Gene Codes Corporation

TCAGENE
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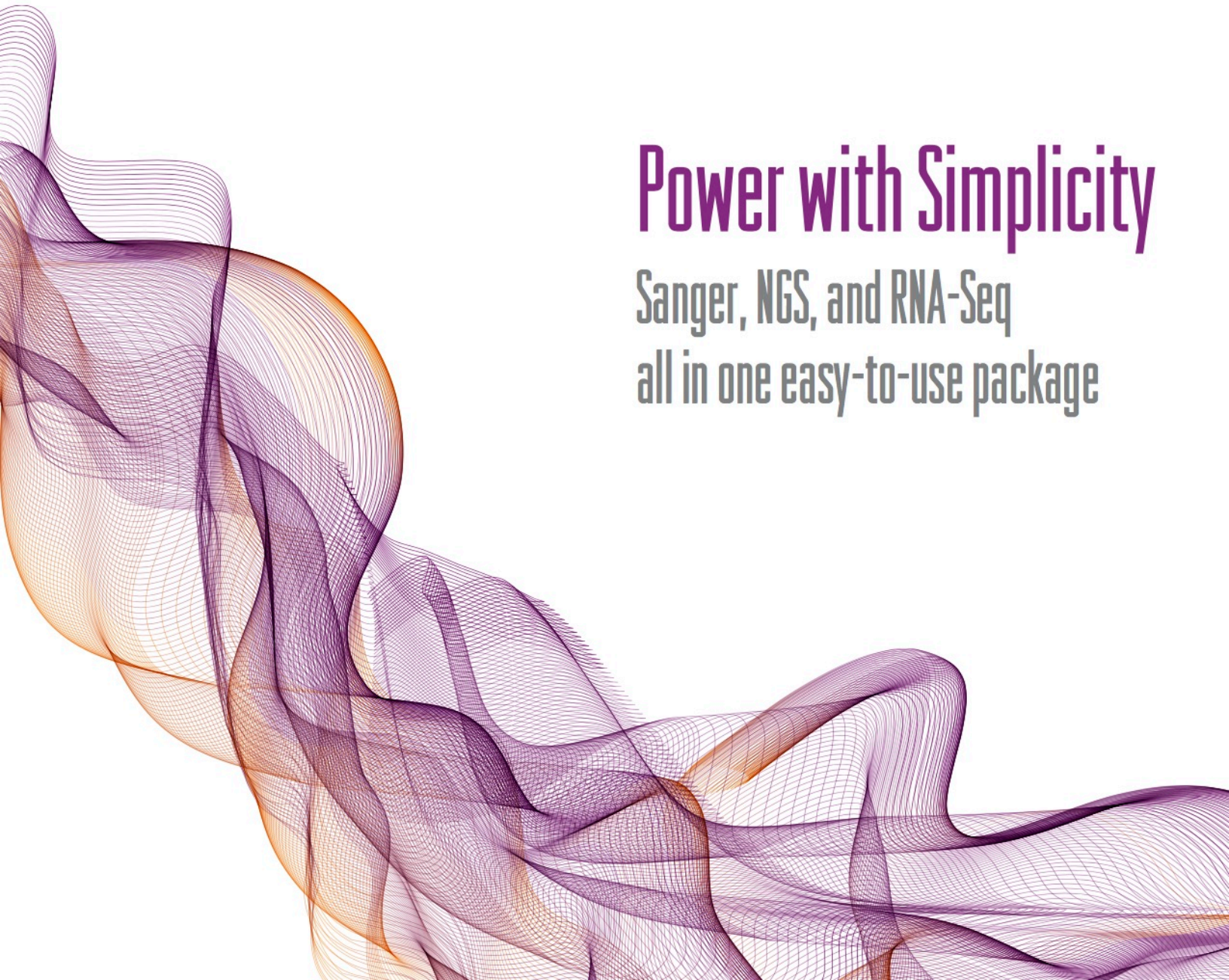
# SEQUENCHER® 5.4

## WITH SEQUENCHER CONNECTIONS



## Power with Simplicity

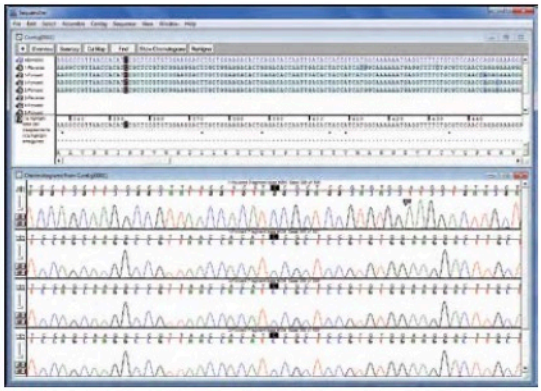
Sanger, NGS, and RNA-Seq
all in one easy-to-use package

