














# BaseSpace® Sequence Hub Apps Quick Guide







Credits are the common currency in which BaseSpace Sequence Hub services are priced. Learn more about [iCredits and billing](#).

Biomedical and Basic Research – Genetic Analysis			
App name	Sequencing application(s)	Key functionality	Vendor
 <b>Amplicon DS</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Targeted Resequencing (TruSight Tumor 26 Panel)</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Somatic Variant Calling</li> <li>Annotation</li> </ul>	<b>illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 4 M reads, 2 x 150 bp cost = 0.70 iCredits/sample
 <b>BWA Aligner</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Whole Genome Sequencing</li> <li>Targeted Sequencing</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Custom reference genome</li> <li>Batch processing</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 100 M reads, 2 x 150 bp cost = 28.10 iCredits/sample
 <b>BWA Enrichment</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Small Variant Calling</li> <li>Annotation</li> <li>Custom Manifest Files</li> <li>Batch processing</li> </ul>	<b>illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 30 M reads, 2 x 75 bp cost = 5.28 iCredits/sample
 <b>Cancer Variant Caller</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Whole-Genome Sequencing</li> <li>Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>Variant Calling</li> </ul>	<b>Samsung</b> <a href="mailto:basespace.qa@samsung.com">basespace.qa@samsung.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>EDGC Annotator</b>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>Variant Annotation</li> <li>Variant Analysis</li> </ul>	<b>EONE-DIAGNOMICS Genome Center</b> <a href="http://www.edgc.com/edgannotator?lang=en">www.edgc.com/edgannotator?lang=en</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>Enrichment</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Small Variant Calling</li> <li>Somatic Variant Calling</li> <li>SV/CNV Calling</li> <li>Annotation</li> <li>Custom Manifest Files</li> <li>Batch processing</li> </ul>	<b>illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: TruSeq Exome (200x mean coverage) 60 M reads, 2 x 75 bp cost = 6.76 iCredits/sample






## Biomedical and Basic Research – Genetic Analysis (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>GeneTalk Variant Analyzer</b></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>Variant Annotation</li> <li>Variant Analysis</li> </ul>	<p><b>GeneTalk</b></p> <p><a href="http://www.gene-talk.de">www.gene-talk.de</a>            Compute Cost: Free            License Cost: n/a</p>
 <p><b>LoFreq Rare Variant Caller</b></p> <p><a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> <li>Oncology</li> </ul>	<ul style="list-style-type: none"> <li>Variant Caller</li> </ul>	<p><b>Genome Institute of Singapore</b></p> <p><a href="http://www.gisapps.org/lofreqbs/contact.htm">www.gisapps.org/lofreqbs/contact.htm</a>            Compute Cost: 3 iCredits per node/hr            License Cost:            - 1 iCredit per 10 GB of input file            - 4 iCredits for 30–39 GB            - 5 iCredits 40–49 GB            - etc.</p>
 <p><b>Melanoma Profiler</b></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> <li>Oncology</li> </ul>	<ul style="list-style-type: none"> <li>Variant Analysis</li> <li>Tumor Normal</li> </ul>	<p><b>Biomatters Ltd.</b></p> <p><a href="http://apps.biomatters.com/melanoma-profiler/welcome">apps.biomatters.com/melanoma-profiler/welcome</a>            Compute Cost: Free</p>
 <p><b>mtDNA Variant Analyzer</b></p> <p><a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> <li>mtDNA Profiling</li> <li>Forensics</li> </ul>	<ul style="list-style-type: none"> <li>Visualizatoin</li> <li>Variant Analysis</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: Free            License Cost: n/a</p>
 <p><b>mtDNA Variant Processor</b></p> <p><a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing</li> <li>mtDNA Profiling</li> <li>Forensics</li> </ul>	<ul style="list-style-type: none"> <li>mtDNA Variant Calling</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: Free            License Cost: n/a</p>
 <p><b>MutationForecaster</b></p>	<ul style="list-style-type: none"> <li>RNA-Seq</li> <li>Variant Analysis</li> </ul>	<ul style="list-style-type: none"> <li>Interpret and validate mutations that affect mRNA splicing and protein coding</li> </ul>	<p><b>Cytognomix Inc.</b></p> <p><a href="http://basespace.mutationforecaster.com">basespace.mutationforecaster.com</a>            Compute Cost: Free            License Cost:            - 1 Day Subscription: 75 iCredits            - 7 Day Subscription: 125 iCredits</p>
 <p><b>MyFLq</b></p> <p><a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>Forensics</li> </ul>	<ul style="list-style-type: none"> <li>STR and SNP query</li> </ul>	<p><b>University Ghent</b></p> <p><a href="http://forensic.ugent.be">forensic.ugent.be</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>

