strandngs

Streamlining NGS Data Management & Analysis

# Reads to Discovery

RNA-Seq | DNA-Seq | ChIP-Seq | Small RNA-Seq | Methyl-Seq | MeDIP-Seq

www.strand-ngs.com

Analyze | Visualize | Annotate | Discover

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## Data Import

**Vendor Platforms:**
- Illumina
- Ion Torrent
- Roche 454
- ABI SOLiD
- Pacific Biosciences

**File Formats:**
- FASTA/FASTQ
- Unaligned BAM
- SAM/BAM
- BED, Counts data
- MiSeq run folder
- VCF/VAL

**Library Layouts:**
- Single end
- Paired end
- Mate paired
- Directional single/paired end

## Alignment

- BWT based algorithm
- SSE/GPU based fast implementation
- Short and long reads alignment
- Single and paired end alignment
- Split read alignment
- Arbitrary gaps and mismatches
- Multiple matches
- Quality/adapter based trimming

## Data QC

**Pre-alignment QC Plots:**
- Base level quality distribution
- Read level quality distribution
- Base composition / quality plots

**Post-alignment QC Plots:**
- Alignment score distribution
- Mapping quality distribution
- Illumina lane/tile QC plots
- Read length distribution plots
- Read quality distribution plots

**Filter Low Quality Reads:**
- Filter by read metrics
- Filter duplicate reads
- Filter multiple mapping reads
- Filter by tile quality
- Filter by region lists

## RNA-Seq

- Gene, exon and transcript level quantification
- Differential gene expression
- Differential gene splicing
- SNPs, MNPs and InDels
- Novel genes
- Novel splice junctions
- Gene Fusions

## DNA-Seq

- WGS, WES, Targeted panels
- SNPs, InDels and SVs
- Annotate with dbSNP, COSMIC
- Effect on transcripts
- SIFT, Polyphen2 predictions
- Multi-sample SNP analysis
- Copy number analysis

## ChIP-Seq

- Peak detection using PICS and MACS
- TF regulation binding sites
- Identify affected genes
- Histone modification sites
- ChIP sample vs control
- Motif detection
- Scan motifs in the genome

## Small RNA-Seq

- Quantification of miRNA, tRNA, snRNA, snoRNA and scRNA
- Novel small RNA prediction
- Differential gene expression
- Target mRNA prediction using TargetScan, PicTar, microRNA.org, PITA

## Methyl-Seq

- Detect hyper- and hypo-methylation
- Detect DMCs and DMRs
- Perform intra-sample analysis
- Perform methylation effect analysis

## MeDIP-Seq

- Normalize using a Calibration curve
- Detect hypo- and hyper-methylation
- Annotate methylation call

## Strand NGS - Server Edition

- Collaborative analysis
- Centralized storage
- Scalable compute
- Web-based interface for system administration
- Easy and flexible deployment

## Biological Interpretations

- GO enrichment, GSEA, GSA
- Single experiment OR Multi-omics analysis
- Identify significant pathways
- Curated / literature-derived pathway rendering
- Intuitive data overlay
- Create custom pathways

## Discovery

**Rich visualizations:**
- Gene view
- Variant support view
- Elastic genome browser

**Managed Annotations:**
- Pre-packaged RefSeq, UCSC, NSEMBL, and dbSNP annotations
- Custom annotations
- BioCyc pathways

**Customization:**
- Jython scripts
- R-scripts
- Configurable pipeline

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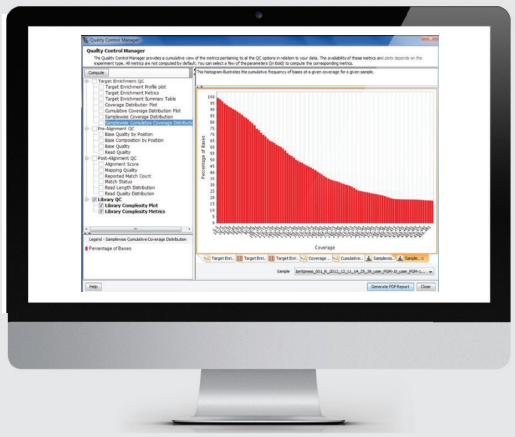
Strand NGS is an integrated platform that provides analysis, management and visualization tools for next generation sequencing (NGS) data generated by cutting-edge NGS instruments like Illumina, Roche, ABI, Ion Torrent, PacBio, SOLiD. It is a cross-platform application with desktop/ server versions and includes a feature-rich Genome Browser that provides custom visualizations to support the interpretation of analysis results. Strand NGS enables users to perform alignment and analysis of RNA-Seq, DNA-Seq, small RNA, Methyl-Seq, MeDIP-Seq and ChIP-Seq data, as well as biological interpretation, including Pathway and Multi-omic analysis.