# Sequencher 5.4 for Sanger Sequencing Analysis

## You're in control with Sequencher's powerful, user-friendly tools and features.

» Sequencher is intuitive, so each step from importing your reads to assembly to searching for SNPs and heterozygotes is straightforward. Sequencher is flexible. You can adjust parameters and preferences and save them to easily standardize your workflow.

## Sequence editing and trimming tools



» Sequencher makes it easy to clean up raw data by trimming vector, low quality base calls, and other artifacts. Rapid editing tools let you correct sequencing errors before or after they have been incorporated into alignments.

## Assembly and alignment

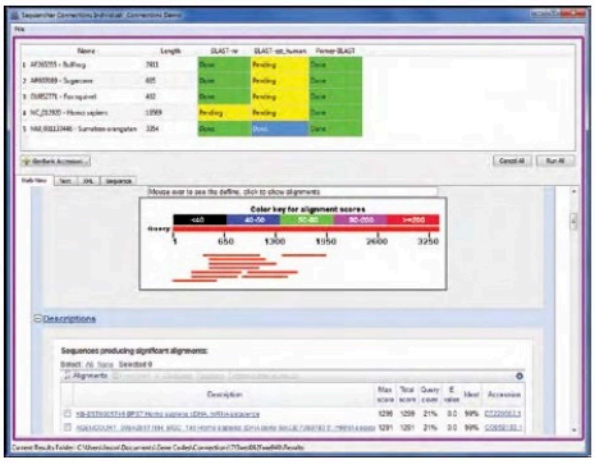
» Perform de novo or reference-based assembly with flexible, understandable parameters. Take advantage of your laboratory's naming conventions to assemble multiple samples from multiple sources using Assembly by Name. Use Clustal or MUSCLE plugins for multiple-sequence alignment.

## Detect SNPs and produce reports

» Analyze traces locally or globally to find secondary, uncalled peaks. Use the Sequencher Variance Table to navigate your assemblies, discover SNPs, and more. Generate reports that quickly and clearly document your findings.

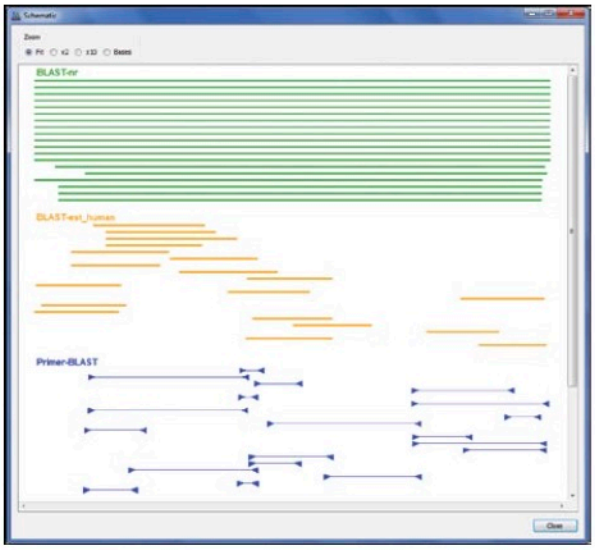
# Sequencher Connections

## Sequencher Connections allows you to run multiple analyses in parallel.



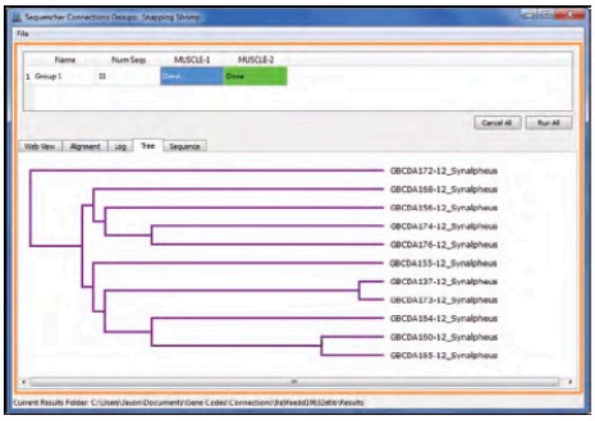
» Sequencher Connections is your portal to local and remote analyses. Connections allows you to run multiple analyses on one or more sequences in parallel. The Connections control panel updates in real time to show you the progress of each analysis on each part of your data, so you can explore them as they complete. Simultaneously run multiple instances of the same application with different parameters and see how the results compare graphically.

