**Project Summary**

This application addresses broad Challenge Area (06) Enabling Technologies and specific Challenge Topic 06-HG-101, “New computational and statistical methods for the analysis of large data sets from next-generation sequencing technologies”. NextGen sequencing has enormous potential to push forward genomics research by allowing researchers to ask new questions and is being rapidly adopted by genomics research groups and clinical diagnostics labs. Increased adoption must be accompanied by advances in high-throughput analysis, strategies for mitigating systemic bias, and new sequence assembly and downstream analysis pipelines. We propose to develop optimized bioinformatics workflows for NextGen sequence assembly, gene expression and genomic variation analysis, and implement them in an end-to-end NextGen workflow and genomic visualization tool. The proposed system, named Aqwa (Automated Query and Workflow Agent), will be an easy-to-use tool for routinely running carry out tasks that would be difficult or impossible without significant bioinformatics resources. No similar system exists and Aqwa will be freely distributed as an open source software package. Aqwa is designed for researchers in large sequencing centers, genomics research groups, and clinical diagnostics laboratories. In addition to saving the time of researchers, the system will ultimately improve the quality of analyses that may lead to significant advances in the understanding, treatment and cure of human diseases.