**Project Narrative**

Rapidly falling NextGen sequencing costs means increasing demand for NextGen bioinformatics infrastructure and tools. Researchers using NextGen data must use computer clusters to handle the huge data volumes and require new analysis pipelines and workflow tools to manage complex pipelines. We propose to develop optimized bioinformatics workflows for NextGen sequence assembly, gene expression and genomic variation analysis workflows, and implement them in an end-to-end NextGen workflow and genomic visualization tool.