## Biomedical and Basic Research – Genetic Analysis (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>Novoalign Generic DNA pipeline</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Variant Calling</li> </ul>	<p><b>Novocraft</b>  <a href="http://www.novocraft.com/products/novoalign">www.novocraft.com/products/novoalign</a>                      Compute Cost: 3 iCredits per node/hr</p>
 <p><b>NuGEN Ovation Target Enrichment</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>• Demultiplexing</li> <li>• Alignment</li> </ul>	<p><b>NuGEN Technologies, Inc.</b>  <a href="http://www.nugen.com">www.nugen.com</a>                      Compute Cost: 3 iCredits per node/hr                      License Cost: n/a</p>
 <p><b>Phy-Mer</b></p>	<ul style="list-style-type: none"> <li>• Mitochondrial Analysis</li> </ul>	<ul style="list-style-type: none"> <li>• Haplogroup Analysis</li> </ul>	<p><b>MEEI Bioinformatics Center (MBC)</b>  <a href="https://github.com/danielnavarrogomez/phy-mer">github.com/danielnavarrogomez/phy-mer</a>                      Compute Cost: 3 iCredits per node/hr                      License Cost: n/a</p>
 <p><b>TruSeq® Amplicon</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Targeted Resequencing</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Small Variant Calling</li> <li>• Somatic Variant Calling</li> <li>• Annotation</li> <li>• Custom Manifest Files</li> <li>• Batch processing</li> </ul>	<p><b>Illumina, Inc.</b>                      Compute Cost: 3 iCredits per node/hr                      License Cost: n/a                      Example Compute Cost:                      TruSight Myeloid Panel                      (5000x mean coverage)                      2.35 M reads, 2 x 150 bp                      cost = 0.78 iCredits/sample</p>
 <p><b>TruSeq Long-Read Assembly</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• TruSeq Synthetic Long Reads</li> </ul>	<ul style="list-style-type: none"> <li>• Assembly of synthetic long reads</li> <li>• Phasing Analysis</li> </ul>	<p><b>Illumina, Inc.</b>                      Compute Cost: Free                      License Cost: n/a</p>
 <p><b>TruSeq Phasing Analysis</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Genetic Analysis</li> <li>• Haplotype Resolution</li> </ul>	<ul style="list-style-type: none"> <li>• Phasing Analysis</li> </ul>	<p><b>Illumina, Inc.</b>                      Compute Cost: Free                      License Cost: n/a</p>



## Biomedical and Basic Research – Genetic Analysis (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>TruSight Tumor 15</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Targeted Resequencing (TruSight Tumor 15 Panel)</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Variant Calling</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: TruSight Tumor 15 Panel (5000x mean coverage) 733 K reads, 2 x 150 bp cost = 0.35 iCredits/sample</p>
 <p><b>TruSight Tumor 170</b></p>	<ul style="list-style-type: none"> <li>Targeted Resequencing (TruSight Tumor 170 Panel)</li> </ul>	<ul style="list-style-type: none"> <li>Variant Calling</li> <li>SV/CNV Calling</li> <li>RNA Fusion Calling</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: Free License Cost: n/a</p>
 <p><b>Tumor Normal</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Whole Genome Sequencing</li> </ul>	<ul style="list-style-type: none"> <li>Variant Calling</li> <li>SV/CNV Calling</li> <li>Annotation</li> <li>Tumor Normal Analysis</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: Whole Genome (80x Tumor/40x Normal mean coverage) 1.8 B reads, 2 x 100 bp cost = 92.88 iCredits/pair of samples</p>
 <p><b>Whole Genome Sequencing</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Whole Genome Sequencing</li> </ul>	<ul style="list-style-type: none"> <li>Alignment</li> <li>Small Variant Calling</li> <li>SV/CNV Calling</li> <li>Annotation</li> <li>Batch Processing</li> </ul>	<p><b>Illumina, Inc.</b></p> <p>Compute Cost: 3iCredits per node/hr License Cost: n/a Whole Genome (30x mean coverage) 300 M reads, 2 x 150 bp cost = 9–12 iCredits/sample depending on sample quality</p>
 <p><b>CrossMap</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Data conversion</li> </ul>	<ul style="list-style-type: none"> <li>Converts genome coordinates between different assemblies</li> </ul>	<p><b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>




