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
Accuracy and Speed Benchmarks

### REFERENCE-GUIDED ALIGNMENT BENCHMARKS

<table>
<thead>
<tr>
<th>Data Set</th>
<th>Number of Samples</th>
<th>Input Data (Gbases)</th>
<th>Assembly Time</th>
<th>Per-Sample Assembly Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salmonella Genome</td>
<td>18</td>
<td>7</td>
<td>69 minutes</td>
<td>2.7 minutes</td>
</tr>
<tr>
<td>Human RNA-Seq</td>
<td>11</td>
<td>69</td>
<td>11 hours</td>
<td>55 minutes</td>
</tr>
<tr>
<td>Human Exome</td>
<td>10</td>
<td>68</td>
<td>8 hours</td>
<td>49 minutes</td>
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<tr>
<td>Human Genome</td>
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<td>112</td>
<td>17 hours</td>
<td>17 hours</td>
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<tr>
<td>Human Genome</td>
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<td>335</td>
<td>43 hours</td>
<td>14 hours</td>
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### DE NOVO TRANSCRIPTOME ASSEMBLY BENCHMARKS

<table>
<thead>
<tr>
<th>Data Set</th>
<th>Number of Reads (Millions)</th>
<th>Transcripts</th>
<th>Average Transcript Length</th>
<th>Assembly Time</th>
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<tbody>
<tr>
<td>Human</td>
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<td>30,342</td>
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<td>Water Bear</td>
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<td>24,960</td>
<td>1,680</td>
<td>30 hours</td>
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### ACCURACY COMPARISONS FOR HUMAN EXOME VARIANT ANALYSIS USING NA12878

<table>
<thead>
<tr>
<th>Workflow</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>False Discovery Rate</th>
<th>True Positives</th>
<th>False Positives</th>
<th>False Negatives</th>
<th>Elapsed Time</th>
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<tbody>
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<td>Lasergene Genomics Suite</td>
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<td>99.999%</td>
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<td>99.995%</td>
<td>7.41%</td>
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<td>99.995%</td>
<td>7.82%</td>
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<td>99.999%</td>
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</tr>
<tr>
<td>BWA Mapper / GATK Haplotype Base Caller</td>
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<td>99.999%</td>
<td>0.97%</td>
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<td>149</td>
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</tbody>
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**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

**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