Library Prep and NGS Pricing Descriptions

Any given sequencing project is a combination of core services with UT-approved rates sized according to the details of the project. Prices shown below are estimates based on typical pricing. According to UT System and UT Austin policy, the GSAF bills for actual expenses which vary with the size and scope of each project.

To create and save a price estimate for future use, create a job request here. If you are seeking price estimates only, please do not submit the request until you have samples ready.

Sequencing prices per lane (HiSeq) or per flow cell (NextSeq and MiSeq)

<table>
<thead>
<tr>
<th>Platform</th>
<th>Run Type</th>
<th>Internal / UT</th>
<th>External Academic</th>
<th>External Commercial</th>
</tr>
</thead>
<tbody>
<tr>
<td>HiSeq 2500</td>
<td>SR 50</td>
<td>$1052</td>
<td>$1331</td>
<td>$1357</td>
</tr>
<tr>
<td>HiSeq 2500</td>
<td>SR 100</td>
<td>$1428</td>
<td>$1806</td>
<td>$1842</td>
</tr>
<tr>
<td>NextSeq 500</td>
<td>SR 75 H.O. (1,3)</td>
<td>$2,302</td>
<td>$2,906</td>
<td>$3,060</td>
</tr>
<tr>
<td>NextSeq 500</td>
<td>PE 75 H.O. (1,3)</td>
<td>$3,826</td>
<td>$4,834</td>
<td>$4,988</td>
</tr>
<tr>
<td>NextSeq 500</td>
<td>PE 150 H.O.</td>
<td>$5,735</td>
<td>$7,250</td>
<td>$7,404</td>
</tr>
<tr>
<td>MiSeq</td>
<td>V2 - 300 cycles</td>
<td>$1,627</td>
<td>$2,054</td>
<td>$2,157</td>
</tr>
<tr>
<td>MiSeq</td>
<td>V2 - 500 cycles (1)</td>
<td>$1,771</td>
<td>$2,236</td>
<td>$2,339</td>
</tr>
<tr>
<td>MiSeq</td>
<td>V3 - 150 cycles</td>
<td>$1,463</td>
<td>$1,847</td>
<td>$1,950</td>
</tr>
<tr>
<td>MiSeq</td>
<td>V3 - 600 cycles (1)</td>
<td>$2,183</td>
<td>$2,758</td>
<td>$2,860</td>
</tr>
</tbody>
</table>

Notes:
1) These run types (bold) are available as shared runs on the GSAF “per-read” pricing schedule.
   - Please see bottom of the page for full explanation of “per-read pricing” and guidelines on lane outputs
2) H.O. is Illumina’s High Output run type. Mid Output is not available under standard pricing (inquire if interested).

Library Preparation Pricing:

- DNA and RNA Library Preps
- 10X Single Cell 3’ Gene Expression, scRNA-Seq
- Metagenomics (ribosomal gene sequencing)
- Genotyping-by-sequencing
- Quality Control by BioAnalyzer
- Tag-Seq Services

NEW: 10X Single Cell 3’ Gene Expression, scRNA-Seq

- Currently offering 10X single cell 3’ Gene Expression v3 library preparation
- Sequencing will be offered on the NextSeq
  - Sequencing charges are independent of library prep charges but can be estimated at around $1154 per 100 Million reads on a NextSeq
  - Currently we will only accept 4 samples at a time for a scheduled 10X run, if you would like to run more please contact Jessica Podnar at gsaf@utgsaf.org for a consultation

<table>
<thead>
<tr>
<th>10X Library Preparation</th>
<th>Cost per sample Internal</th>
<th>Cost per sample External</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Sample, Library Prep Only</td>
<td>$2156.44</td>
<td>$2727.90</td>
</tr>
<tr>
<td>Each additional sample, up to 4 total, Library Prep Only</td>
<td>$1916.44</td>
<td>$2424.30</td>
</tr>
</tbody>
</table>

Tag-Seq Services

- TagSeq is a new service offered by the GSAF, this is a 3’ RNA based library prep utilizing the intrinsic properties of a reverse transcriptase
  - Evaluation of TagSeq, a reliable lowcost alternative for RNaseq
  - Profiling gene expression responses of coral larvae (*Acropora millepora*) to elevated temperature and settlement inducers using a novel RNASeq procedure
- RNA submitted must be high quality and should be normalized, preferred concentration for the RNA is between 10-100 ng/ul providing at least 25 microliters
  - Samples must be submitted in 96 well plates
• If Trizol/Tri-Reagent was used for extraction samples should go through a column clean up

