strandngs

Streamlining NGS Data Management & Analysis

Reads to Discovery

DNA-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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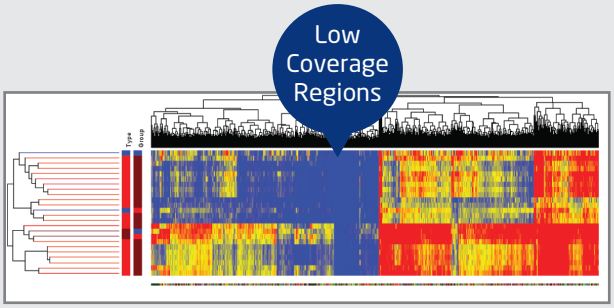
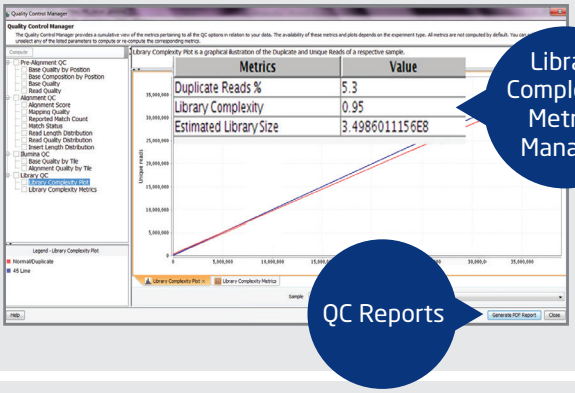
Targeted Re-sequencing Analysis

- Import BED file of target regions.
- Filter reads outside target regions.
- Evaluate efficacy of targeted re-sequencing.
- Identify target regions with low coverage across samples.
- Detect SNPs and other variants on targeted regions.



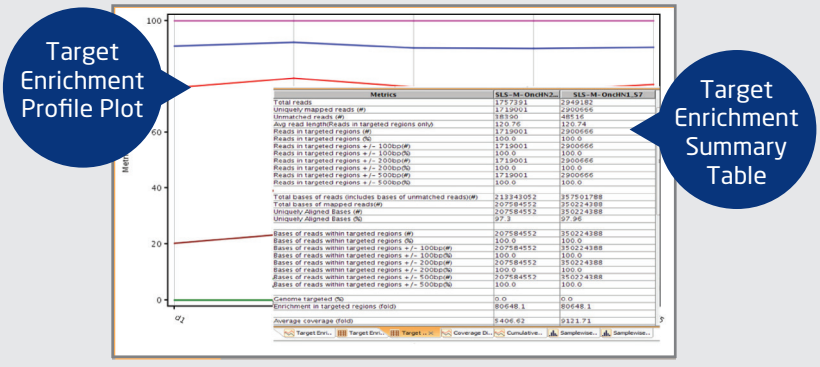
Quality Control Manager: Library QC

- Multiple quality inspection options including pre-alignment, post-alignment, vendor-specific QC and Library QC.
- Automatically generates a QC report for every sample.
- Export QC report as a pdf document.



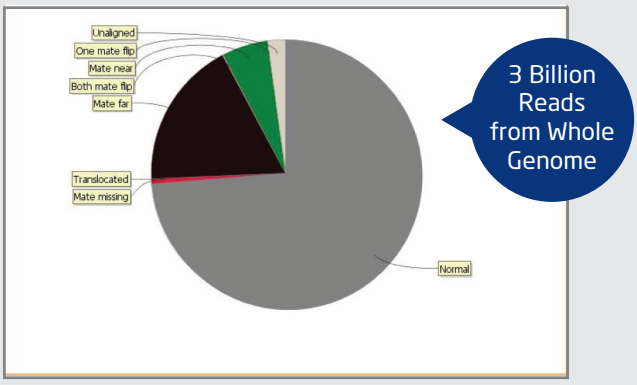
Quality Control Manager: Target Enrichment QC

- Efficiently analyze data generated from target enrichment sequencing experiments.
- Target region-based quality control for your customized panels.
- Assess coverage distribution across target regions, including target enrichment profile plot, metrics, summary table, and sample-wise base frequency coverage distribution.



Whole Genome Analysis

- Perform Whole Genome analysis on human or other organisms on your desktop.
- Regular desktop machine with 4GB RAM, 4 cores, and 2TB hard disk.