## Data Handling, Data Quality Control (QC), and Data Visualization

App name	Sequencing application(s)	Key functionality	Vendor
 <b>Elastic Genome Browser</b>	<ul style="list-style-type: none"> <li>• Resequencing (human)</li> </ul>	<ul style="list-style-type: none"> <li>• Genome Browser</li> <li>• Visualizations</li> </ul>	<b>Strand Life Sciences</b> <a href="http://www.strandls.com">www.strandls.com</a> Compute Cost: Free License Cost: n/a
 <b>FASTA Upload</b>	<ul style="list-style-type: none"> <li>• Data Import</li> </ul>	<ul style="list-style-type: none"> <li>• Import FASTA files</li> </ul>	<b>BioBam Bioinformatics S.L.</b> <a href="http://www.biobam.com/basespaceapps">www.biobam.com/basespaceapps</a> Compute Cost: Free License Cost: n/a
 <b>FASTQ Toolkit</b>	<ul style="list-style-type: none"> <li>• FASTQ Manipulation</li> </ul>	<ul style="list-style-type: none"> <li>• Sub-sampling</li> <li>• Adapter Trimming</li> <li>• Base Trimming</li> <li>• Quality Trimming</li> <li>• Read Filtering</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>FASTQC</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Data QC</li> </ul>	<ul style="list-style-type: none"> <li>• Base QC Profile</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>Genome Profiler</b>	<ul style="list-style-type: none"> <li>• Resequencing (human)</li> </ul>	<ul style="list-style-type: none"> <li>• Genome Browser</li> <li>• Visualizations</li> </ul>	<b>Biomatters Ltd.</b> <a href="http://apps.biomatters.com/melanoma-profiler/welcome">apps.biomatters.com/melanoma-profiler/welcome</a> Compute Cost: Free License Cost: n/a
 <b>Integrative Genomics Viewer</b>	<ul style="list-style-type: none"> <li>• Whole Genome Sequencing</li> <li>• Targeted Resequencing</li> <li>• ChIP-Seq</li> <li>• RNA-Seq</li> </ul>	<ul style="list-style-type: none"> <li>• Genome Browser</li> <li>• Visualizations</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: Free License Cost: n/a
 <b>SRA Import</b>	<ul style="list-style-type: none"> <li>• Data Import</li> <li>• General NGS</li> </ul>	<ul style="list-style-type: none"> <li>• Imports NGS data from NCBI Sequence Read Archive to BaseSpace Sequence Hub using SRA accession number</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>SRA Submission</b>	<ul style="list-style-type: none"> <li>• Data Export</li> <li>• General NGS</li> </ul>	<ul style="list-style-type: none"> <li>• Submission of data to NCBI SRA</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a





## Data Handling, Data Quality Control (QC), and Data Visualization (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <b>USC BigWig Generator</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Data Conversion</li> </ul>	<ul style="list-style-type: none"> <li>Convert data to BigWig file format</li> </ul>	<b>Ramsingh Lab Keck-Hematology</b> <a href="https://github.com/RamsinghLab">github.com/RamsinghLab</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>Variant Calling Assessment Tool</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Data QC</li> </ul>	<ul style="list-style-type: none"> <li>Comparison of variant call sets</li> <li>SNV and Indel statistics</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a






