ECSEQ BIOINFORMATICS

RNA-Seq

Explore The Transcriptome And Its Variability With Ease.

KEY BENEFITS

Rapid Results
Our skilled team of professional bioinformaticians delivers results quickly.

Expert Solutions
Rely on in-depth bioinformatics experience and up-to-date scientific methods.[1]

Excellent Support
Always have somebody to discuss your bioinformatics issues.

Flexible Analyses
Employ an analysis strategy that is adjusted to your needs.

Trustable Results
Our RNA-Seq analyses have been tested and validated in many projects.

High Data Security
Securely transfer and access your data and the results.

Explore & Share your Results
Comprehensive interactive HTML reports included.

Best-in-class Methods
Get the most biologically relevant information out of your data.

[1]Discover our RNA-seq expertise at ecseq.com/analysis/RNA-Seq

Current methods of next-generation sequencing offer the opportunity to investigate the entire transcriptome in an essentially unbiased way. Compared with traditional microarray approaches, gene expression analyses are possible at a broader dynamic range: RNA-Seq data can be used to find novel transcripts, splice sites, gene fusions, sequence variants and other variations that allow a more comprehensive biological understanding on the RNA level.

RNA-Seq is a well-established method and our researchers have proven expertise in its analysis. Our protocols are approved by renowned experts in the field and our analyses have been published in high-impact, peer reviewed journals (find details under ecseq.com/analysis/RNA-Seq)

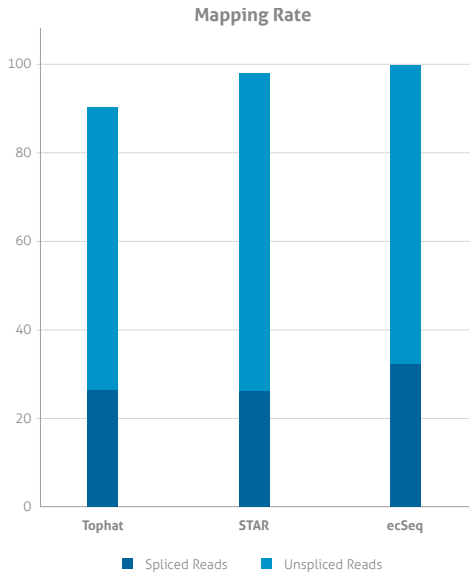
High-Sensitivity RNA-Seq Alignment

Our RNA-Seq analyses rely on our ultra-sensitive mapping approach, which is specifically adjusted to recover spliced sequencing reads. This results in a higher mapping rate and increased number of spliced reads than competitors, like Tophat or STAR, while delivering the same high sensitivity of 98% (see Figure). In other words, we are not only able to extract more valuable information from the sequencing data, but also more biologically relevant insights. The improved mapping rate, with more spliced reads, results in higher detection levels of splice junctions. The latter are critical for analyzing isoform expression, alternative splicing, circular RNAs and other trans-splicing events.

"Higher mapping rate means more valuable biological information"

Gene Expression Profiling And Differential Expression Analysis

Our optimized gene expression analysis enables rapid discovery of functional biomarkers with RNA-Seq data. Depending on the protocol used and goal followed, our scientists select the optimal preprocessing and mapping strategy. Quantification and differential expression analyses can be carried out on the level of genes, transcripts, exons or even genomic regions. The accuracy of

