illumina®

Unlock insights from RNA-Seq studies

Explore transcriptomics data and gain a deeper understanding of gene expression with Partek™ Flow™ software

Partek Flow software offers a user-friendly bioinformatics solution for analyzing and visualizing RNA-Seq data, empowering researchers of all skill levels to maximize insights from transcriptomics data.

Advanced visualization tools
Create informative, publication-ready visualizations with just a few clicks

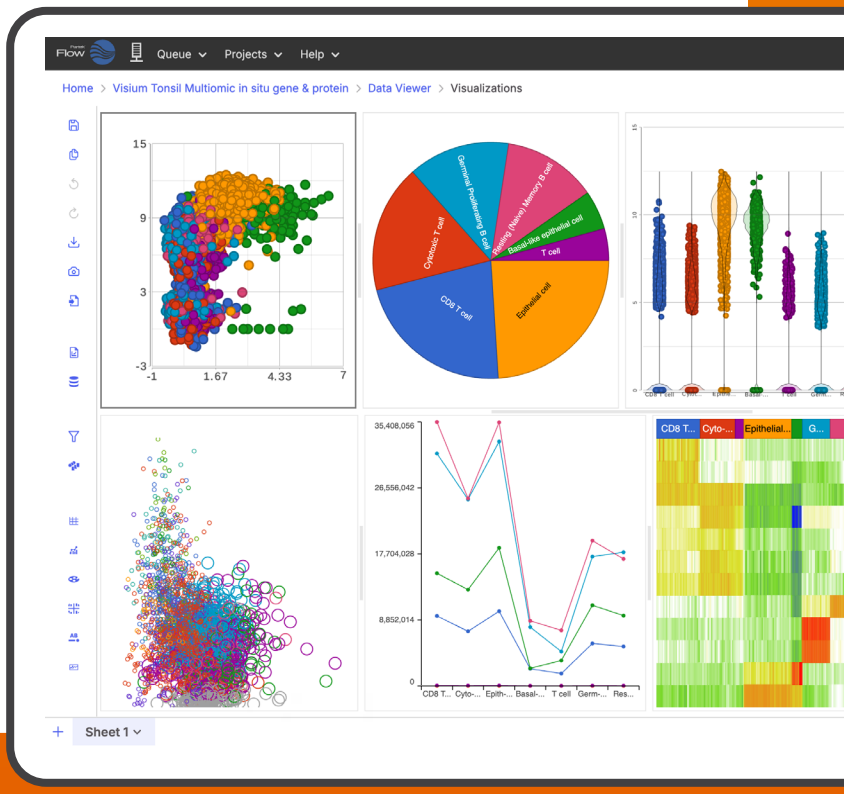
Point-and-click analysis
Analyze data easily with an intuitive, context-sensitive interface

Powerful statistics
Access industry standard statistical algorithms for results you can trust

Customizable workflows
Build custom analysis pipelines visually and share with collaborators

Partek Flow tools for RNA-Seq analysis

- Principal component analysis (PCA)
- Differential expression analysis (LIMMA, ANOVA, DESeq2, and more)
- Interactive dot plot, volcano plot, heat map, scatter plot, chromosome view, and Venn Diagram
- Gene ontology and KEGG pathway enrichment
- K-means, hierarchical, and graph-based clustering



Powerful analysis and visualization tools

Whether looking for patterns of gene expression changes in time series data, building a classification model from published data, or discovering biomarkers by identifying correlation between, Partek Flow software has the tools for easily analyzing and visualizing your RNA-Seq data.

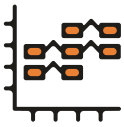
Cross-platform integration for multiomic insights

Analyzing multiple omics data sets in parallel provides a more complete view of the molecular mechanisms underlying phenotypes. Partek Flow software enables integration and side-by-side visualization of data from multiple assay types, including RNA-Seq, ChIP-Seq, ATAC-Seq, microRNA expression, and microarray analysis.

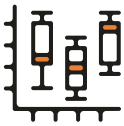
Steps in the **RNA-Seq analysis workflow**