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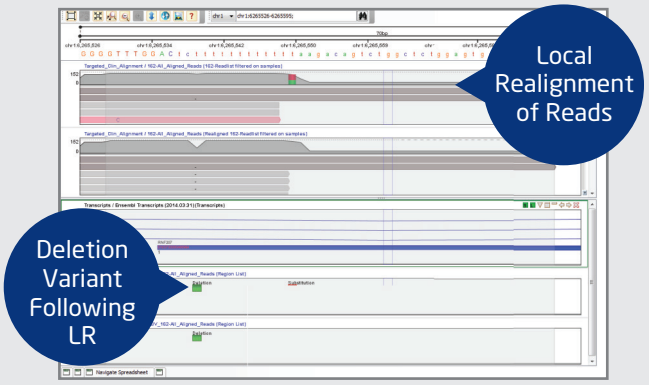
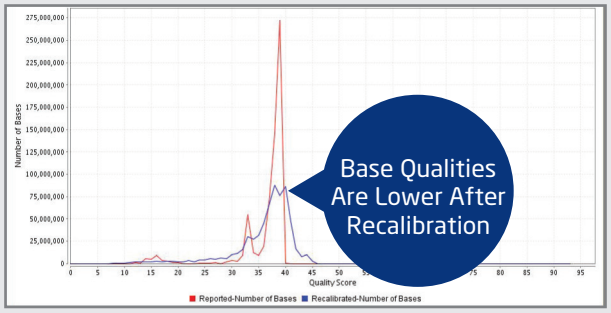
Local Realignment (LR)

- Reads with alignment artifacts around InDels can be realigned using information from multiple reads.
- Helps in getting rid of spurious substitutions and reduces false-positive variant calls.



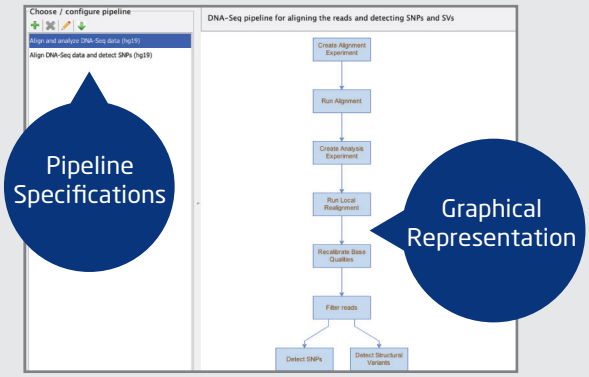
Base Quality Score Recalibration (BQSR)

- Recalibrates base quality scores to reduce errors and systemic biases.
- Uses contexts like machine cycle and dinucleotide context to recalibrate the reported base quality scores.
- Helps reduce false-positive variant calls.



Pipeline Execution

- Analysis pipelines that include filters, local realignment, base quality recalibration, and SNP detection.
- Additional pipelines that start from alignment of raw reads or direct import of aligned samples.
- Customization of pipelines for individual runs.



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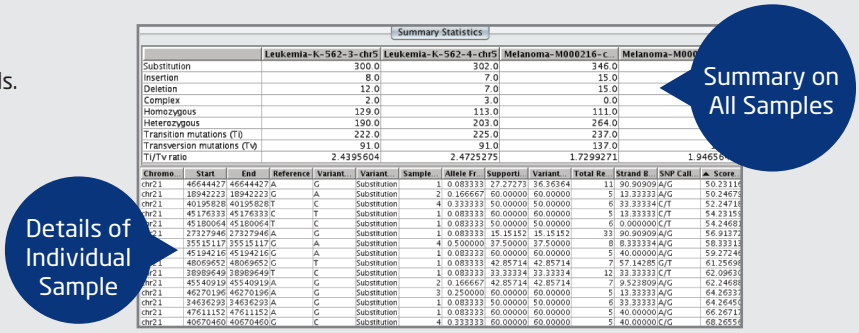
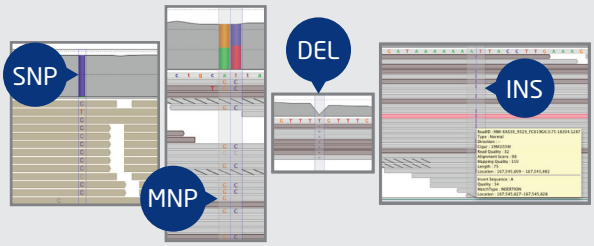
Variant Detection

- SNP Detection algorithm to detect SNPs, MNPs, and small InDels.
- View summary statistics of variants across samples.
- Visualize details of variants in each sample, along with dbSNP annotations.
- Support for VCF and VAL import.



