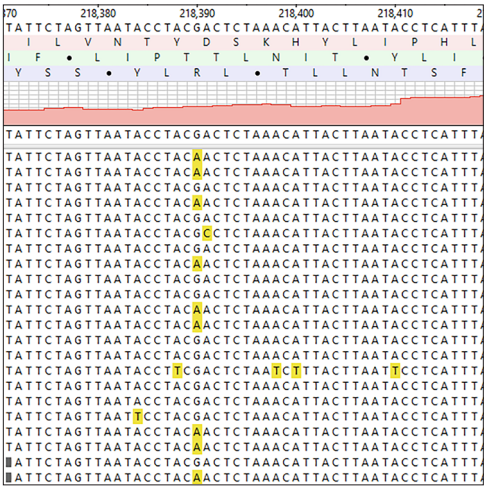
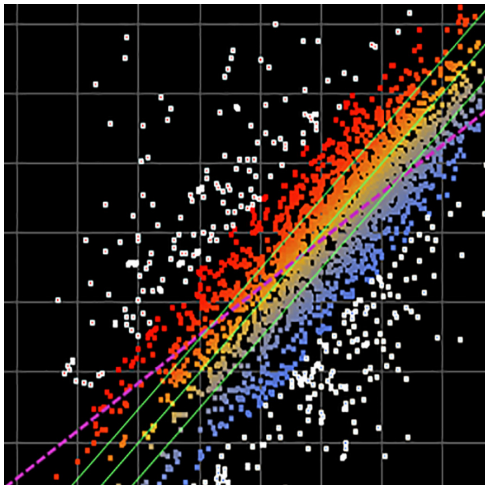
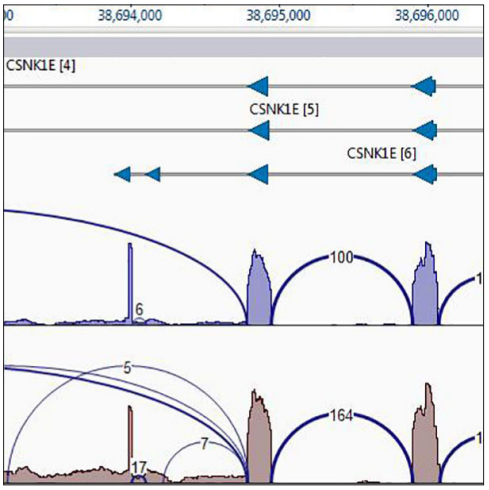
DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

LASERGENE GENOMICS

Supporting all major NGS workflows and technologies







RESEQUENCING AND GENOTYPING

- Reference guided alignment for any size project
- Cancer genomics
- Viral genome analysis, including support for ARTIC network protocols
- Copy number variation (CNV) calculation
- 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

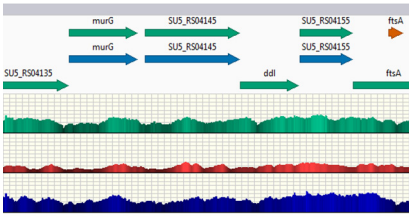
Accuracy and Speed Benchmarks

REFERENCE-GUIDED ALIGNMENT BENCHMARKS

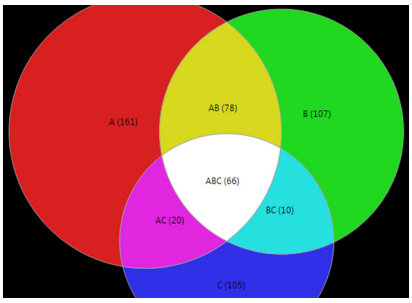
Data Set	Number of Samples	Input Data (Gbases)	Assembly Time	Per-Sample Assembly Time
Salmonella Genome	18	7	69 minutes	2.7 minutes
Human RNA-Seq	11	69	11 hours	55 minutes
Human Exome	10	68	8 hours	49 minutes
Human Genome	1	112	17 hours	17 hours
Human Genome	3	335	43 hours	14 hours

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	**99.56%**	**99.999%**	**1.29%**	**15,272**	**200**	**67**	**1.3 hr**
CLC Bio Genomics Workbench	99.18%	99.995%	7.41%	15,553	1,245	288	3.1 hr
Geneious	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*

Contact Us

608.258.7420 tel
866.511.5090 toll free

0.808.234.1643 U.K.
0.800.182.4747 Germany

3801 Regent Street
Madison, WI 53705

www.dnastar.com
info@dnastar.com