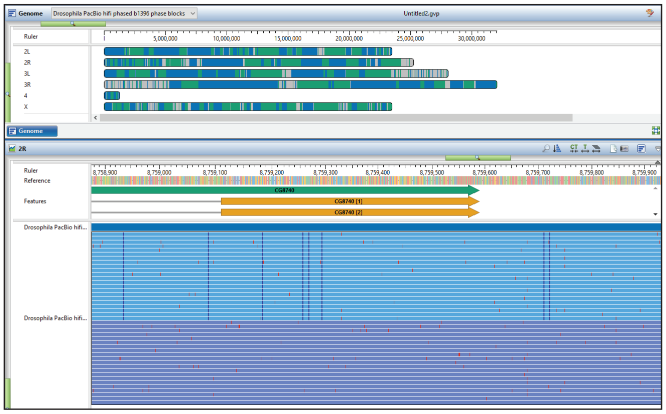
DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

Lasergene 18.0 New Feature Highlights

Phased Variant Analysis

New diploid phasing algorithm for long-read data sets as large as the complete human genome.

- View phased/unphased regions across the whole genome using customizable color schemes.
- View phased SNPs on separate rows of the variants table.
- Export phased consensus blocks.

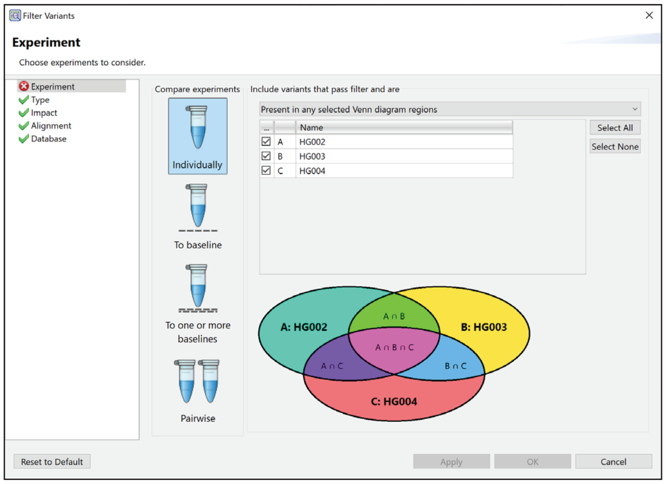


Above: GenVision Pro showing a single phase block from a Drosophila assembly. The wild-type haplotype has no SNPs, while a mutant haplotype has several SNPs.

Variant Comparison Across Samples

Import SeqMan NGen assemblies, BAM, and/or VCF files into GenVision Pro and compare variants between samples.

- Filter variants based on a Venn diagram, on single or multiple baseline controls, on paired samples (e.g., normal vs. tumor), on the percentage of samples containing the variant, and many other options. Save a filter or set it as the default filter for future projects.
- View Variant Annotation Database information for human samples assembled in SeqMan NGen.
- Create sets of variants and compare them to one another. Export variants and sets of variants in VCF format.



Include variants that pass filter and are: Present in any selected Venn diagram regions

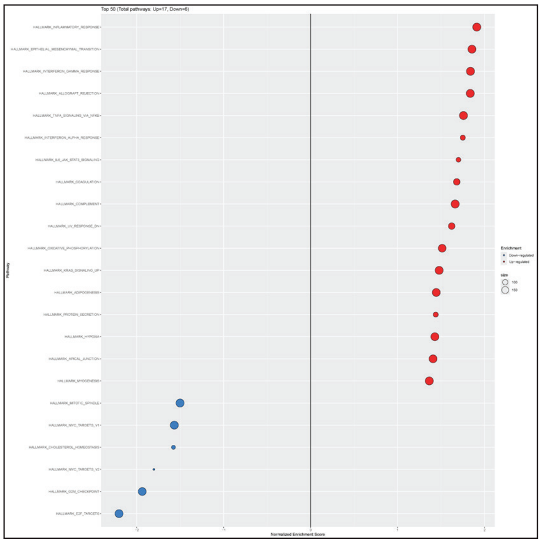
...		Name
☑	A	HG002
☑	B	HG003
☑	C	HG004

Above: The numerous filtering options in GenVision Pro can easily help locate variants of interest.

Gene Set Enrichment Analysis (GSEA)

GSEA is a specialized version of the RNA-Seq differential expression workflow that focuses on groups of genes that share some commonality, such as regulation, chromosomal location, or biological function.

- Learn whether a predefined set of genes shows statistically significant differences between two biological states (e.g., phenotypes).
- Choose any of 31 human, 19 mouse, *C. elegans*, and yeast analysis options.
- View the output in a specialized bubble plot.



Above: a GSEA bubble plot from set of human samples.