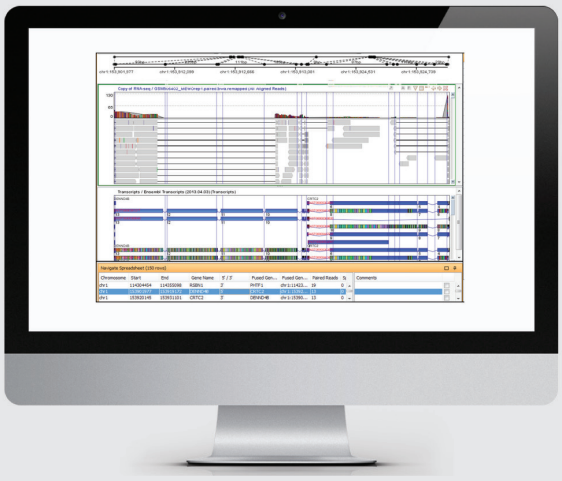
## Data Quality Control

Various quality inspection options including pre-alignment, post-alignment, vendor-specific, and library QC plots along with multiple filtering steps ensure that any poor quality data is kept out of the analysis.



## Genome Browser

A feature-rich Genome Browser provides custom visualizations of the analysis results. Annotation data, such as cytobands, genes, and transcripts, as well as results from various analyses, such as peak regions, SNPs, and gene fusions can be simultaneously viewed as individual tracks. The elastic genome browser can display multiple genomic regions simultaneously. Each genomic region can be viewed at a different zoom level, allowing for uninteresting regions to be collapsed and interesting regions to be expanded. You can also launch copy number visualizations using the web browser.



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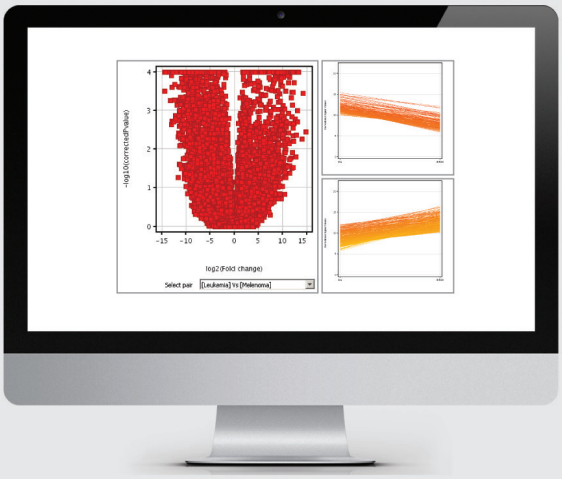
# Alignment

Strand NGS provides support for aligning reads to a genome for small RNA reads, DNA reads (for ChIP-Seq and DNA-Seq applications), and RNA reads (spliced and unspliced reads) from sequencing platforms like Illumina, Ion Torrent, ABI, SOLiD, Roche 454, and Pac Bio. The tool is equipped with the Strand NGS aligner, a proprietary algorithm based on the Burrows Wheeler Transform. Strand NGS aligner can handle both short reads and long reads, allows an arbitrary number of gaps and mismatches, handles both single end and paired end reads. Adapters can be trimmed using the integrated Cutadapt feature. Strand NGS also supports split read alignment for detecting long InDels and translocations.

# RNA-Seq

Strand NGS supports an extensive workflow for the analysis and visualization of RNA-Seq data, which includes standard differential expression analysis for different experimental conditions, as well as differential splicing analysis. It supports discovery of novel genes, exons, and novel splice junctions. The tool aids detection of variants and gene fusion events in the transcriptome.



