

**Research Development Fund – SPRING 2019 Application Template****Application Title: Addition of Genomic Optical Mapping Capabilities at Texas A&M University****Lead contact for RDF Application:****Name – Andrew Hillhouse****Department – Veterinary Pathobiology****Email address – hillhouse@tamu.edu****Phone number – (979) 458-5678****Key Participating Units: College of Agriculture and Life Sciences, College of Medicine, School of Public Health, College of Science, College of Veterinary Medicine and Biomedical Sciences****Anticipated Request Amount (\$): \$345,200****Executive summary of this application to utilize Research Development Funds:**

This proposal seeks to enhance the tools available for Texas A&M genomics research by adding optical DNA mapping capabilities through the Bionano Genomics Saphyr system to the existing tools available through the Texas A&M Institute for Genome Sciences and Society (TIGSS) Shared Molecular Biology Core. The TIGSS Genomics Core has provided access to equipment, services, and training for molecular biology and genomics research to the scientific community of the Texas A&M system for over 4 years. The Bionano Genomics Saphyr is a bench-top instrument used to manipulate and image extremely long molecules of specifically labeled genomic DNA. These labeled DNA molecules are used to generate genome-spanning *de novo* physical maps in a robust and extremely high-throughput manner and is an extremely powerful tool for identifying a variety of genomic structural variations including insertions, deletions, genomic inversions and copy number variations.

Sequencing of DNA and RNA molecules has become an invaluable and necessary component of much of modern biological research. Genome sequencing is a powerful tool for understanding the roles that genes and genetics play in ecology, environmental biology, development, and disease. The Texas A&M campus is fortunate to have multiple tools available for different aspects of genome research and each of these tools is specialized in their focus and applications including Illumina short read sequencing, Pacific Biosystems Long read sequencings and 10x Genomics Linked Read sequencing. An increasingly accepted approach for genome assembly and analysis requires an integration of data from multiple technologies in an effort to maximize the amount of information obtained from an organism's genome while minimizing the amount of errors in the final genome. This approach has been used successfully for projects like those proposed in the Vertebrate genome project (<https://vertebrategenomesproject.org>) and helps to produce the highest quality genome assemblies available. With a maximum output of over 500 equivalently sized genomes per year, the Bionano Saphyr will help to expand the capabilities of genomic research is at Texas A&M university.