strandngs

Streamlining NGS Data Management & Analysis

Reads to Discovery

RNA-Seq Analysis

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

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Analyze | Visualize | Annotate | Discover

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RNA-Seq Analysis

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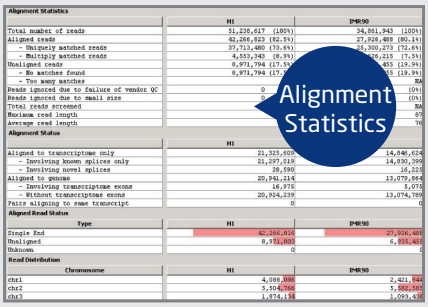
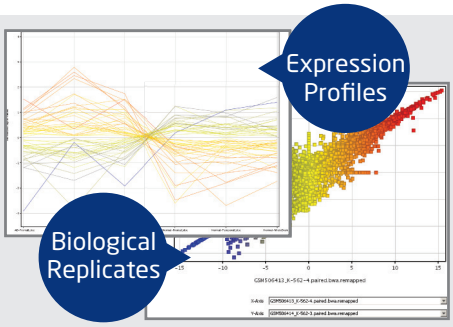
Alignment and Data QC

- Alignment against the transcriptome as well as the whole genome to enable detection of novel splice forms and genes.
- Handles variable length reads and paired reads as well.
- Allows arbitrary number of gaps and mismatches.
- Options for trimming adaptors, low quality bases and screening reads against standard screening databases.
- Perform RNA specific QC for genic regions and gene types.



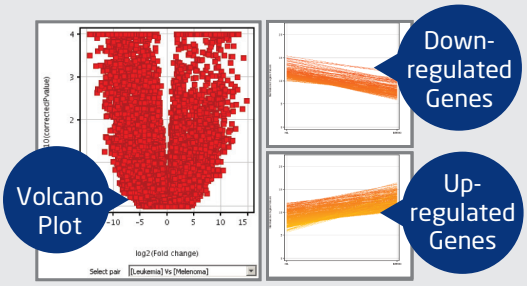
Quantification & Normalization

- Expression values at gene, exon and transcript levels.
- Appropriate handling of partially overlapping reads and multiple mapping reads.
- DESeq, RPM, TMM and Quantile methods for normalization.
- Experiment grouping supports large scale project handling.



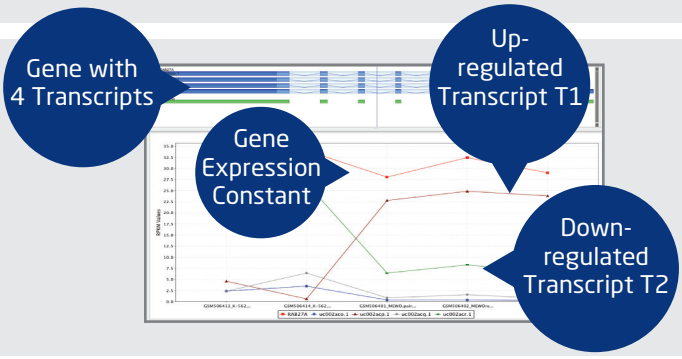
Differential Expression

- t-Test, Mann-Whitney, N-way ANOVA for identifying differentially expressed genes under different experimental conditions.
- Multiple Testing Correction using Benjamini Hochberg, Storey, Bonferroni, etc.
- Fold Change computation and visualization.



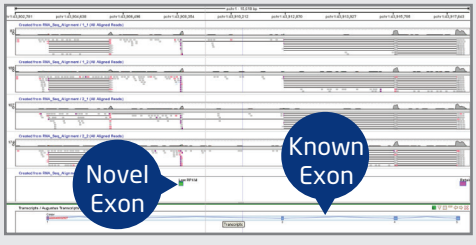
Differential Splicing

- EM algorithm to de-convolute gene counts to transcript counts.
- Identification of differentially spliced genes.
- Visualization in the gene view.



Novel Discovery

- Detection of novel genes, novel splice junctions, and novel exons in known genes.
- Differential expression analysis of novel genes and contribution of novel exons to differential splicing.
- Prioritization of novel regions using conservation score.



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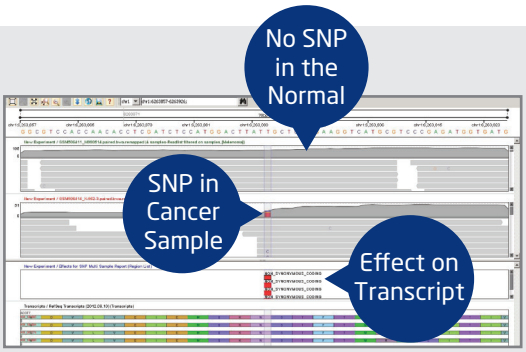
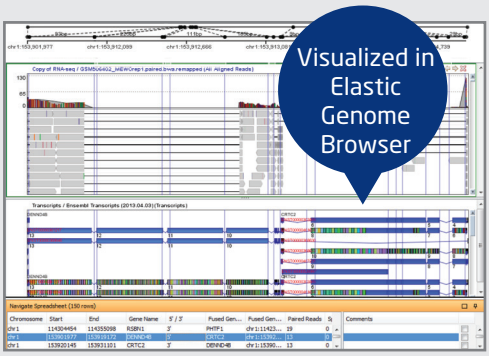
Transcriptome Variant Detection

- SNP, MNP, and InDel detection.
- Annotation with dbSNP to identify known/novel mutations.
- Prediction of effects such as non-synonymous coding, frameshift, splice-site, etc. on transcripts.
- Identify significant SNPs using an intuitive filtering framework.