Lasergene 18.0 New Feature Highlights (continued)

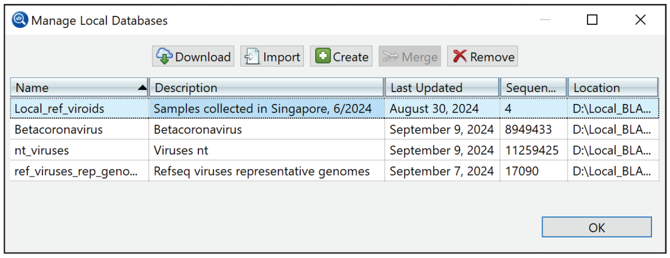
Other Features in GenVision Pro

- Import/export BAM, VCF, multi-sample VCF, and GFF files, in addition to .assembly files.
- Load multiple file types into the same GenVision Pro session and compare them side-by-side.
- Visualize BED and other region tracks across whole genome.

Search Sequences in a Custom Local Database

Create secure local sequence databases in GenVision Pro, Protean 3D, SeqMan Ultra, and MegAlign Pro.

- Upload local files or import sequences from NCBI, with over 30 databases to choose from.
- Merge, expand, rename, and/or delete local databases using the Local Database Manager.
- Local searches are 5-25x faster than online searches.



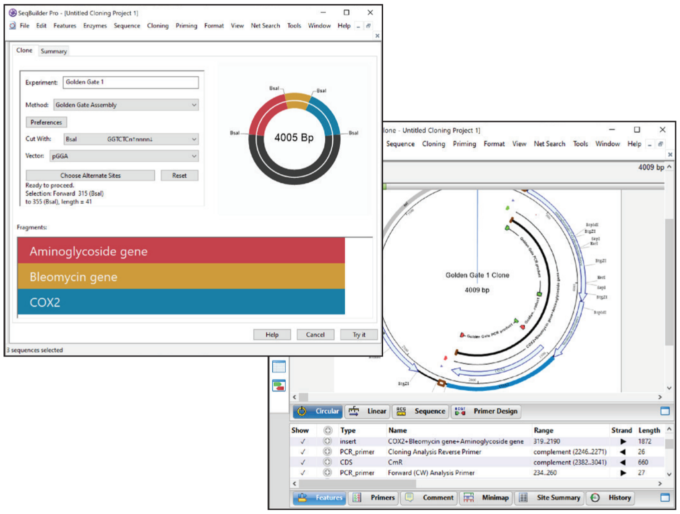
Name	Description	Last Updated	Sequen...	Location
Local_ref_viroids	Samples collected in Singapore, 6/2024	August 30, 2024	4	D:\Local_BLA...
Betacoronavirus	Betacoronavirus	September 9, 2024	8949433	D:\Local_BLA...
nt_viruses	Viruses nt	September 9, 2024	11259425	D:\Local_BLA...
ref_viruses_rep_geno...	Refseq viruses representative genomes	September 7, 2024	17090	D:\Local_BLA...

Above: Easily import or download sequence files and databases with the Local Database Manager.

Golden Gate Cloning

SeqBuilder Pro now supports Golden Gate virtual cloning, for precise and scarless clones.

- Set up the clone with a simple wizard that detects likely failures and provides helpful feedback.
- Use any number of inserts, and digest and ligate vector and inserts simultaneously.
- View features for all components of the clone.
- Effortlessly remove unwanted restriction sites (domestication).



Experiment: Golden Gate 1
Method: Golden Gate Assembly
Cut With: BsaI GGTCTCn↑nnnn↓
Vector: pGGA
Ready to proceed.
Selection: Forward 315 (BsaI) to 355 (BsaI), length = 41
3 sequences selected

Show	Type	Name	Range	Strand	Length
✓	insert	COX2+Bleomycin gene+Aminoglycoside gene	319..2190	▶	1872
✓	PCR_primer	Cloning Analysis Reverse Primer	complement (2246..2271)	◀	26
✓	CDS	CmR	complement (2382..3041)	◀	660
✓	PCR_primer	Forward (CW) Analysis Primer	234..260	▶	27

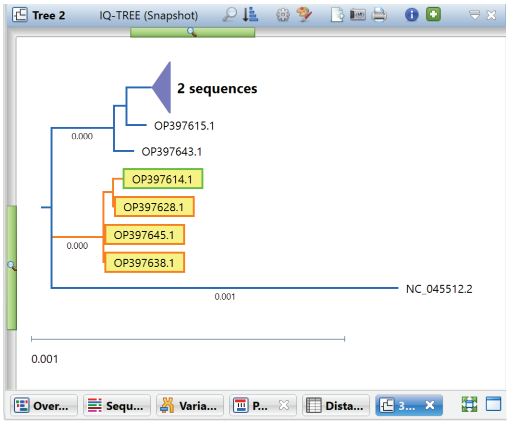
Above: SeqBuilder Pro's guided workflow makes it simple to create and view a virtual Golden Gate clone.

Other Cloning Enhancements

- Easily add new vectors to the already-comprehensive vector catalog, including TA and TOPO cloning vectors.
- Quickly create a new selector from enzymes applied to the sequence.

Phylogenetic Trees Built with IQ Tree

MegAlign Pro now offers the IQ Tree algorithm for building phylogenetic trees. This method is fast, accurate, and supports bootstrapping.



Above: The IQ Tree output is fully customizable and can be exported as a publication-quality image.

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