## Run multiple BLAST searches simultaneously.




» As an example of how you can use Connections, you can connect with NCBI over the internet and BLAST your DNA sequences against multiple GenBank databases, run the same query sequences using different parameters, and simultaneously use Local Blast to search databases stored on your machine. At the same time, you can be running PrimerBlast to design primers and check their specificity. And with 5.4, you can save your Sequencher Connections sessions and view your results later, even after they have expired on the NCBI website.

## Perform multiple-sequence alignments with MUSCLE.



» Another example of using Connections is trying different variable settings for multiple-sequence alignments and comparing the resulting phylogenetic trees. You can run the same sets of sequences at the same time with different parameter settings, or test the impact of adding or removing some samples from your alignment. As each alignment completes, the indicator in the Connections control panel turns green to let you know that the data is ready to review, even while other analyses are still running.

# Sequencher 5.4 for NGS Analysis

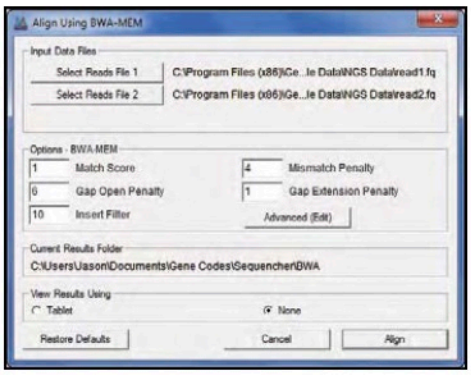
## Use the top tools developed by bioinformatics researchers with an easy-to-use interface.

Most NGS tools utilize the command line. Sequencher provides an interface that gives access to all of the power of those tools, without the command line.

For each algorithm, Sequencher let you use recommended settings or set up Advanced parameters. Each Advanced parameter is accompanied by a description and setting it is as easy as a single click and changing the values to suit your data.

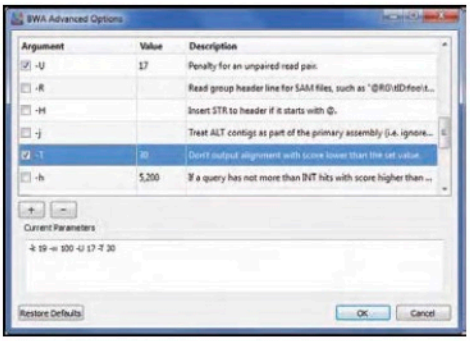
### Perform de novo assembly or reference-guided alignment without the command line.

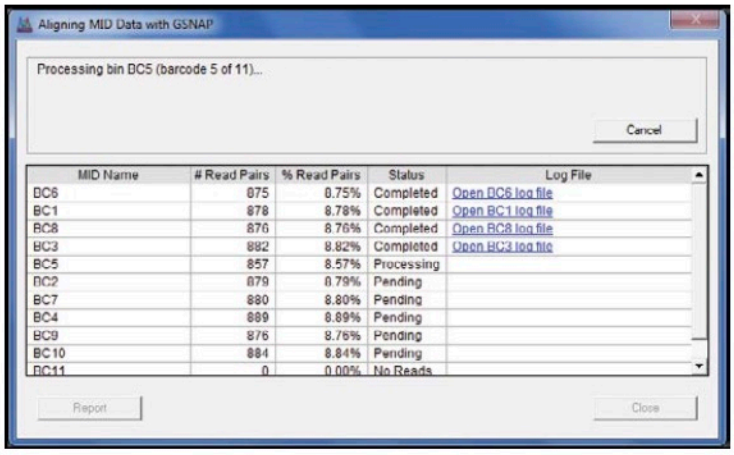
» Sequencher has a plugin lineup featuring Velvet for de novo assembly and Maq, GSNAP, and BWA for reference-guided alignment. With GSNAP you can perform SNP-tolerant alignments and SNP analysis, generate methylation reports from bisulfite-treated DNA, and perform A-to-I RNA-editing tolerant alignments.