## Gene Expression and Regulation

App name	Sequencing application(s)	Key functionality	Vendor
 <b>ChIPSeq</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>DNA-Protein Interactions</li> <li>ChIPSeq</li> </ul>	<ul style="list-style-type: none"> <li>Uses MACS for peak identification and HOMER for motif discovery</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>Cufflinks Assembly &amp; DE</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Transcriptome Mining</li> <li>Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>Assembly of novel transcripts</li> <li>Differential Expression</li> </ul>	<b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: mRNA: 25 M reads, 2 x 75 bp cost = 11.25 iCredits/sample total RNA: 50 M reads, 2 x 75 bp cost = 23.49 iCredits/sample
 <b>DESeq2</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>Transcriptome Mining</li> <li>Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>Differential Expression</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: mRNA: 25 M reads, 2 x 75 bp cost = 37.64 iCredits/sample totalRNA: 50 M reads, 2 x 75 bp cost = 75.28 iCredits/sample

## Gene Expression and Regulation (continued)



App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>Genomatix Pathway System (GePS)</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Transcriptome</li> <li>• ChIP-Seq</li> <li>• Methyl-Seq</li> <li>• Oncology</li> </ul>	<ul style="list-style-type: none"> <li>• Pathway Analysis</li> <li>• Genomatix</li> </ul>	<p><b>Genomatix</b>  <a href="http://www.genomatix.de">www.genomatix.de</a>            Compute Cost: Free            License Cost: 7 Day            Subscription: 70 iCredits</p>
 <p><b>iPathwayGuide</b></p>	<ul style="list-style-type: none"> <li>• Transcriptome</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Pathway Analysis</li> </ul>	<p><b>Advaita Bio</b>  <a href="http://www.advaitabio.com">www.advaitabio.com</a>            Compute Cost: Free            License Cost:            - Single Report: 149 iCredits            - Annual Subscription: 1995 iCredits</p>
 <p><b>MethylKit</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Methylation Profiling</li> <li>• Whole Genome Sequencing</li> <li>• Targeted Sequencing</li> </ul>	<ul style="list-style-type: none"> <li>• Analyze WGBS and targeted bisulfite sequencing data</li> </ul>	<p><b>BaseSpace Labs</b>  <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>MethylSeq</b></p>	<ul style="list-style-type: none"> <li>• Whole Genome Sequencing</li> <li>• Targeted Resequencing</li> <li>• ChIP-Seq</li> <li>• RNA-Seq</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Methylation Calling</li> <li>• Custom manifests</li> <li>• Custom Genome</li> <li>• Batch Processing</li> </ul>	<p><b>Illumina, Inc.</b>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a            Example Compute Cost:            TruSeq Methyl Capture            55 M reads, 2 x 100 bp            cost = 19.53 iCredits/sample</p>
 <p><b>miRNAs Analysis</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Small RNA sequencing</li> <li>• miRNA Profiling</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Differential Expression</li> </ul>	<p><b>B&amp;Gu @ University of Torino</b>  <a href="http://mirnasanalysisbasespaceapp.blogspot.it">mirnasanalysisbasespaceapp.blogspot.it</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a            Example Compute Cost:            5 M reads, 1 x 50 bp            cost = 0.78 iCredits/sample</p>
 <p><b>NextBio Annotates RNA-Seq</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Transcriptome</li> <li>• Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>• Gene Annotation using BaseSpace Correlation Engine</li> </ul>	<p><b>BaseSpace Labs</b>  <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>NuGEN Ovation Fusion Detection</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Targeted RNA-Seq</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Fusion Detection</li> </ul>	<p><b>NuGEN Technologies, Inc.</b>  <a href="http://www.nugen.com">www.nugen.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>

