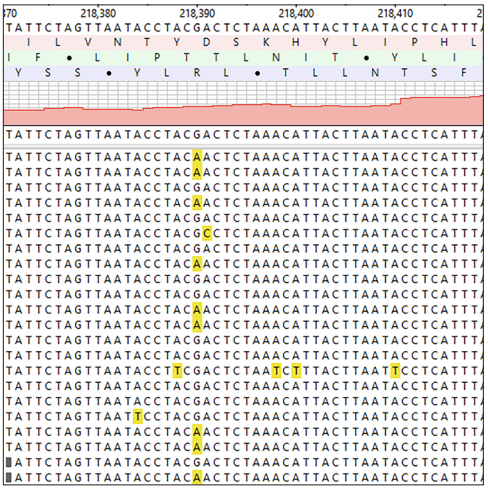
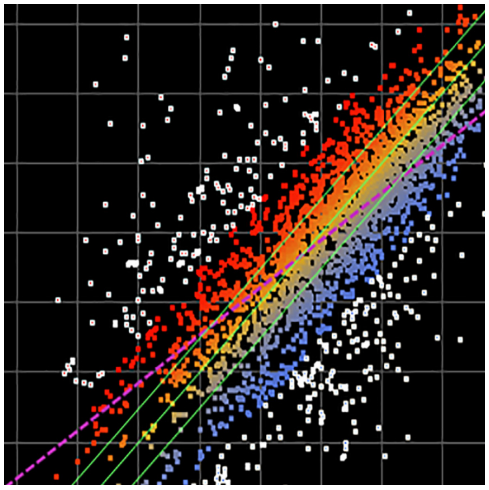
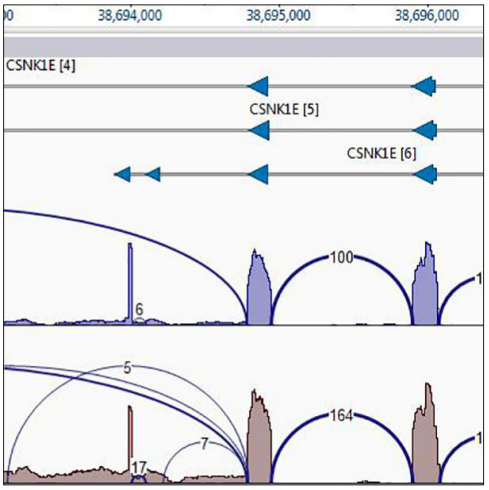
DNASTAR®
Software for Life Scientists

LASERGENE GENOMICS

Supporting all major NGS workflows and technologies







RESEQUENCING AND GENOTYPING

- Reference guided alignment for any size project
- Cancer genomics
- Copy number variation (CNV) calculation
- Sanger validation of NGS assemblies and variant calls
- Variant detection accuracy >99%
- SNP to structure worklfow for modeling impact of mutations on protein structure

GENOME ASSEMBLY AND EDITING

- *De novo* genome assembly and contig editing
- Hybrid *de novo* assembly with closely related reference for contig ordering and scaffolding
- Gap closure for genomic alignments

TRANSCRIPTOME ANALYSIS

- *De novo* transcriptome assembly with auto-mRNA annotation
- RNA-Seq gene expression analysis and statistics, including DESeq2 and EdgeR
- ChIP-Seq peak detection
- Microarray analysis
- miRNA discovery, quantification, and gene expression
- Combined analysis and visualization of gene expression data from multiple technologies

METAGENOMICS

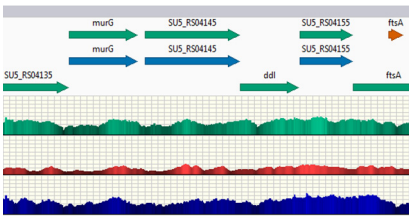
- Alignment of metagenomic sequencing data to biome genomes and gene databases
- *De novo* assembly of novel sequences

Perform NGS assembly, alignment, and variant calling quickly and accurately

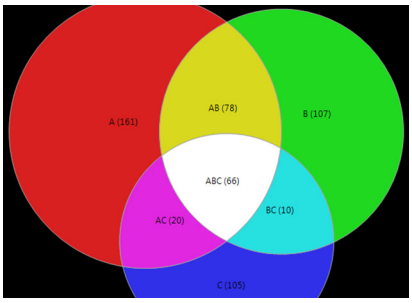
Accuracy and Speed Benchmarks

REFERENCE-GUIDED ALIGNMENT BENCHMARKS				
Data Set	**Number of Samples**	**Input Data (Gbases)**	**Assembly Time**	**Per-Sample Assembly Time**
Salmonella Genome	18	7	69 minutes	2.7 minutes
Human RNA-Seq	11	69	11 hours	55 minutes
Human Exome	10	68	8 hours	49 minutes
Human Genome	1	112	17 hours	17 hours
Human Genome	3	335	43 hours	14 hours

DE NOVO TRANSCRIPTOME ASSEMBLY BENCHMARKS				
Data Set	**Number of Reads (Millions)**	**Transcripts**	**Average Transcript Length**	**Assembly Time**
Human	100	30,342	975	15 hours
Water Bear	45	24,960	1,680	30 hours



Multiple genome assemblies



Venn diagram used to compare SNPs, genes & peaks

ACCURACY COMPARISONS FOR HUMAN EXOME VARIANT ANALYSIS USING NA12878							
Workflow	**Sensitivity**	**Specificity**	**False Discovery Rate**	**True Positives**	**False Positives**	**False Negatives**	**Elapsed Time**
Lasergene Genomics Suite	**99.56%**	**99.999%**	**1.29%**	**15,272**	**200**	**67**	**1.3 hr**
CLC Bio's Genomics Work-bench 8.0	99.18%	99.995%	7.41%	15,553	1,245	288	3.1 hr
Geneious 8.1	91.68%	99.995%	7.82%	14,827	1,257	1,346	2.9 hr
BWA Mapper / GATK Unified Genotyper	99.09%	99.999%	1.08%	15,161	166	139	6.0 hr
BWA Mapper / GATK Haplotype Base Caller	99.14%	99.999%	0.97%	15,168	149	132	6.3 hr

Sequencing Platforms
Illumina
Ion Torrent
PacBio

Operating Systems
Windows
Macintosh

DNASTAR Cloud

Hardware Requirements
16-32 GB RAM
Quad-Core 3 GHz processor
Two 1-4 TB hard drives*
**For ref-guided alignments on local computers*

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