<table>
<thead>
<tr>
<th>Tag-Seq Cost (Library Prep and Sequencing, HiSeq 2500 SR50)</th>
<th>Cost per sample Internal</th>
<th>Cost per sample External</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard Coverage (3-5 M reads)</td>
<td>$61.46</td>
<td>$77.75</td>
</tr>
<tr>
<td>High Coverage (7-10 M reads)</td>
<td>$87.76</td>
<td>$111.02</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Tag-Seq Cost (Library Prep and Sequencing, HiSeq 2500 SR100)</th>
<th>Cost per sample Internal</th>
<th>Cost per sample External</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard Coverage (3-5 M reads)</td>
<td>$70.81</td>
<td>$89.57</td>
</tr>
<tr>
<td>High Coverage (7-10 M reads)</td>
<td>$106.46</td>
<td>$134.67</td>
</tr>
</tbody>
</table>

**IF min sample number is not met $270 added for internal and $340 for external**

**DNA and RNA library preps:**

**DNA** low cost high throughput - wide size range, ~400 bp insert size. Minimum batch size of 8 samples per project. For fewer than 8 samples, your job will be queued until a minimum batch size of 8 is reached. Price includes indexing and final QC by BioAnalyzer and qPCR. See this web page for sample input guidelines.

**RNA** low cost high throughput - size range typically ~200 nt; “dUTP” directional protocol. Always processed in batches of at least 8; if you submit fewer than 8 samples, your job will be queued until a minimum batch size of 8 is reached. Price includes indexing and QC by BioAnalyzer on final lib only and qPCR. Please request a BA if you need to check the quality of the RNA before we proceed to library prep. See this web page for sample input guidelines.

Prices listed are per sample. For projects with 8 or less samples, a flat fee per project is charged as shown.

<table>
<thead>
<tr>
<th>Type of Library Preparation Procedure</th>
<th>Samples</th>
<th>Internal / UT Network</th>
<th>External Academic</th>
<th>External Commercial</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA High-Throughput with index</td>
<td>8 or more</td>
<td>$101</td>
<td>$127</td>
<td>$137</td>
</tr>
<tr>
<td>RNA directional WITH poly-A enrichment and index</td>
<td>8 or more</td>
<td>$206</td>
<td>$280</td>
<td>$283</td>
</tr>
<tr>
<td>RNA directional WITH ribosomal removal and index</td>
<td>8 or more</td>
<td>$301</td>
<td>$381</td>
<td>$416</td>
</tr>
<tr>
<td>RNA directional with index - NO removal of ribosomal RNA</td>
<td>8 or more</td>
<td>$141</td>
<td>$179</td>
<td>$206</td>
</tr>
<tr>
<td>Added fee/project for services with fewer than 8 samples</td>
<td>7 or less</td>
<td>$331</td>
<td>$462</td>
<td>$551</td>
</tr>
</tbody>
</table>

**Metagenomics assays on the Illumina MiSeq:**

**Metagenomics assay:** This service starts with normalized (i.e. equal concentration and volume) gDNA and includes amplification using one of the GSAF provided primer sets chosen by the customer as shown on this web page. The service is calibrated to deliver at least 10,000 2x250 bp paired-end sequences from the Illumina MiSeq platform for at least 90% of the samples submitted, assuming there is reasonable amount of DNA to amplify. To minimize jackpot effects, PCR is performed in triplicate for each sample and re-pooled.

The library preparation is a two-step process, a gene-specific PCR then a second PCR to add the dual indexes. The PCR targets the bacterial 16S V4/V5 region, the 16S V4 region, or fungal ITS region, as specified by the client. Gel-based QC is performed on a sampling of 10% of the samples post amplification. Genomic DNA is expected as input; the GSAF does not provide DNA extraction services at this time. See this web page for sample input guidelines and note that DNA concentrations should be normalized before submission. The GSAF can normalize your sample concentrations for an additional charge.

Prices vary slightly depending on the actual number of samples processed, so the prices are provided for reference and planning purposes. Submit a job request to get accurate, approved pricing.

