



Streamlining NGS Data Management & Analysis

Reads to Discovery

Data Import, Alignment, and Quality Control

RNA-Seq

DNA-Seq

ChIP-Seq

Small
RNA-Seq

Methyl-Seq

MeDIP-Seq

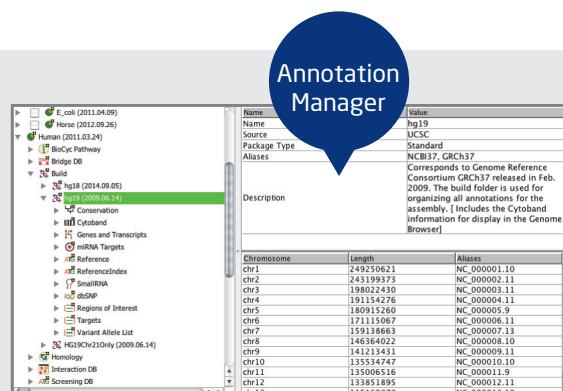
www.strand-ngs.com

Analyze | Visualize | Annotate | Discover

strand 
New Generation Healthcare

Comprehensive Annotations

- Pre-packaged gene and transcript annotations from UCSC, RefSeq and ENSEMBL for all model organisms.
- SNP annotations from dbSNP and COSMIC, SIFT/Polyphen scores from dbNSFP, small RNA annotations, miRNA target prediction databases, screening databases and more.
- Ability to create annotations for other organisms from gbk/gtf files or FASTA files.



Import Data

- File Formats - FASTA/FASTQ, Unaligned BAM, SAM/BAM, Counts data.
- Library Layouts - Single End, Paired End, Mate Paired as well as Directional layouts.
- Vendor Platforms - Illumina, Ion Torrent, 454 Roche, SOLiD, PacBio.

Experiment Metadata

Choose Meta Data
Select the appropriate organism, build, sequencing platform and library layout.

Organism:

Build:

Gene Annotation:

Sequencing Platform:

Library layout:

NOTE: All reads from the sample for analysis. Make sure they are aligned to the correct reference genome.

Type	Selected files/samples	Sample Name
<input type="checkbox"/>	Leukemia-K-562-3-chr5	Leukemia-K-562-3-chr5
<input type="checkbox"/>	Leukemia-K-562-4-chr5	Leukemia-K-562-4-chr5
<input type="checkbox"/>	Melanoma-M000216-chr5	Melanoma-M000216-chr5
<input type="checkbox"/>	Melanoma-M000921-chr5	Melanoma-M000921-chr5

Buttons: Help, << Back, Next >>, Finish, Cancel

Data Files

Alignment with Strand NGS aligner

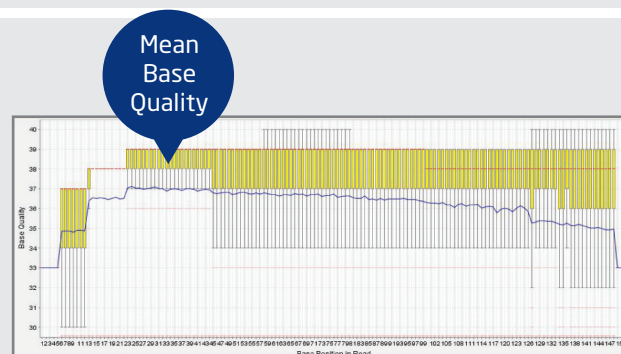
- Alignment for small RNA, DNA-Seq, ChIP-Seq and RNA-Seq data.
- Targeted region alignment for resequencing applications. Handles variable length reads, arbitrary number of gaps and mismatches and paired reads as well.
- Split read alignment for detecting long InDels and translocations.
- Options for trimming adaptors, low quality bases and screening reads against standard databases.
- Aligns ~8 million DNA reads against hg19 per hour per core on a 64GB RAM machine.

Alignment Statistics

Alignment Statistics		H1	IM-90
Total number of reads		81,238,617 (100%)	34,881,943 (100%)
Aligned reads		73,766,623 (90.8%)	27,925,488 (80.1%)
- Uniquely matched reads		25,300,273 (72.6%)	14,830,399 (46.2%)
- Multiply matched reads		48,466,350 (59.2%)	13,095,089 (37.5%)
Unaligned reads		7,472,000 (9.2%)	6,956,455 (20.0%)
- No matches found		0 (0.0%)	0 (0.0%)
- Too many matches		0 (0.0%)	0 (0.0%)
Reads ignored due to failure of vendor QC		0 (0.0%)	0 (0.0%)
Total reads screened		81,238,617	34,881,943
Maximum read length		101	70
Average read length		36	36
Alignment Status		H1	IM-90
Aligned to transcriptome only		21,325,609	14,946,624
- Involving known splices only		21,297,019	14,830,399
- Involving novel splices		28,590	16,225
Aligned to genome		20,941,214	13,079,864
- Involving transcriptome exons		16,975	5,075
- Without transcriptome exons		20,924,239	13,074,789
Pairs aligning to same transcript		0	0
Aligned Read Status		H1	IM-90
Single End		42,066,815	27,925,488
Unaligned		8,731,803	6,956,455
Unknown		0	0
Read Distribution		H1	IM-90
Chromosome			
chr1		4,368,888	2,421,944
chr2		5,156,266	5,888,848
chr3		1,874,154	1,093,430

