**Project Narrative**

Rapidly falling NextGen sequencing costs mean increasing demand for NextGen bioinformatics infrastructure and tools. Researchers using NextGen data to ask new questions need high-throughput methods to handle the huge data volumes and new analysis pipelines for assembly and other analyses. We propose to develop optimized bioinformatics workflows for NextGen sequence assembly, gene expression and genomic variation analysis and integrate them into a software system, named Aqwa (Automated Query and Workflow Agent), which will serve as an end-to-end NextGen workflow and genomic visualization tool.