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## Small RNA-Seq

Strand NGS supports expression analysis of various small RNA species, supports detection of novel small RNA genes, and their classification. After quantification of reads, identify differentially expressed small RNA genes, and visualize the results in a small RNA-specific gene view. The miRNA targets of interesting small RNA genes can be predicted using multiple target prediction databases like TargetScan, PicTar, TarBase, microRNA.org, and PITA.

## DNA-Seq

The DNA-Seq workflow provides options for the analysis of whole genome, whole exome and targeted re-sequencing data. Detect variants (SNPs, MNPs and InDels), with dbSNP, predict functional risk using dbNSFP and identify the effect of non-synonymous coding SNPs on alternate transcripts of a gene. Large structural variations including insertions, deletions, inversions, and translocations can also be detected with paired-end, mate-paired, split read data. In addition, copy number variations can be detected in samples using tumor-normal pairs or using a reference coverage profile.

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## Methyl-Seq

Strand NGS supports analysis and visualization of bisulfite treated methyl-seq data – from whole genome or targeted experiments. Within this workflow detect methylation in individual samples and identify differentially methylated cytosines across samples / target regions and also study methylation effects at the genic level. Further downstream analysis such as GO and pathway analysis can be performed on the set of affected genes.

## MeDIP-Seq

Strand NGS supports genome-wide methylation analysis using MeDIP-Seq data. The workflow supports data normalization before estimating the methylation signal and identifies differential methylation events across a pair of conditions. These regions can be further annotated based on their location with respect to known genes. Downstream analysis such as GO, pathway analysis can be performed on selected entities.

## ChIP-Seq

The ChIP-Seq workflow provides the ability to identify transcription factor binding sites and histone modification sites using the PICS and MACS peak detection algorithms. It supports the ability to detect motifs in the peak regions using GADEM, and scan for known motifs in the genome or region of interest.

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## Biological Interpretation

Strand NGS provides biological interpretation and discovery tools such as GO analysis, Gene Ontology enrichment, GSEA, NLP derived interaction network analysis, and pathways analysis. The pathway module in Strand NGS also supports pathway rendering from WikiPathways, BioCyc and BioPAX. Integrated multi-omics analysis can be performed by overlaying data from genomics, transcriptomics, and epigenomics experiments.


## Server Edition

Enterprise version of Strand NGS is designed to cater to the needs of multi-member teams working on NGS data analysis and facilitates collaborative analysis through group and individual level permissions. It enables central storage of data and analysis results with support for scheduled and incremental backups. The Extensive API allows the use of third party applications and it is optimized for scalable and efficient NGS data analysis.

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# About Strand

A History of Innovative Genomic Research

Strand Life Sciences is a global genomic profiling company and leader in precision medicine diagnostics, aimed at empowering cancer care and genetic testing for inherited diseases. Strand works with physicians and hospitals to enable faster clinical decision support for accurate molecular diagnosis, prognosis, therapy recommendations, and clinical trials. The Strand Center for Genomics & Personalized Medicine is India's 1st and only CAP & NABL accredited NGS laboratory.

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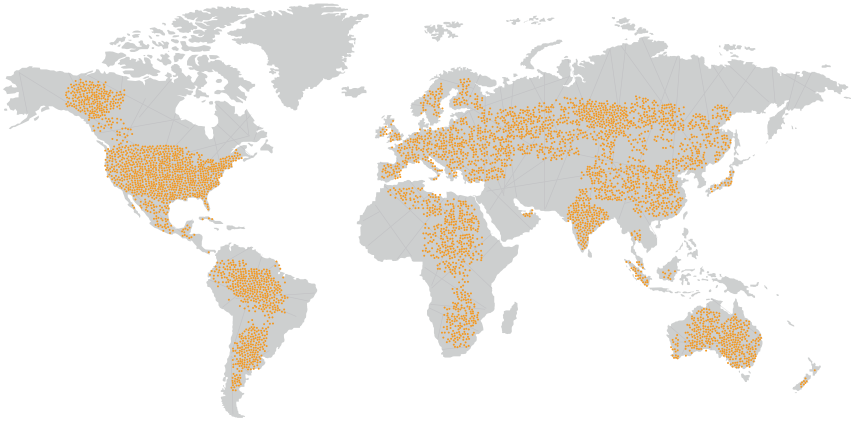

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For 15 years, our genomics products and solutions have facilitated the work of leading researchers and medical geneticists in over 2,000 laboratories and 100 hospitals around the world.

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