

APPLICATIONS

- RNA-seq & ChIP-seq
- Comparative Gene Expression
- Alternative splicing analysis
- Transcriptome profiling
- New gene discovery

KEY HIGHLIGHTS

- Easy to use: Click And Go® automatic workflows
- Relevant analyses: designed from scientific literature
- Reliable results: cutting edge methods & Quality Controls
- Intuitive interface, interactive graphics and dynamic charts
- Integromics technical assistance and customer support
- Scalable: single desktop or flexible server mode

REQUIRED INPUT

- Genomic alignments of reads (BAM or SAM format)
- Gene model annotation (GTF format, already provided for model organisms)

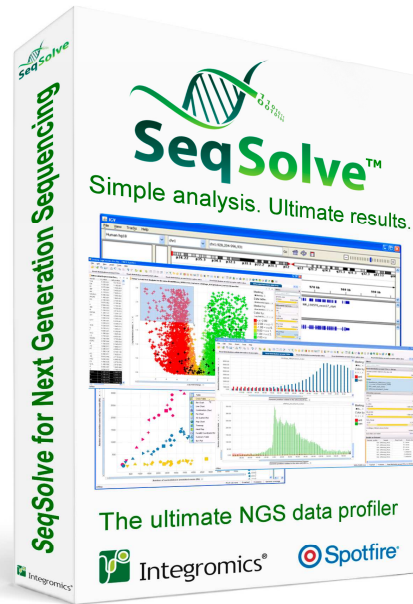
COMPATIBLE WITH

- any annotated species
- any NGS technology

TRIALS, INFOS & WEBINARS

www.integromics.com/ngs

The ultimate NGS data profiler

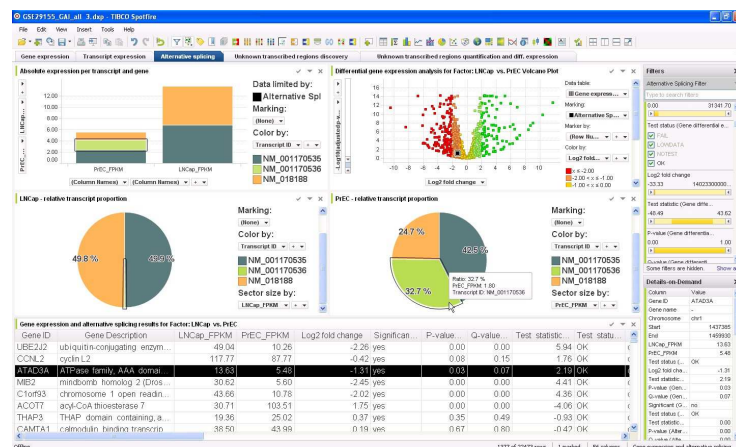


SeqSolve™ from Integromics® is an advanced and user-friendly software solution for the tertiary analysis of “Next Generation Sequencing” (NGS) data. By integrating state-of-the-art bioinformatics methods into one-click analysis workflows, SeqSolve provides scientists with a unique combination of cutting edge algorithms and intuitive user experience.

Its Click And Go® technology enables the automatic processing of the data and includes a Smart Quality Control system, which makes it both simple to use for non-experts and reliable in terms of biological results.

Simple analysis. Ultimate results.

- One-click RNA-seq and ChIP-seq workflows for automated and easy analyses
- Integration of peer-reviewed NGS tools (Cufflinks, SAMtools, IGV, MACS)
- Statistics for comparative analyses to support your results with significance
- Unique Quality Controls to monitor library complexity, gene coverage bias, etc
- Alternative Splicing analysis with transcripts relative abundances
- Automatic detection of new genes (“transfrags”) with differential expression
- Antisense transcription report, genome-wide profiling of read distributions, etc
- Server mode available for remote, scalable and distributed processing
- Real-time interactive graphics powered by industry-leading TIBCO® Spotfire®
- Simple export of results and data to .ppt, .xls or .pdf reports



Differential gene expression report with comparative analysis of alternative splicing between tumour and control RNA samples. Expression fold-change and p-value are dynamically displayed for each gene (volcano plot) as well as the relative abundance of each transcript isoform (pie charts).

