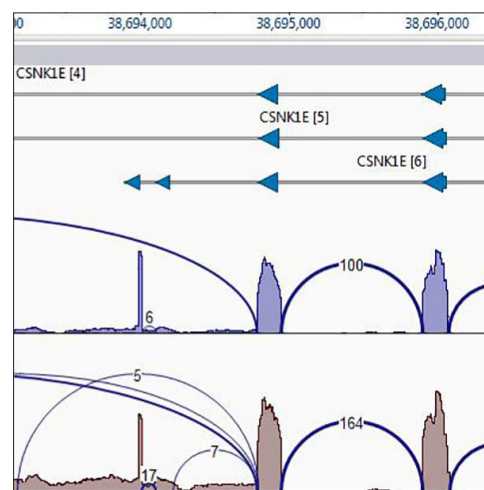
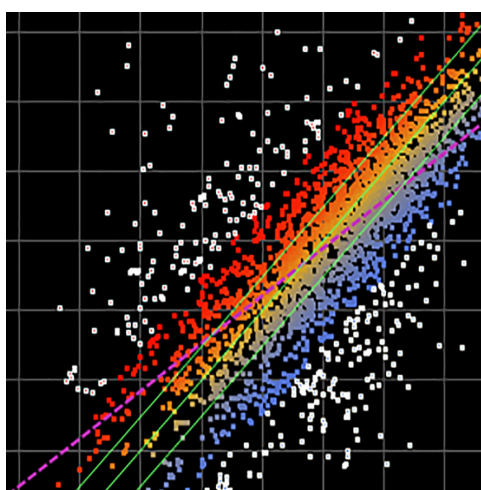
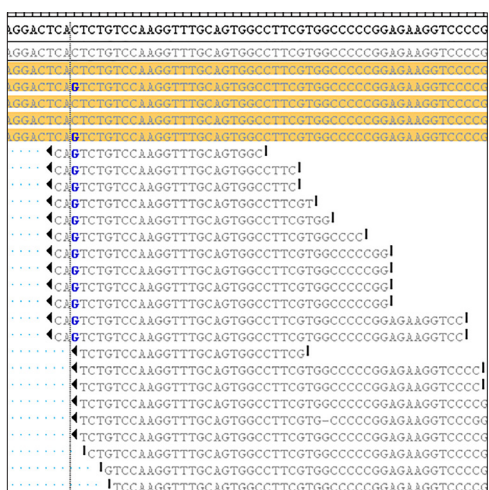


LASERGENE GENOMICS

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 workflow for modeling impact of mutations on protein structure

GENOME ASSEMBLY AND EDITING

- *De novo* genome assembly and contig editing
- Editing and gap closure for reference-guided 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 and quantification
- Combined analysis and visualization of gene expression data from multiple technologies

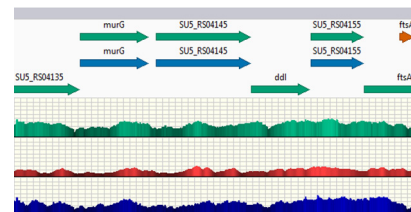
METAGENOMICS

- 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

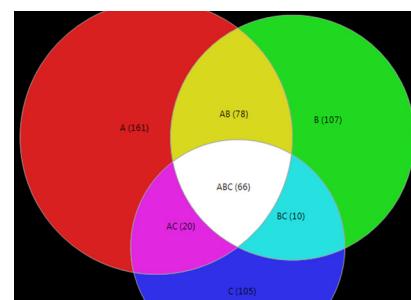
Accuracy and Speed Benchmarks

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



Multiple genome assemblies

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



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 Workbench 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



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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