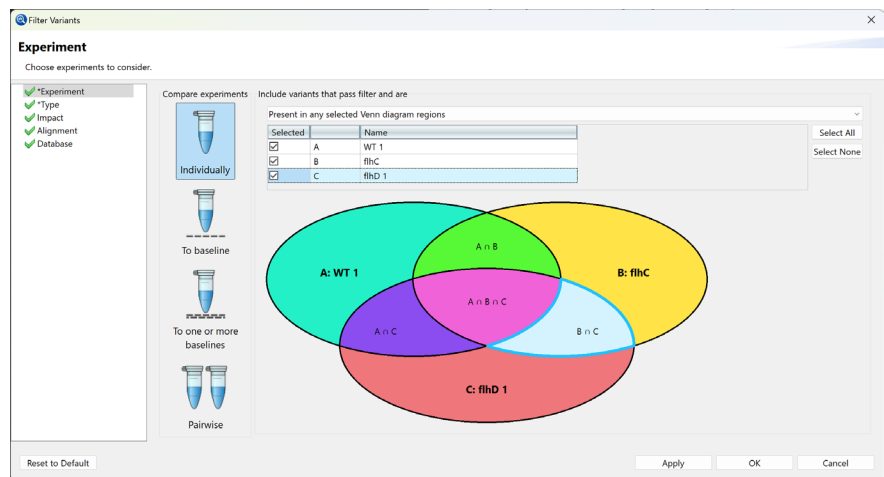
Right: Workflow categories in the SeqMan NGen project setup wizard.



# 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.

Right: 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.

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