Alignment

Quality control



Quantification



Differential analysis

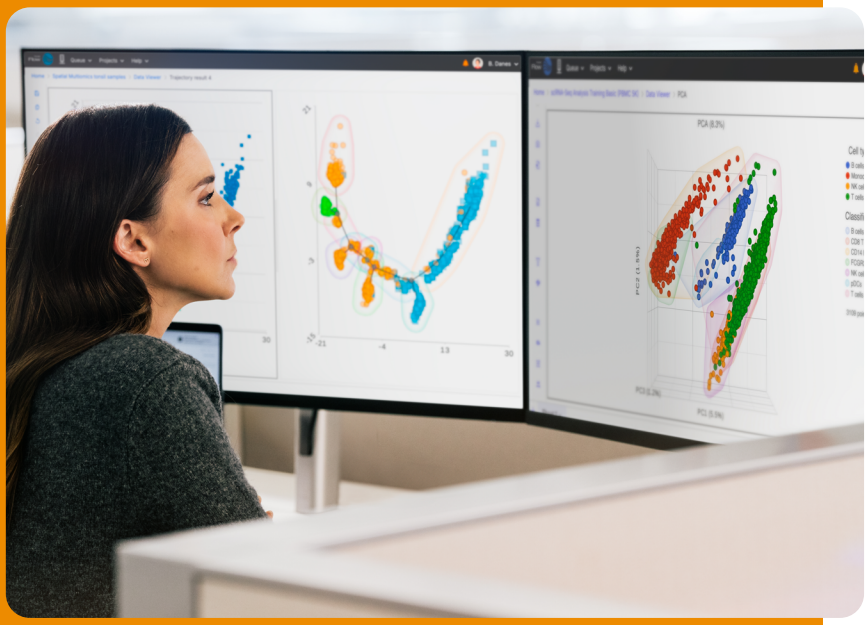
Biological interpretation

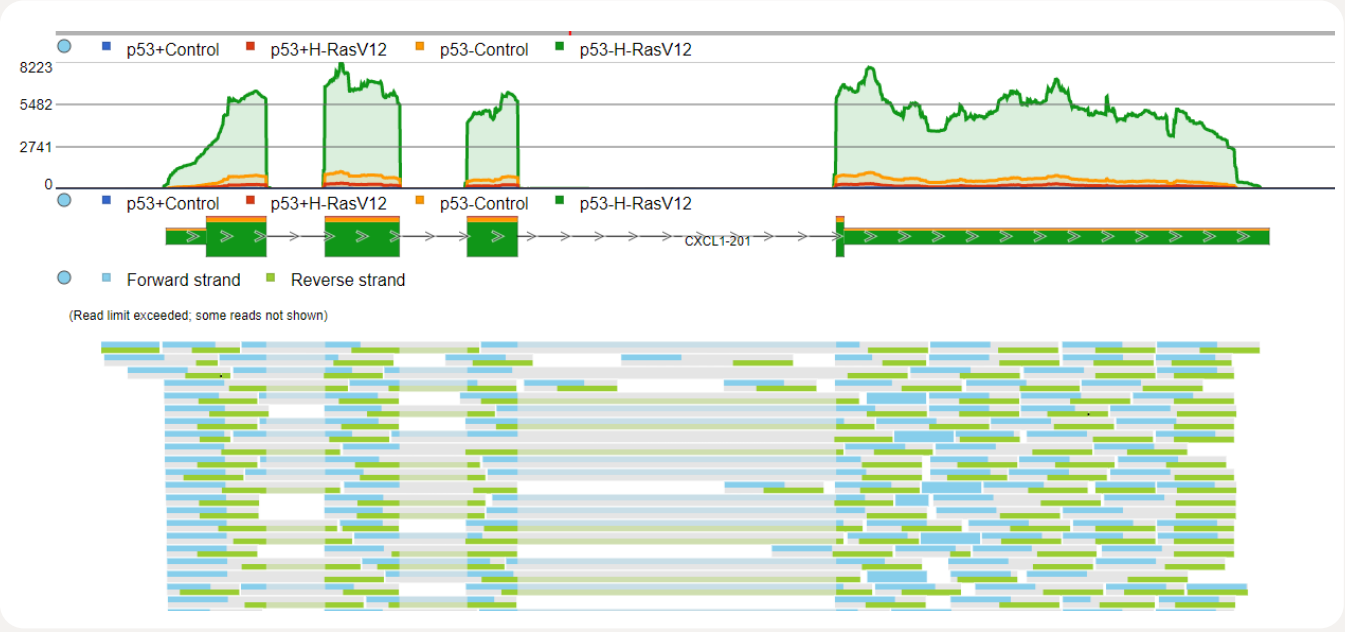
Data to **biological insights in a single solution**

- Start the RNA-Seq analysis pipeline with either unaligned, aligned, or quantified reads, followed by trimming adapter sequences and low-quality bases
- Align reads to any reference genome or transcriptome using popular aligners, including STAR, GSNAP, Bowtie 2, TMap, HISAT-2, and more
- Use Salmon for ultrafast pseudoalignment and transcript quantification
- Map aligned reads to any public or user-defined transcriptome database
- Normalize data using total count, RPKM, and TMM
- Detect differentially expressed genes or transcripts
- Identify alternatively spliced transcripts and fusion genes
- Remove technical noise with flexible feature filtering options