<table>
<thead>
<tr>
<th>Number of Samples</th>
<th>Internal / UT Network</th>
<th>External Academic</th>
<th>External Commercial</th>
</tr>
</thead>
<tbody>
<tr>
<td>176 or more</td>
<td>$28.77</td>
<td>$36.25</td>
<td>$41.02</td>
</tr>
<tr>
<td>50-175 samples</td>
<td>Add $369 / project</td>
<td>Add $464 / project</td>
<td>Add $554 / project</td>
</tr>
<tr>
<td>&lt; 50 samples</td>
<td>Inquire</td>
<td>Inquire</td>
<td>Inquire</td>
</tr>
</tbody>
</table>

**IMPORTANT CAUTION:** The V4/V5 region assay we use is KNOWN to amplify Eukaryotic 18S rRNA genes as well as bacterial 16S V4/V5. If your sample may have Eukaryotic DNA (e.g. host), we have an alternative V4 region (only) assay but you MUST NOTE THIS in the Brief Description of your sequencing request.

**Note:** If you are submitting a mixed population (e.g. bacterial & fungal, or bacterial & eukaryote host, etc.) you should assay your samples before submission to ensure you have the proper concentration of the target DNA, not simply total DNA. Samples submitted with insufficient target DNA may result in excessive primer-dimer or off-target products which produce no useful data. These will still be charged according to the pricing table.
**GBS services**

Genotyping by Sequencing (GBS) services- Please email the GSAF to inquire about this service

**BioAnalyzer Quality Control**

Agilent BioAnalyzer traces on final libraries are included in sample preparation prices. All other Agilent BioAnalyzer assays are a flat $15.90 per sample for internal customers and $19.57 for external academic customers.

**Explanation of yields and the GSAF "per-read" pricing:**

The UT GSAF is known for offering our "per-read" pricing option, so when applicable, clients are not required to purchase a full lane or a full flow cell of sequence data. This is a cost-effective way to do many NGS experiments, such as metagenomics, genotyping-by-sequencing, RNA-seq, and whole genome bacterial sequencing, among others.

However, "per-read" pricing is not available on every run type, and there are some constraints: **PLEASE NOTE CHANGES TO HISEQ**

- Minimum read counts per-sample are as follows:
  - Illumina MiSeq V2 or V3: 1 million reads
  - Illumina NextSeq 500: the larger of 40 million reads per project or 20 million reads per sample.
  - Illumina HiSeq 4000: 20 million reads per single sample; 10 million reads/sample if submitting 2 or more.

- All indexes (barcodes) must be pre-screened for potential conflicts. (See the **Important Note** below.)
- Samples with dual-indexes may not be run in partial lanes on any platform - they must be run in their own whole lane.
- We commonly achieve 210 to 230 million reads per lane on GSAF-prepared libraries (generally lower on SE runs) or more from HiSeq 2500 high output lanes and expect to achieve >240 million for HiSeq 4000 lanes.
- **We do not guarantee a minimum yield of sequences from a lane with customer-prepared libraries.** If you request a full lane of sequence, you will be charged for a full lane of sequence unless something has gone wrong with the instrument or entire flow cell (i.e. the problem is instrument related and not library related).

To calculate "per-read" pricing, we assume:

- a yield of 240 million reads per lane from each HiSeq 4000 lane
- a yield of 200 million reads per lane from each HiSeq 2500 lane
- a yield of 13 million reads per lane from MiSeq V2 and 22 million reads per lane from MiSeq V3
- a yield of 330 million reads per run from NextSeq 500, all run types.

When you request "per-read" pricing, you specify a minimum and a target read count, there is no guarantee but we always try our best to at least hit the minimum, if we do not hit the min you are only charged for the number of reads received. Your maximum charge (and thus the estimate you will receive when you submit your project) will be based on the target read count.

**IMPORTANT NOTE:**

The choice of indices matters. If you are constructing your own finished libraries, we recommend contacting the GSAF before assigning indices to your samples. If, for example, you use TruSeq Index 1 to 6 repeatedly, the wait time may be significantly longer since they will conflict internally and with other projects. Please consider using other indices or have the GSAF prepare your libraries.

Libraries with standard TruSeq or Nextera indices may be multiplexed in a lane. Libraries created by the GSAF can be multiplexed up to 60 samples per lane for DNA or RNA, 672 samples per lane for 16S-based metagenomics or ddRAD.

Libraries with in-line barcodes must be provided pooled by the customer and run in their own lane.

**Payment and turn-around time**

All finished libraries submitted for sequencing will bear a nominal charge for quality assessment and sample handling. This charge is per tube submitted. Lane prices shown above include this charge for 1 sample per lane.

The "Internal UT Rate" is charged when payment comes from an account internal to UT Austin. All other service is charged at the External Rate.

Typical turn-around times are 4-6 weeks for HiSeq 4000 runs, and 2-4 weeks for NextSeq 500 and MiSeq runs.