## Gene Expression and Regulation (continued)







App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>RNA Express</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Transcriptome Mining</li> <li>• Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>• Assembly of novel transcripts with STAR</li> <li>• Differential Expression with DESeq</li> </ul>	<p><b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: mRNA: 25 M reads, 2 x 75 bp cost = 2.28 iCredits/sample totalRNA: 50 M reads, 2 x 75 bp cost = 4.55 iCredits/sample</p>
 <p><b>RNA-Seq Alignment</b> Demo Data Link Demo Data Link Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Transcriptome Mining</li> <li>• Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment (STAR or TopHat)</li> <li>• Gene Counts</li> <li>• Transcripts Counts</li> <li>• Annotation</li> <li>• Variant Calling</li> <li>• Fusion Detectin</li> <li>• Novel Transcript Assembly</li> <li>• Batch Processing</li> </ul>	<p><b>Illumina, Inc.</b> 1.8 License Cost: n/a Example Compute Cost: mRNA: 25 M reads, 2 x 75 bp cost = 6.02 iCredits/sample totalRNA: 50 M reads, 2 x 75 bp cost = 12.04 iCredits/sample</p>
 <p><b>Small RNA</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Small RNA sequencing</li> <li>• miRNA Profiling</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Classification of miRNAs, isomiRs, and piRNAs</li> <li>• Novel miRNA &amp; pre-miRNA discovery</li> <li>• Differential Expression</li> <li>• Batch processing</li> </ul>	<p><b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>
 <p><b>SureCell RNA Single-Cell</b> Demo Data Link Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Transcriptome Mining</li> <li>• Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>• Cell Counts</li> <li>• Alignment</li> <li>• Gene Counts</li> <li>• Cell Filtering</li> <li>• Transcripts Counts</li> <li>• Reporting</li> </ul>	<p><b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 1000 cells, 100 K reads/cell 100 M reads, 1 x 75 bp cost = 8.15 iCredits/sample</p>
 <p><b>TruSeq Targeted RNA</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Targeted Gene Expression</li> </ul>	<ul style="list-style-type: none"> <li>• Gene Expression</li> </ul>	<p><b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>









## Microbial Genomics and Metagenomics

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>16S Metagenomics</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>16S rRNA Microbial Communities Profiling</li> </ul>	<ul style="list-style-type: none"> <li>Taxonomic classification of microbial communities</li> <li>Batch processing</li> </ul>	<p><b>Illumina, Inc.</b> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 100 K reads, 2 x 300 bp cost = 1.28 iCredits/sample</p>
 <p><b>DeepChek®-HBV</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Viral Typing: <ul style="list-style-type: none"> <li>- HBV</li> <li>- HCV</li> <li>- HIV</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>Viral Typing</li> <li>Drug Resistance</li> </ul>	<p><b>ABL S.A.</b> <a href="https://ablsa.com/diagnostic-solutions/deepchek-assays">ablsa.com/diagnostic-solutions/deepchek-assays</a> Compute Cost: Free License Cost: 40 iCredits</p>
 <p><b>DeepChek®-HCV</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Viral Typing: <ul style="list-style-type: none"> <li>- HBV</li> <li>- HCV</li> <li>- HIV</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>Viral Typing</li> <li>Drug Resistance</li> </ul>	<p><b>ABL S.A.</b> <a href="https://ablsa.com/diagnostic-solutions/deepchek-assays">ablsa.com/diagnostic-solutions/deepchek-assays</a> Compute Cost: Free License Cost: 45 iCredits</p>
 <p><b>DeepChek®-HIV</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Viral Typing: <ul style="list-style-type: none"> <li>- HBV</li> <li>- HCV</li> <li>- HIV</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>Viral Typing</li> <li>Drug Resistance</li> </ul>	<p><b>ABL S.A.</b> <a href="https://ablsa.com/diagnostic-solutions/deepchek-assays">ablsa.com/diagnostic-solutions/deepchek-assays</a> Compute Cost: Free License Cost: 65 iCredits</p>
 <p><b>GENIUS Metagenomics: Know Now</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Metagenomics</li> </ul>	<ul style="list-style-type: none"> <li>Bacterial ID</li> </ul>	<p><b>CosmosID</b> <a href="http://www.cosmosid.com/basespace-landing">www.cosmosid.com/basespace-landing</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>
 <p><b>IgReC</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Targeted Sequencing</li> <li>RNA-Seq</li> <li>Immunology</li> </ul>	<ul style="list-style-type: none"> <li>Reconstrs full-length adaptive immune repertoires from Rep-Seq data</li> <li>Alignment</li> </ul>	<p><b>Center for Algorithmic Biotech.</b> <a href="https://yana-safonova.github.io/ig_repertoire_constructor">yana-safonova.github.io/ig_repertoire_constructor</a> <a href="mailto:igtools_support@googlegroups.com">igtools_support@googlegroups.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a</p>
 <p><b>Kraken Metagenomics</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>Shotgun Metagenomics</li> </ul>	<ul style="list-style-type: none"> <li>Host DNA Removal</li> <li>Taxonomic Classification</li> </ul>	<p><b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 4 M reads, 2 x 300 bp cost = 1.16 iCredits/sample 40 M reads, 2 x 300 bp cost = 11.16 iCredits/sample</p>