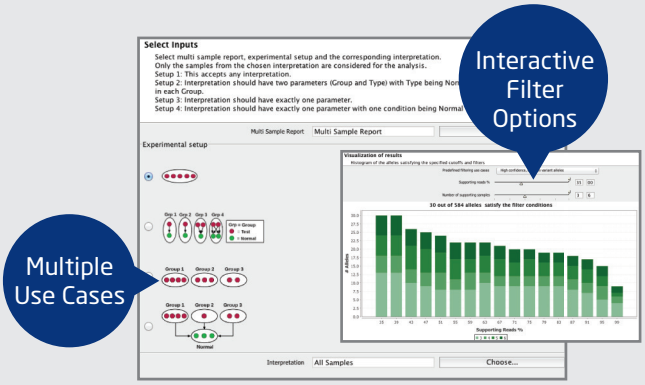
Visualize Variants

- Drag and drop SNP results into the genome browser.
- Visualize SNPs, MNPs, and InDels along with read coverage, as well as other annotations.



Find Significant SNPs

- Multiple use cases including normal-tumor, multi-group comparisons, low-frequency mutations, rare variant analysis, and somatic mutations.
- Cluster significant SNPs and samples to detect patterns visually.
- Identify significant SNPs using an intuitive filtering framework.



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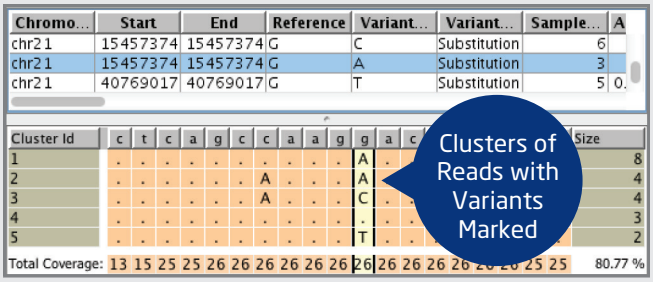
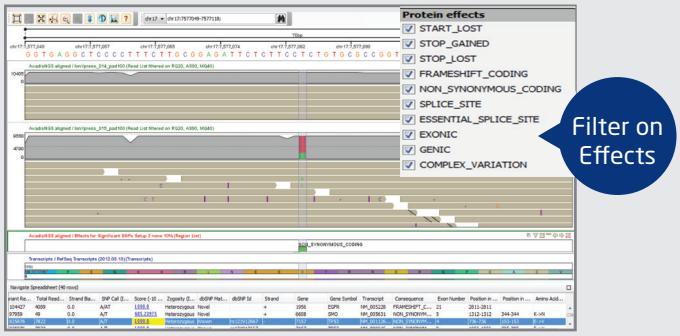
Variant Support View

- Intuitive visualization to verify individual SNPs.
- Color by base quality or mapping quality.
- Cluster reads to make variant locations stand out.
- Annotate clusters with strand information.



SNP Effect Analysis

- Identify effect of detected SNPs on transcripts.
- Variety of effects including non-synonymous coding, splice site, stop gained, etc.
- Visualize along with the amino acid sequences for transcripts.
- Ability to filter on interesting effects.
- Annotate with COSMIC and other external databases.



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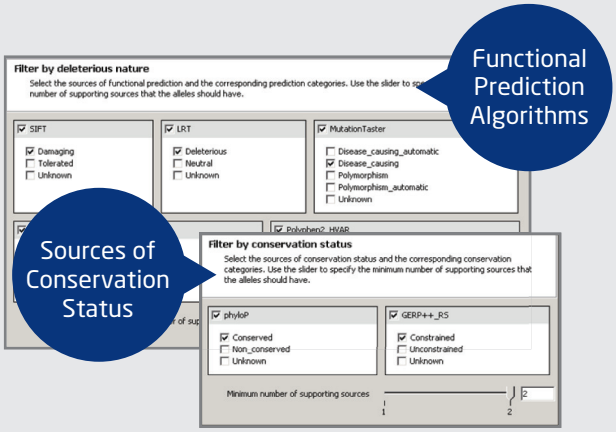
Find Damaging Variants

- Filter variants based on functional annotations for non-synonymous variants from dbNSFP.
- Identify damaging variants based on prediction scores from SIFT, Polyphen, LRT, Mutation Taster, and Mutation Assessor.
- Filter based on conservation scores from phyloP and GERP++_RS.
- Filter based on allele frequencies from 1000 genomes.