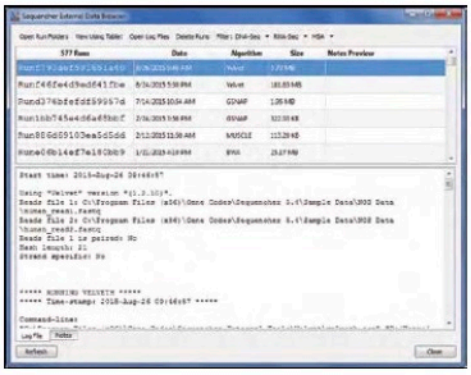



### Multiplex ID for barcoded data

» Use Multiplex ID barcodes with GSNAP, BWA-MEM, or Velvet to sequence a mixture of DNA samples in a single run.



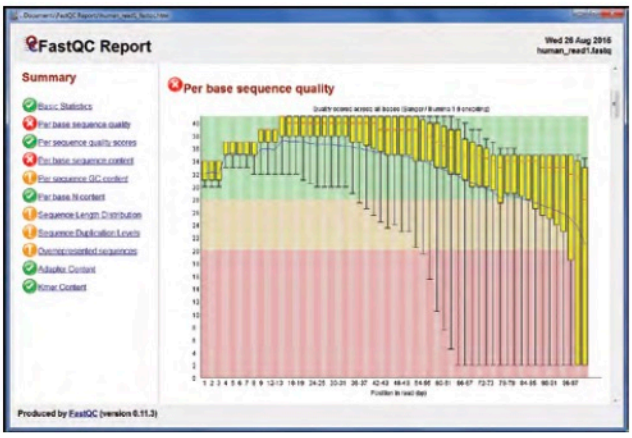



# Sequencher 5.4 for NGS Analysis

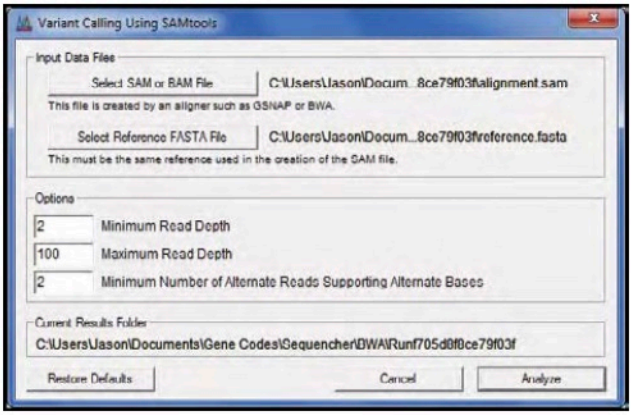
## Check the quality of your FastQ reads files.

» A new plugin added for Sequencher 5.4 is FastQC which allows you to produce quality control reports of your data. Check up to 11 different metrics including per base and per sequence quality and GC content.



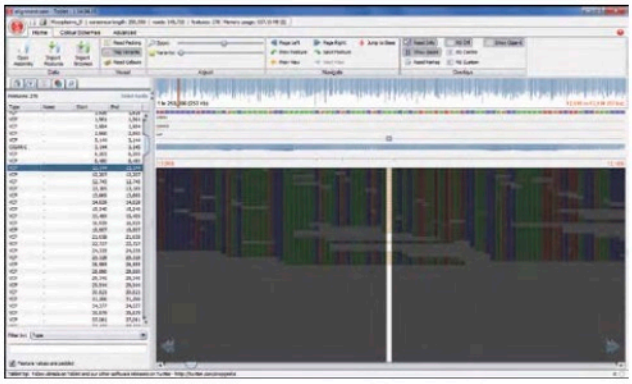

## Variant calling

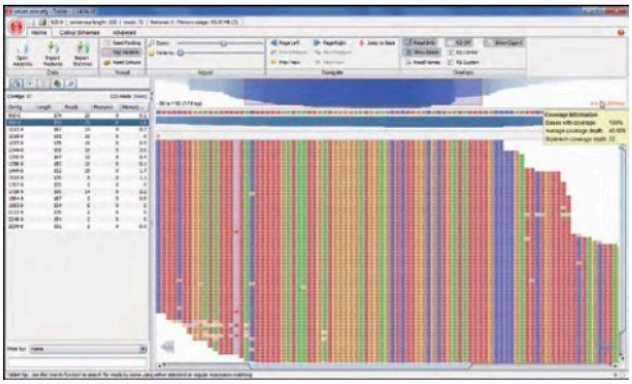
» With Sequencher 5.4 you can now utilize SAMtools to analyze the output from your GSNAP or BWA-MEM alignments for variants, saved in the standard VCF format. Then explore the alignments and the variants in the Tablet genome browser.