## Microbial Genomics and Metagenomics (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>MetaPhlan</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Metagenomics</li> </ul>	<ul style="list-style-type: none"> <li>• Phylogenetic Analysis</li> </ul>	<p><b>The Huttenhower Lab</b>  <a href="http://huttenhower.sph.harvard.edu/metaphlan">huttenhower.sph.harvard.edu/metaphlan</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>MiXCR Immune Repertoire Analyzer</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Targeted Sequencing</li> <li>• RNA-Seq</li> <li>• Immunology</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Visualization</li> </ul>	<p><b>MLaboratory</b>  <a href="http://milaboratory.com">milaboratory.com</a>  <a href="mailto:support@milaboratory.com">support@milaboratory.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>PEDANT™ SequenceAnalyzer</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Microbial</li> </ul>	<ul style="list-style-type: none"> <li>• Bacterial Sequence Analysis</li> </ul>	<p><b>Biomax Informatics AG</b>  <a href="http://www.biomax.com/product/pedant-pro-sequence-analysis-suite">http://www.biomax.com/product/pedant-pro-sequence-analysis-suite</a>            Compute Cost: Free            License Cost: - 15 KB - 2 iCredits</p>
 <p><b>Prokka Genome Annotation</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Microbial</li> </ul>	<ul style="list-style-type: none"> <li>• Prokaryotic Genome Annotation</li> </ul>	<p><b>BaseSpace Labs</b>  <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>QIIME Preprocessing</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Microbiome Analysis</li> </ul>	<ul style="list-style-type: none"> <li>• Taxonomic classification of microbial communities</li> <li>• Phylogenetic reconstruction</li> <li>• Batch processing</li> </ul>	<p><b>QIIME Development Team</b>  <a href="http://qiime.org">qiime.org</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a            Example Compute Cost:            100 K reads, 2 x 300 bp            cost = 0.04 iCredits/sample</p>
 <p><b>QIIME Visualizations</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Microbiome Analysis</li> </ul>	<ul style="list-style-type: none"> <li>• Visualization</li> </ul>	<p><b>QIIME Development Team</b>  <a href="http://qiime.org">qiime.org</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a            Example Compute Cost:            100 K reads, 2 x 300 bp            cost = 0.71 iCredits/sample</p>



## Microbial Genomics and Metagenomics (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <b>Rescaf</b>	<ul style="list-style-type: none"> <li>• Microbial</li> </ul>	<ul style="list-style-type: none"> <li>• Improves quality of scaffold sequences</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>SEAR: Antibiotic Resistance</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Metagenomics</li> <li>• Microbiome</li> </ul>	<ul style="list-style-type: none"> <li>• Construct Antimicrobial Resistance Genes</li> </ul>	<b>University of Cambridge</b> <a href="https://github.com/will-rowe/SEAR">github.com/will-rowe/SEAR</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>SPAdes Genome Assembler</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Microbial</li> </ul>	<ul style="list-style-type: none"> <li>• <i>De novo</i> Assembly</li> </ul>	<b>Algorithmic Biology Lab</b> <a href="http://cab.spbu.ru/spades">cab.spbu.ru/spades</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 5 MB genome with 100x coverage 833 K reads, 2 x 300 bp cost = 7.30 iCredits/sample
 <b>SRST2</b> <a href="#">Demo Data Link</a> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Microbial ID</li> </ul>	<ul style="list-style-type: none"> <li>• MLST Typing</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>String Graph Assembler</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Mid-size Genome Assembler</li> </ul>	<ul style="list-style-type: none"> <li>• Assembly</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a
 <b>Velvet de novo Assembly</b> <a href="#">Demo Data Link</a>	<ul style="list-style-type: none"> <li>• Microbial</li> </ul>	<ul style="list-style-type: none"> <li>• <i>de novo</i> Assembly</li> </ul>	<b>BaseSpace Labs</b> <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a> Compute Cost: 3 iCredits per node/hr License Cost: n/a Example Compute Cost: 5 MB genome with 100x coverage 833 K reads, 2 x 300 bp cost = 1.53 iCredits/sample