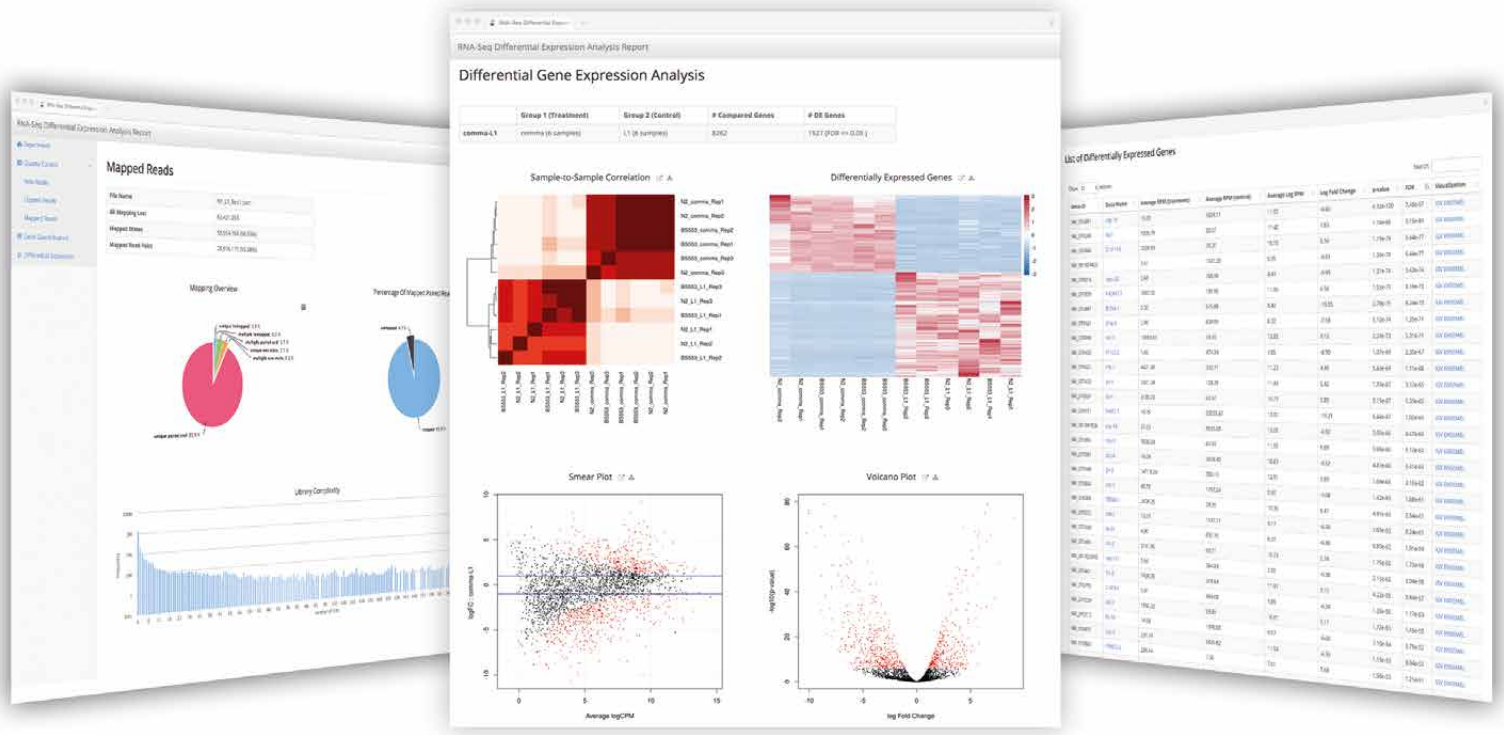


expression quantification is improved by scientifically sound handling of reads aligning to multiple genomic loci. The high mapping rate also increases the power for detecting differential expression (especially in the case of low-quality reference genomes). Optionally, a gene ontology analysis can be added to gain further biological insights.

In-Depth Transcriptome Analysis

RNA sequencing moreover provides valuable data to explore the transcriptome for non-standard events. The information provided in spliced reads enables the prediction of novel transcript isoforms, alternative splicing events, fusion genes, circularized RNAs and others. Besides synthetic gene modifications, like inserted/deleted genomic sequences, RNA editing sites and alternative polyadenylation events can be discovered. Non-standard transcripts, like fusion genes and circular RNAs, which have a major impact on the development of several diseases, including cancer, diabetes, and obesity, are regularly overseen in RNA-Seq data sets. Since they are widely used as diagnostic and prognostic markers and play a major role in current biomedical research, we have developed sophisticated methods to identify and verify these.

Interactive HTML Reports



Basic Analyses

- Sequencing Data Quality Control
- Adapter Clipping
- Bad-End Quality Trimming
- High-Sensitivity Read Mapping
- Mapping Quality Control
- Gene Quantification
- Differential Gene Expression

Additional Analyses

- GO Analysis
- RNA-Editing Prediction
- Fusion Gene Detection
- NEW: Circularized RNA Analysis
- Exon Retention Identification
- Alternative Polyadenylation Analysis
- and more!

End-to-end NGS Solutions

For all RNA-Seq applications we also offer end-to-end RNA-Seq analysis, including

- Sample Preparation
- Next-Generation Sequencing
- Bioinformatics Data Analysis

Contact one of our scientists and discuss your project!

Use the callback service on our website **www.ecseq.com** or write to support@ecseq.com

About Us

ecSeq GmbH is a bioinformatics solution provider focusing on next-generation sequencing technologies. Since 2012 ecSeq GmbH provides data analysis services and bioinformatics training for various NGS applications.

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