Structural Variant Analysis

- Structural variant detection on paired end and split read data.
- Identify large structural variants including large insertions, deletions, inversions, and translocations.
- Verify using Elastic Genome Browser.

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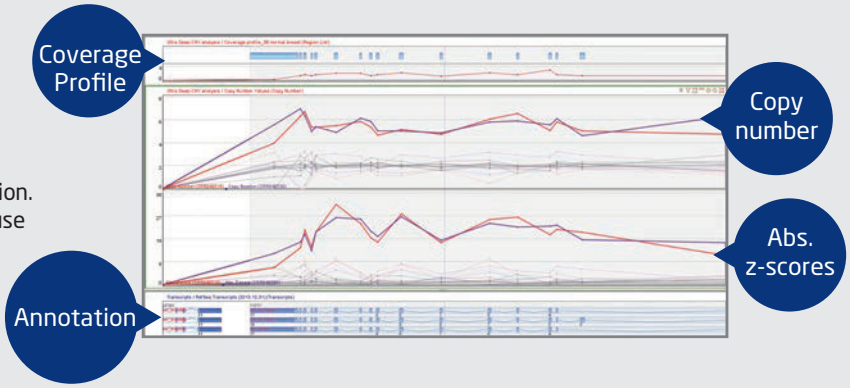
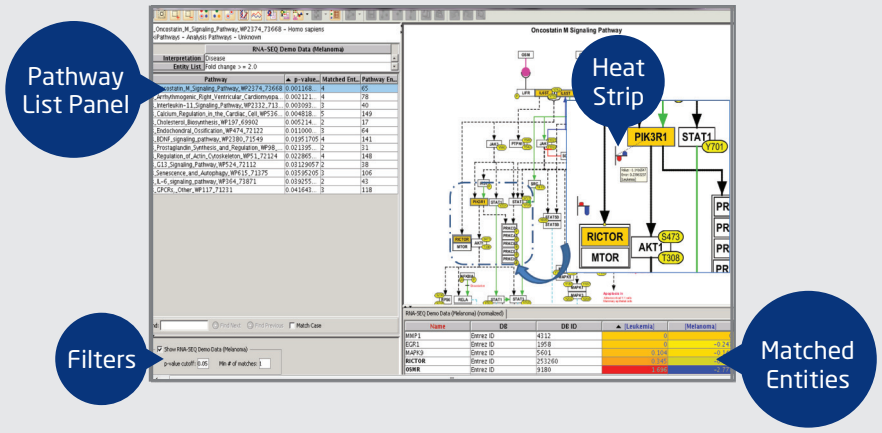
Copy Number Variant (CNV) Analysis

- Detects CNV regions in group of samples.
- Includes GC bias correction as a preprocessing step.
- Includes estimation of sample ploidy and normal cell contamination.
- Ability to create coverage profiles from a group of samples and use it for subsequent CNV analysis across experiments.
- Verify CNV's using the Genome Browser and specially designed web based visualization



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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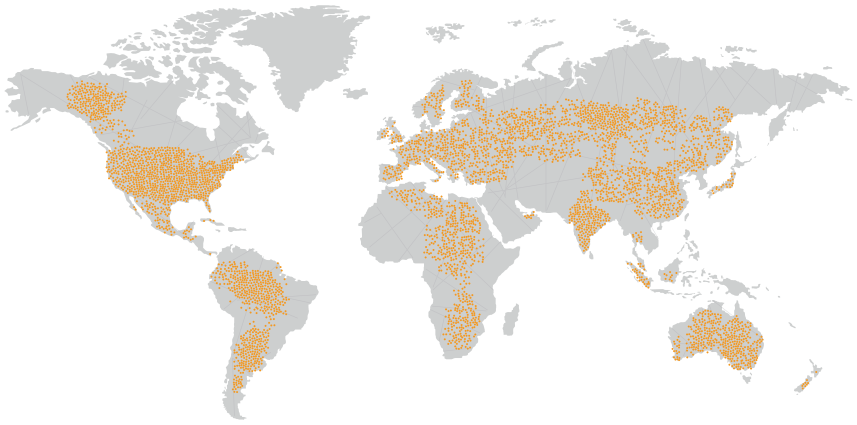

A Trusted Partner to Companies Worldwide

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.

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