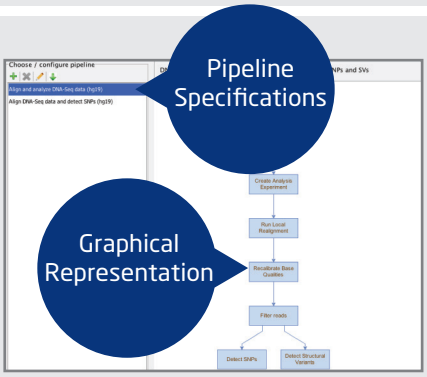
Gene Fusions

- Gene fusions detected from spliced and paired reads.
- Detection of read through transcripts.
- Gene fusions involving paralogs and pseudogenes marked as such to help filter out false positives.



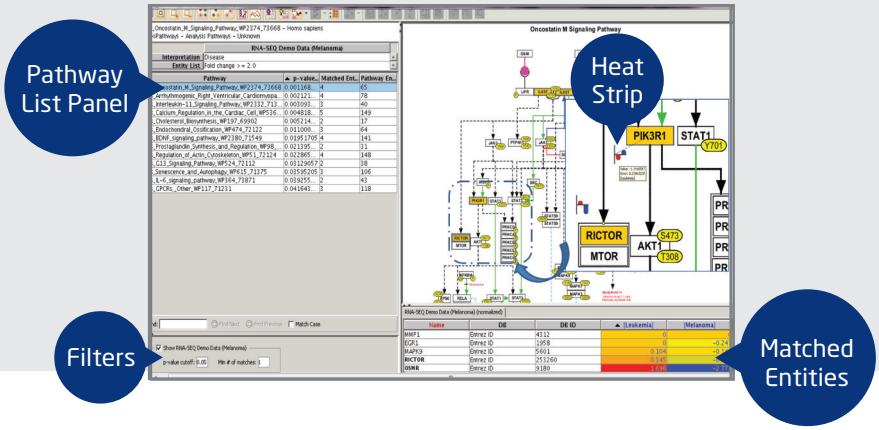
Pipeline Execution

- Pipelines that run in the background.
- Analysis pipeline includes filters and quantification.
- Pipelines support alignment of raw reads and direct import of aligned samples.
- Customization of pipelines for individual runs.



Pathway Analysis

- Single Experiment Analysis (SEA) identifies enriched pathways for the genes from a single experiment type.
- Multi-Omic Pathway Analysis (MOA) from multiple genomics and transcriptomics experiments.
- Overlay differentially expressed entities on curated pathways.
- Choose from curated pathways like WikiPathways, BioCyC pathways, BioPAX pathways or literature-derived networks like NLP and MeSH.
- Find significant pathways for differentially expressed genes.



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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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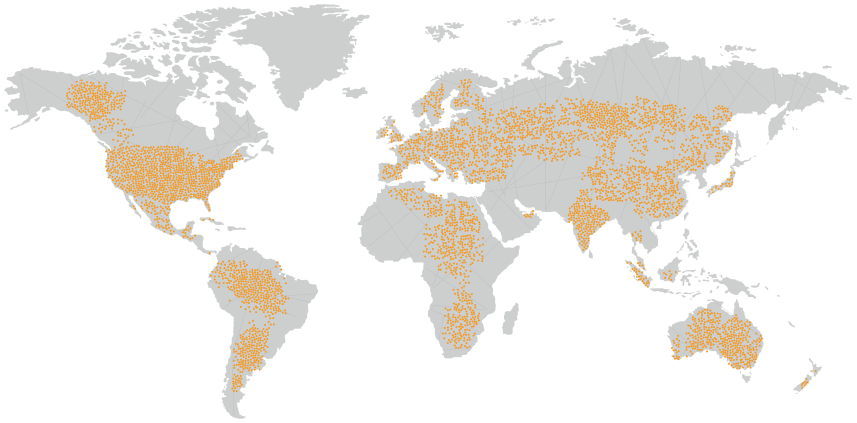

A Trusted Partner to Companies Worldwide

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.

Strand Life Sciences Pvt. Ltd
5th Floor, Kirloskar Business Park, Bellary Road, Hebbal, Bangalore 560024
Phone:+91-80-40 (787263) Fax: +91-80-4078-7299

Contact us
sales@strandngs.com
USA: 1-800-752-9122 ROW: +1-650-353-5060

support@strandngs.com
USA: 1-800-516-5181 ROW: +1-650-288-4559