## Viewing assemblies and alignments.

» View your NGS results using Tablet in a number of different modes. Get information on individual reads and read pairs and arrange the stacking of the reads to reveal pairings. Customize the color of the individual bases, variants, read types, and read groups. Annotate alignments with GTF and VCF files. Tablet has controls to enable translations, zoom in and out, as well as highlight variant bases, making it a cinch to explore your reads.

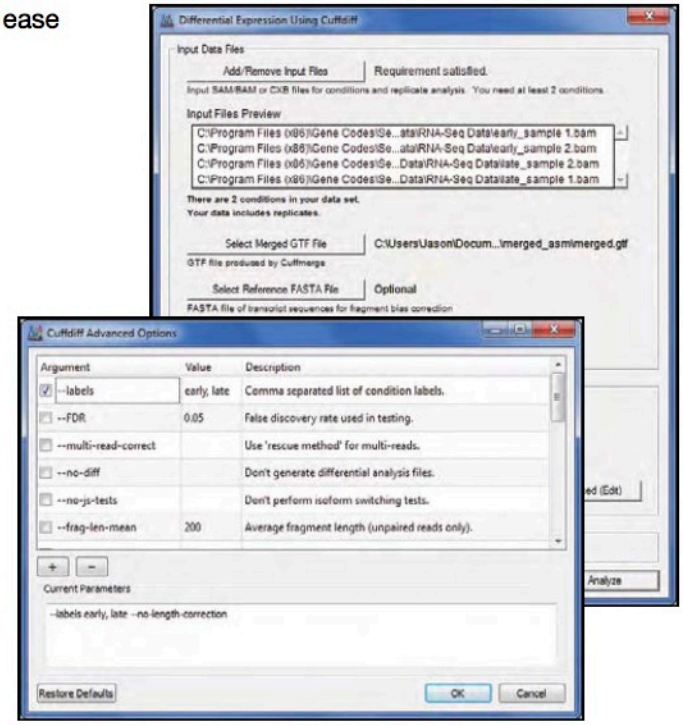




# Sequencher 5.4 for RNA-Seq Analysis

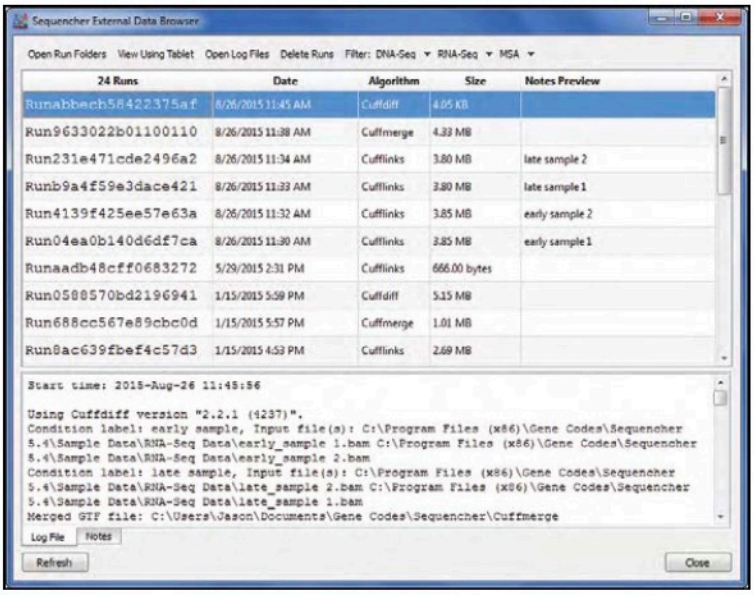
## Easily perform powerful RNA-Seq analyses with Sequencher's user-friendly interface.

Extend Sequencher with more options for RNA-Seq analysis. Plug-in algorithms from the Cufflinks[1] suite can be downloaded right from the Gene Codes website (www.genecodes.com), including tools for normalizing and quantifying NGS data. In addition, the graphical user interface lets you have complete and easy-to-understand control of Advanced options that would require you to set flags and in-line parameters if you were using the same tools from the command line. Add annotated replicates to your workflow with ease using Sequencher's Conditions and Replicates editor.




## Unique tools to help you organize and streamline your analyses

» Sequencher's External Data Browser makes it easy to track and organize your NGS runs. Add free-form text annotations to each run to remind you about data and parameters. View any alignment in Tablet without opening its project and delete old space-consuming runs without having to spend time searching for them.