## Proteomics

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>OpenSWATH</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Mass Spec</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>Aebersold Group @ ETH Zurich</b>  <a href="http://www.openswath.org">www.openswath.org</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>OpenSWATH Assay Generator</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Mass Spec</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>Aebersold Group @ ETH Zurich</b>  <a href="http://www.openswath.org">www.openswath.org</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>Protein Expression Assembler</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Mass Spec</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>SCIEX</b>  <a href="http://sciex.com">sciex.com</a>  <a href="mailto:swathcloudsupport@sciex.com">swathcloudsupport@sciex.com</a>            Compute Cost: Free            License Cost: n/a</p>
 <p><b>Protein Expression Extractor</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Mass Spec</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>SCIEX</b>  <a href="http://sciex.com">sciex.com</a>  <a href="mailto:swathcloudsupport@sciex.com">swathcloudsupport@sciex.com</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>Protein Expression Workflow</b> Demo Data Link</p>	<ul style="list-style-type: none"> <li>• Mass Spec</li> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>SCIEX</b>  <a href="http://sciex.com">sciex.com</a>  <a href="mailto:swathcloudsupport@sciex.com">swathcloudsupport@sciex.com</a>            Compute Cost: Free            License Cost: n/a</p>
 <p><b>RNA-Seq Translator</b></p>	<ul style="list-style-type: none"> <li>• Proteomics</li> <li>• RNA-Seq</li> </ul>	<ul style="list-style-type: none"> <li>• Uses <i>de novo</i> transcriptome assembly to generate protein sequences</li> </ul>	<p><b>Yale University</b>  <a href="mailto:rob.kitchen@yale.edu">rob.kitchen@yale.edu</a>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>

## Proteomics (continued)

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>SWATH to MRM Builder</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Small RNA sequencing</li> <li>• miRNA Profiling</li> </ul>	<ul style="list-style-type: none"> <li>• Alignment</li> <li>• Classification of miRNAs, isomiRs, and piRNAs</li> <li>• Novel miRNA &amp; pre-miRNA discovery</li> <li>• Differential Expression</li> <li>• Batch processing</li> </ul>	<p><b>Illumina, Inc.</b>            Compute Cost: 3 iCredits per node/hr            License Cost: n/a</p>
 <p><b>SWATHAtlas Ion Library Generator</b></p>	<ul style="list-style-type: none"> <li>• Proteomics</li> </ul>	<ul style="list-style-type: none"> <li>• Protein Analysis</li> </ul>	<p><b>Institute for Systems Biology</b>  <a href="http://www.swathatlas.org">www.swathatlas.org</a>            Compute Cost: Free            License Cost: n/a</p>

## Quality

App name	Sequencing application(s)	Key functionality	Vendor
 <p><b>PicardSpace</b>  <a href="#">Demo Data Link</a></p>	<ul style="list-style-type: none"> <li>• Data QC</li> </ul>	<ul style="list-style-type: none"> <li>• Calculates alignment metrics</li> </ul>	<p><b>BaseSpace Labs</b>  <a href="mailto:basespacelabs@illumina.com">basespacelabs@illumina.com</a>            Price: Free for .bam &lt;1            Compute Cost: Free            Compute Cost: Free MB            1 iCredit for .bam &gt; 1            Compute Cost: Free            Compute Cost: Free MB            License Cost: n/a</p>