About Us

The GSAF is a full service sequencing core that provides both Sanger and Next Generation Sequencing services, in addition to a library prep and quality check services, open access to equipment and training. The GSAF works directly with the bioinformatics core who can provide assist in any of your analysis needs to data storage solutions.

Weare housed in approximately 2,000 square feet of controlled-access laboratory space and are an experienced NGS facility. Launched in 2008, the GSAF currently processes over 10,000 NGS samples per year.

Instruments in our lab:

- Illumina NovaSeq 6000 (one)
- Illumina MiSeq sequencers (three)
- Illumina NextSeq 500 sequencer (two)
- Covaris S220 and E220 Adaptive Focused Acoustic shearing devices
- Agilent BioAnalyzer 2100
- Agilent TapeStation
- Invitrogen Qubit fluorimeter and Thermoscientific Fluoroskan
- Tecan Evo and Hamilton Nimbus
- 10x Chromium system
- Ion Torrent S5

Lab protocols we are experienced with:

- Creation of fragment DNA sequencing libraries for all Illumina next-gen sequencers
- Creation of mate-pair sequencing libraries between 1.5kb and 4kb for Illumina next-gen sequencers
- Creation of RNA-seq libraries from total RNA, small RNA, and immuno-precipitated RNA for Illumina next-gen sequencers
- Creation of amplicon libraries (particularly 16s and ITS regions) for the Illumina next-gen sequencers
- Human exome and custom capture with the Agilent SureSelect, Illumina TruSeq, and Nimblegen SeqCap EZ kits
- Sample and library QC using the Agilent BioAnalyzer, Picogreen and Ribogreen fluorimetry, qPCR, and spectrophotometry

Computational and software resources:

- The bioinformatcis group maintains a wide range of tools for NGS analysis and assemblyand can assist with all of your analysis needs, please visit them here.
- Need your own server or access to one of ours, here is an explanation of the Biomedical Research Computing services with instructions for getting an account.
- In addition, the GSAF uses and works with the TACC bioinformatics group, supporting tools and applications suitable to the TACC environment.
- Want to get started? Contact us
- New to Unix? Check out some Unix and Perl resources for beginners.

Our Mission and Vision

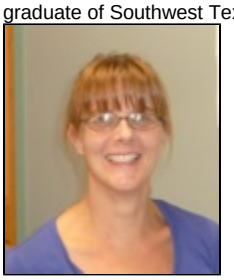
Vision: The GSAFs vision is to be a world-class genomic analysis center in terms of data quality, breadth of available methods, and productivity.

Mission: The mission of the Genome Sequencing and Analysis Facility is to provide the best quality analytical results with the best value to life science researchers.

Our People

Jessica Wheeler Podnar
Associate Director
(512) 232-5924
MBB 3.210
gsaf@utgsaf.org

Jessica joined the GSAF in June 2010 as the facility lab manager, when she came on board the core was focused on 454 and SOLiD sequencing but soon transitioned to focus Illumina platforms. She has a wealth of knowledge covering library preparation, sequencing and project planning. She is an active member in the DNA Sequencing Research Group as part of Association of Biomolecular Resource Facilities. Prior to joining the university Jessica worked at Sierra Sciences, a biotech company located in Reno NV, 4 years as a researcher and laboratory manager in the cell culture division. She is a graduate of Southwest Texas State University.



Heather Deiderick
Post-doctoral researcher
(512) 475-9725
Heather is one of several PhD scientists on staff and has years of experience with all manner of molecular biology techniques. She currently specializes in working with researchers to develop new approaches and protocols for the GSAF. If you want to try something new with NextGen sequencing, contact us. We are eager to try new methods to get you the data you need!

Gabriella Huerta
Research Engineering Scientist
Associate IV
(512) 475-9725
Gabriella manages the Illumina sequencing operations and contributes to all aspects of the genomic sequencing enterprise. Every library barcode, concentration and quality control metric is carefully scrutinized by Gabriella, as she performs the complex task of setting up the sequencing runs to assure the highest quality results. With prior experience running NGS operations at Perlegen Sciences and Pfizer, Gabriella has the depth of experience to get the jobs done right.

Matt Barnette
Research Engineering Scientist
Associate III
(512) 475-9725
Matt is the genomic library preparation master. Whether RNA or DNA, short fragments or long, simple steps or complex, there is no procedure Matt has not tamed. When not keeping rhythm on the drums for a local band, Matt is busy writing scripts to help our internal processes run efficiently and accurately.

Holly Stevenson
Research Engineering Scientist
Associate III
Holly is a PhD scientist with prior experience applying and tailoring genetic technologies to cancer research and clinical studies at the National Cancer Institute. She joined GSAF in 2017 and has over 15 years of experience in molecular biology methods. She currently aids customers by preparing a variety of DNA/RNA libraries, assists in operating our Illumina sequencers, and helps in testing and implementing new NGS services.

Juili Kelvekar
Research Engineering Scientist
Associate II
Juili helps in managing Sanger sequencing as well as NextGen sequencing core and contributes to DNA/RNA library preparation, QA analysis, routine Sanger sequencing and maintaining Bio analyzers. She has a versatile background in nanotechnology and Biomedical engineering and worked on many complex research projects. Her prior experience involved synthesizing contrast agents for disease detection and for therapeutic drug delivery. She is very detailed oriented and like to work on different challenging projects.
Tina pic

Tina Arredondo
Research Engineering Scientist
Associate II
Insert Bio for Tina