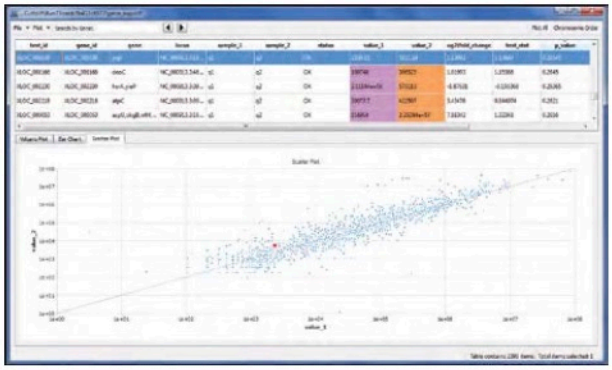



[1] Cole Trapnell, Brian A Williams, Geo Pertea, Ali Mortazavi, Gordon Kwan, Marijke J van Baren, Steven L Salzberg, Barbara J Wold, and Lior Pachter. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotechnology 28, 511–515 (2010).

# Sequencher 5.4 for RNA-Seq Analysis

## Design publication-quality plots and charts with Sequencher's customizable visualization tools.

Sequencher has easy-to-use visualization tools that allow you to produce high-quality charts and plots without worrying about command-line statistical programming or forcing your data into a spreadsheet. Choose your data and view your results as a Scatter Plot, Volcano Plot, or Bar Chart.

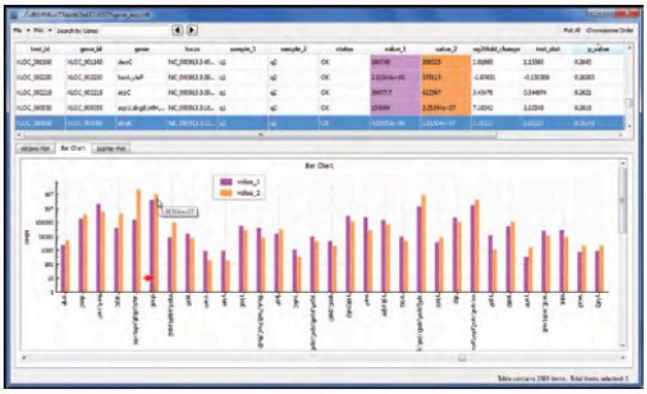


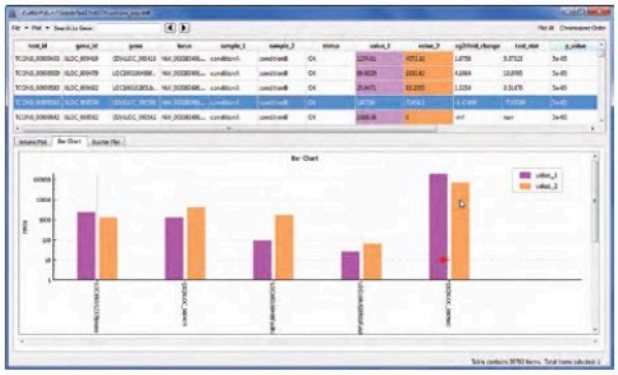
### Interactive charts and plots

» The charts and plots are linked to the underlying data. Search by gene name or geneID to locate your data of interest. Click on a bar or data point to view more information in the data table, or click on a line in the data table to locate that data point in the graph.

### Customize and export charts and plots.

» Sequencher allows you to select and plot on only the genes you want to focus on. Sort the data and then choose which rows you want to include or exclude from your plot. Once you have the graph you want, you can export it as a high-resolution png file.





# Make the move to Sequencher 5.4 for powerful, easy-to-use analysis for all of your sequencing data.

## With your Sequencher licenses you get:

» Free upgrades and unlimited technical support for one year

» Flexible licensing options designed to meet your needs

Licenses are available for Windows, Macintosh, or Dual Platform. You can choose between a Standalone License, a Shared Network License, or an Institution-Wide Site License, and decide whether you want a USB license key (dongle) or a software-based dongle-free license.

**We won't throw you in the deep end.** Your Sequencher license comes with unlimited technical support for one year. Our extensive tutorials and videos show you how to get the most out of your data with Sequencher.

**Visit www.genecodes.com to download Sequencher 5.4. Request an evaluation license to try Sequencher today.**

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