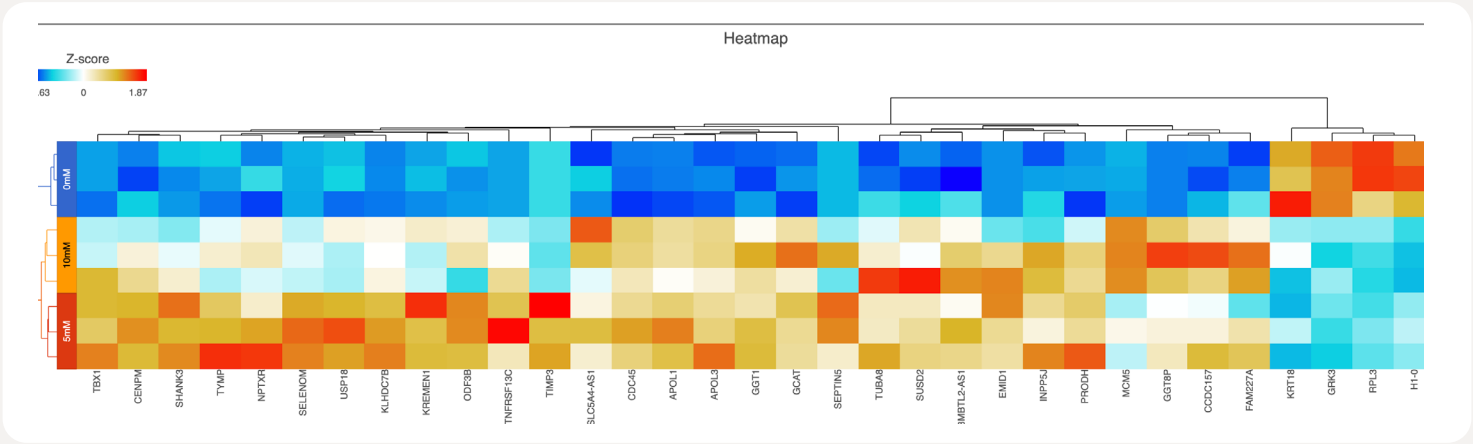
Multiple ways to **explore RNA-Seq data**

Transform raw RNA-Seq data into interactive figures and maximize biological insights from your transcriptomics research. The integrated genome browser in Partek Flow software makes visualizing isoforms and differential expression fast and easy.

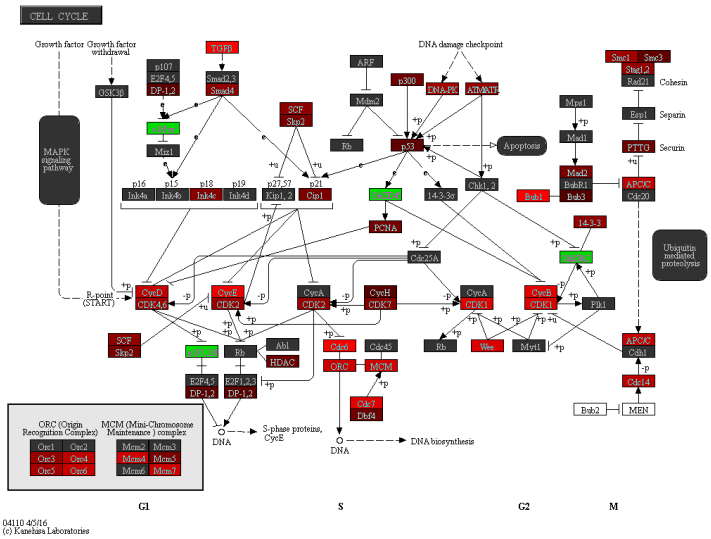




Visualize reads against a reference genome, compare experimental groups, and measure isoform abundances.



Visualize large amounts of multi dimensional data, compare gene expression patterns between experimental groups, and identify clusters of rows with similar values using heat maps.



Analyze enriched pathways visually by color coding KEGG pathway maps with fold-changes or p-values.

Learn more

Partek Flow software

Request a free 14-day trial

Abbreviations: ANOVA, analysis of variance; API, application programming interface; ATAC-Seq, assay for transposase-accessible chromatin with sequencing; ChIP-Seq, chromatin immunoprecipitation with sequencing; GSNAP, gene set analysis; KEGG, Kyoto encyclopedia of genes and genomes; QA, quality assurance; QC, quality control; REST, representational state transfer; RPKM, reads per kilobase of transcript per million mapped reads; STAR, spliced transcripts alignment to a reference; TMap, Torrent mapping alignment program; TMM, trimmed mean of M-value.

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