**Genomics and Bioinformatics Service**
101 Gateway, Suite A
College Station, TX 77845
www.txgen.tamu.edu

*If you have any questions related to starting new projects, study design, pricing, & collaborations. please contact Dr. Charlie Johnson (charlie@ag.tamu.edu)*

*If you have any questions or concerns about your samples, or the submission process, please contact Dr. Richard Metz rmetz@tamu.edu.*

**DO NOT BRING SAMPLES UNLESS YOU HAVE A SIGNED QUOTE/SCOPE-OF-WORK**

**Sample Submission Guidelines:**
Good quality starting material is paramount to completing a successful sequencing project. Although we perform initial quality control (QC) analyses, we highly suggest that you check your samples for quality before submitting them. If a sample does not pass our QC tests, it will delay your project and may require you submit a suitable replacement. Initial QC costs are included in our library prep costs, but you will be charged for additional QC assessments of replacement samples.

Pricing and additional contact information can be found on our website (www.txgen.tamu.edu).

**Labeling your samples/Plates**: Please keep sample names short and easy to read and make sure tubes and/or plates are clearly and unambiguously labeled. You will be asked to send an electronic version of the sample names and any QC measures you may have performed (concentration and OD ratios, gel images, etc.). Once a sample is submitted for processing any remaining material will not be returned unless arrangements have been made. Investigators should retain a portion of each sample for follow-up validation studies.

**Format**: We prefer samples to be delivered in **96-well plates** with the **same volume** (preferably 50µl) in each well. Failure to do so will delay your project or incur more cost as it is time consuming for us to measure and adjust volumes.

**RNA (including RNA-Seq and small RNA-Seq…):** Total RNA should be DNase-treated and dissolved in nuclease-free water. The $OD_{260}/OD_{280}$ and $OD_{260}/OD_{230}$ ratios should be close to 2.0. For most cases, we require at least 1.5-2.0 µg of total RNA in a volume of 50µl (30-40 ng/µl final concentration). Please adjust your sample volumes to 50µl before submitting.

We suggest using column-based kits such as those made by Qiagen and Ambion. If you are using a phenol-based purification system (such as Trizol), further purify the RNA using a column based cleanup procedure to ensure contaminating RNases and phenols are removed. ***Note that small RNA isolation requires kits specifically designed (e.g. mirVana) to retain the low molecular weight RNA species***

**DNA (DNA-Seq, Re-sequencing, WSG, de novo genomes, BACs and Amplicons…):** Genomic DNA should be treated with RNase and dissolved in EB (10nM Tris-HCl, pH 7.5-8.0), TE (10mM Tris-HCl, 0.1mM EDTA, pH 8.0) or nuclease-free water. The $OD_{260}/OD_{280}$ and $OD_{260}/OD_{230}$ ratios should be close to 1.8 or higher. We require at least 2-5.0µg of high molecular weight, intact DNA in a volume of 50-100µl. Please adjust your sample volumes to this range before submitting.

> **gDNA for de novo Genome Sequencing (Mate-Pair libraries):** Assembling novel whole genomes is aided by sequencing multiple sized inserts using the mate-pair library approach. This requires much larger amounts of high molecular weight DNA than standard techniques. In addition to the requirements above, gDNA must be largely intact (>20kb). We require at least 20-30µg in 500-750µl TE.
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> **Amplicons**: Talk to us before planning an amplicon sequencing project.

There are many methods and commercial kits for isolating DNA and each has its advantages and disadvantages depending on the species and tissue source. Ask us if you are unsure which method will give the best DNA.

**Libraries:** If you are submitting pre-made libraries, we require at least 20µl of 10ng/µl or higher. Final libraries should be in EB (10mM Tris-HCl, pH 8.0) or RB (10mM Tris-HCl, 0.1% Tween, pH 8.0). We require that you contact us first when using a home-brew prep to discuss optimal strategies and possible complications. ***We are not responsible for failed runs due to library prep if we did not make the libraries, you will be charged regardless of outcome.***