

Geospiza GeneSifter® Analysis Edition Product Update for v3.3

GeneSifter® Analysis Edition adds new levels of analysis and data visualization to its Next Generation Sequencing support with splice index analysis and base variant calling as well as updated support for Affymetrix miRNA and Gene/Exon ST microarrays.

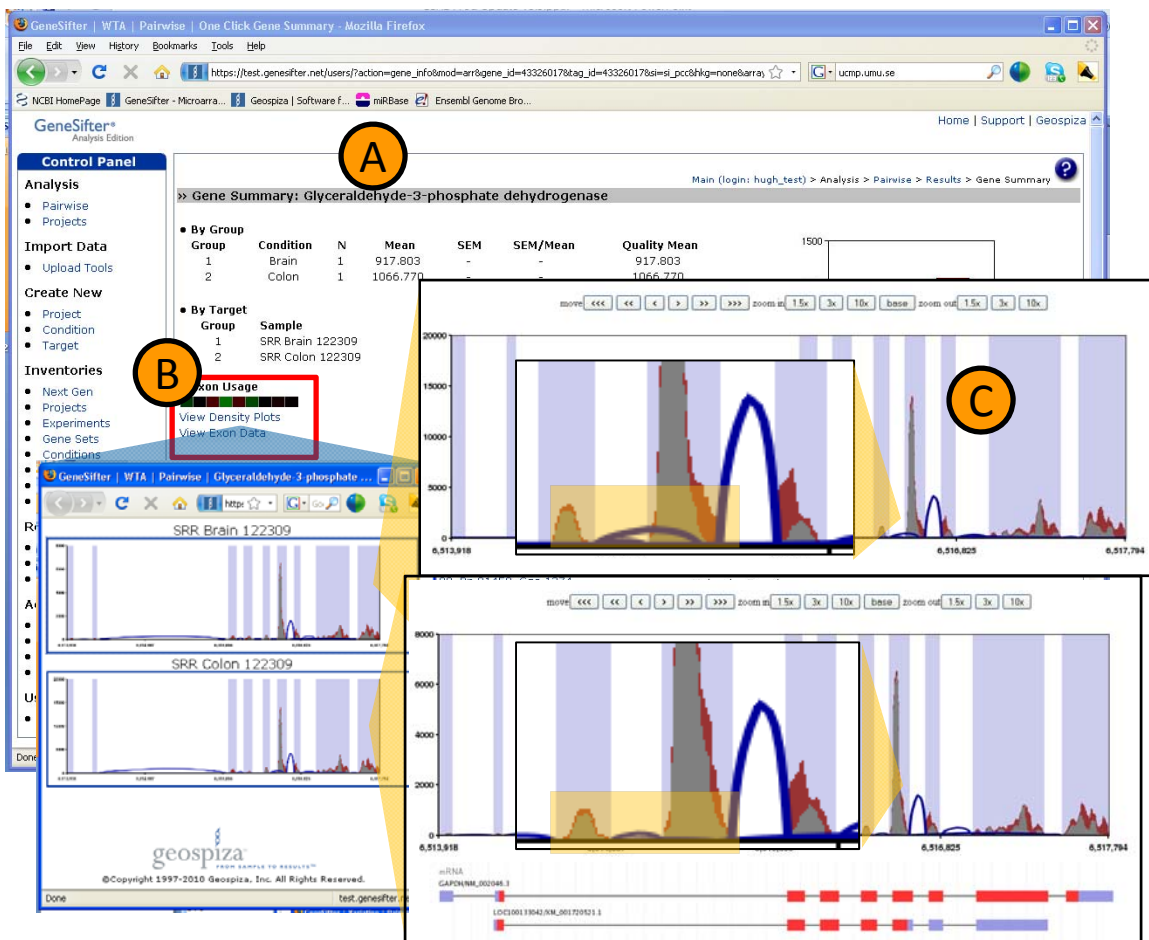
Identifying differential splicing between samples requires tools that can sift through 25,000 -100,000 or more possible genes and/or transcript variants to pull out the top candidates for further analysis. GeneSifter provides these tools for researchers to analyze data in a biologically meaningful way with the capability to not only qualify data by differential expression and statistical significance, but also by functional importance using GO ontology or KEGG pathway analysis. GeneSifter now supports a new level of analysis with splice index analysis of whole transcriptome data, which allows comparisons of two experimental groups (replicate samples supported) to identify those genes with splicing differences.

Summary of Updates

Next Generation

Sequencing

- Splice Index Analysis
- Enhanced “One Click Gene Summary” **A**
- Splicogram **B**
- Integrated Next Gen results **C**
- Base variant calling *
- Interactive Read viewer *



* Available as part of the Whole Transcriptome Pipeline.

Figure 1 – Splice Index analysis. Compare splicing differences between two individual or groups of samples and drill into your data from gene to individual base level and see exactly how each gene in your sample(s) is differentially expressed exon by exon and splice event by splice event.

Read Viewer – Variant base level visualization and analysis added to NGS support.

With GeneSifter's Read Viewer, you can instantly view your sequence data -- anywhere in the genome. View variants in your data, such as single nucleotide variants, insertions, and deletions, and verify 'by eye' that your reads are aligned correctly. Consensus sequence with quality values for every base are available for instant viewing. The GeneSifter Read Viewer is especially powerful in combination with gene sorting. After sorting your data by gene expression level or number of variants, you will be one click away from the most biologically interesting parts of your data. Don't rely on tables of numbers in a spreadsheet – use GeneSifter and see your data for yourself.

Base Variant Viewer

- Interactive viewer **A**
- Consensus sequence calls **B**
- SNVs and indels **C**



Platforms Supported

Next Generation Sequencing

- Illumina – Genome Analyzer, II, IIx, IIe, and HiSeq2000
- Life Technologies – SOLiD2, 3 and 3+

Microarrays

- Affymetrix
- Illumina
- Agilent
- Nimblegen
- Custom spotted

Figure 2 – Read Viewer. Short reads from an aligned sample are presented relative the reference sequence. The reference, consensus sequence, and quality scores can easily be viewed giving you the ability to see with confidence each read and base.

Other updated features:

- Full support for Affymetrix (Human, Mouse, and Rat) Gene and Exon 1.0 ST microarrays.
- Full support for Affymetrix miRNA microarray.
- Integrated and sortable transcript lists to make searching NGS data easier and more efficient.
- Option to export reports in .xls format.