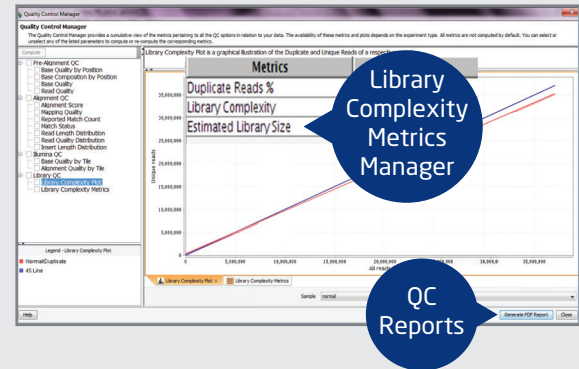
Quality Control Plots

- Base and read quality distributions.
- Base composition and quality distributions by position in read.
- Read length and insert length distributions.
- Alignment score and mapping quality distributions.
- Mate status QC plot.
- Vendor-specific QC plots.
- Targeted region QC.



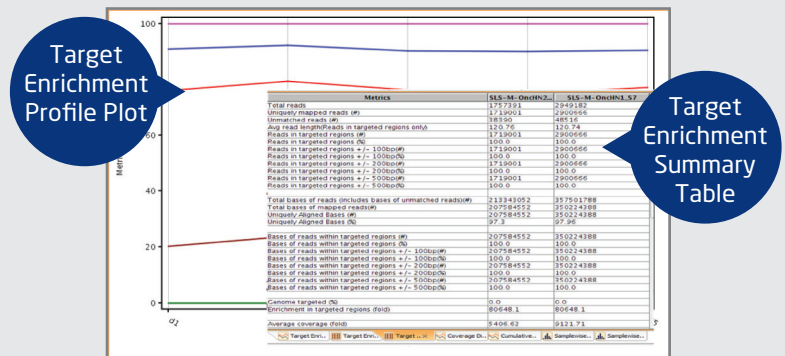
Quality Control Manager: Library QC

- 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.



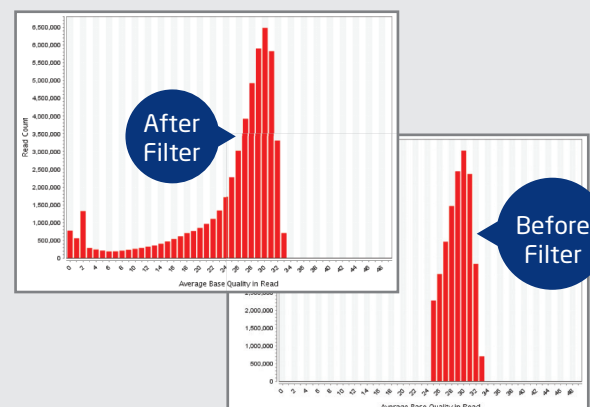
Quality Control Manager: Target Enrichment QC

- Efficiently analyze data generated from targeted resequencing 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.



Filter Low Quality Reads

- Filter by read quality metrics.
- Filter by targeted regions of interest.
- Filter duplicate reads and multiple mapping reads.
- Filter by samples.

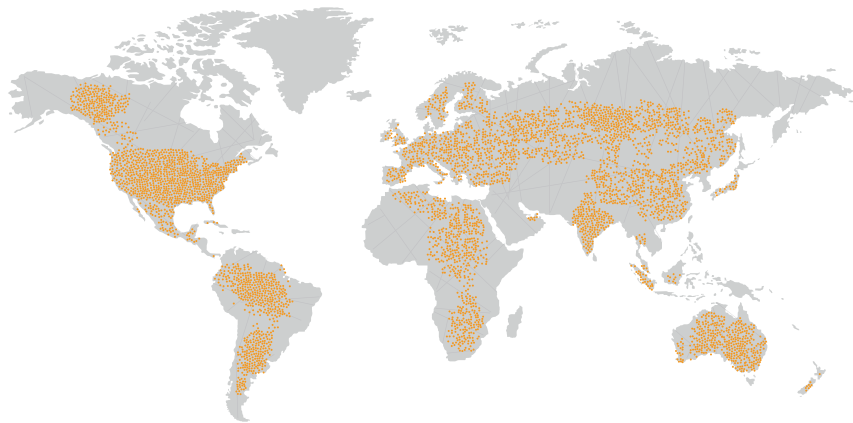


About Strand

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.

www.strandls.com



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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