

Franklin University

FUSE (Franklin University Scholarly Exchange)

Learning Showcase 2014

International Institute for Innovative Instruction

11-14-2014

Genomic Sequencing Data Analysis Workflow for Bioinformatics Core Facilities

Selen A. Yilmaz
Ohio State University

Jie Zhang
Ohio State University

Gulcin Ozer
Ohio State University

Follow this and additional works at: <https://fuse.franklin.edu/ss2014>



Part of the [Genetics and Genomics Commons](#)

Recommended Citation

Yilmaz, Selen A.; Zhang, Jie; and Ozer, Gulcin, "Genomic Sequencing Data Analysis Workflow for Bioinformatics Core Facilities" (2014). *Learning Showcase 2014*. 46.
<https://fuse.franklin.edu/ss2014/46>

This Presentation is brought to you for free and open access by the International Institute for Innovative Instruction at FUSE (Franklin University Scholarly Exchange). It has been accepted for inclusion in Learning Showcase 2014 by an authorized administrator of FUSE (Franklin University Scholarly Exchange). For more information, please contact karen.caputo@franklin.edu.

From Sequencing to Discovery

Genomic Sequencing Data Analysis Workflow for Bioinformatics Core Facilities

The James



Selen A. Yilmaz, MS.^{1,2}, Jie Zhang, PhD.^{1,2}, Gulcin Ozer, PhD.^{1,2}

¹Department of Biomedical Informatics, The Ohio State University College of Medicine, Columbus, OH

²Biomedical Informatics Shared Resource, Comprehensive Cancer Center, The Ohio State University Wexner Medical Center, Columbus, OH

Introduction

The Biomedical Informatics Shared Resource (BISR) at the Ohio State University Wexner Medical Center focuses on

What?

High-throughput genomic sequencing data analyses

Why?

To answer an increasingly diverse range of biological questions

How?

Using state-of-the-art informatics tools and high-quality informatics analysis

High-throughput Sequencers

Gene Expression: RNA-seq
Expression quantification • Differential expression • Alternative splicing • Non-coding RNA • Variant detection • Allelic expression imbalance

Epigenome: ChIP-seq, Methyl-seq
Alignment • Peak detection • Comparative analysis • Visualization

Resequencing: Exome-seq, Whole Genome Sequencing
Alignment • SNP calling • Small and large INDELS • Copy number variation • Gene fusion/translocation

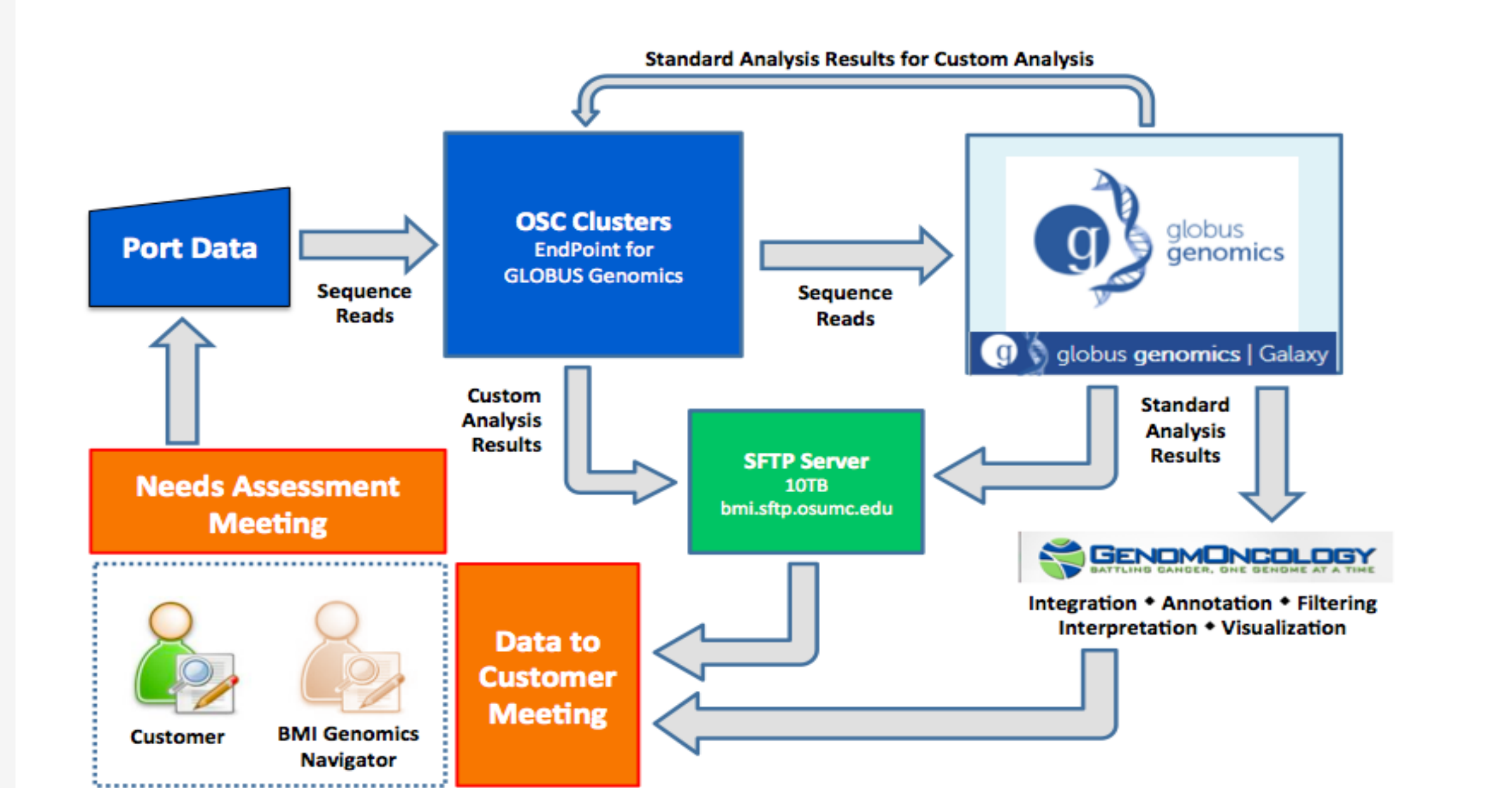
Small RNA-seq
Alignment • Expression and Counts • Known miRNAs • Novel miRNAs

Integration • Visualization • Hypothesis Discovery

Mining and integration of public datasets and annotations

Applications of Next Generation Sequencing (NGS)

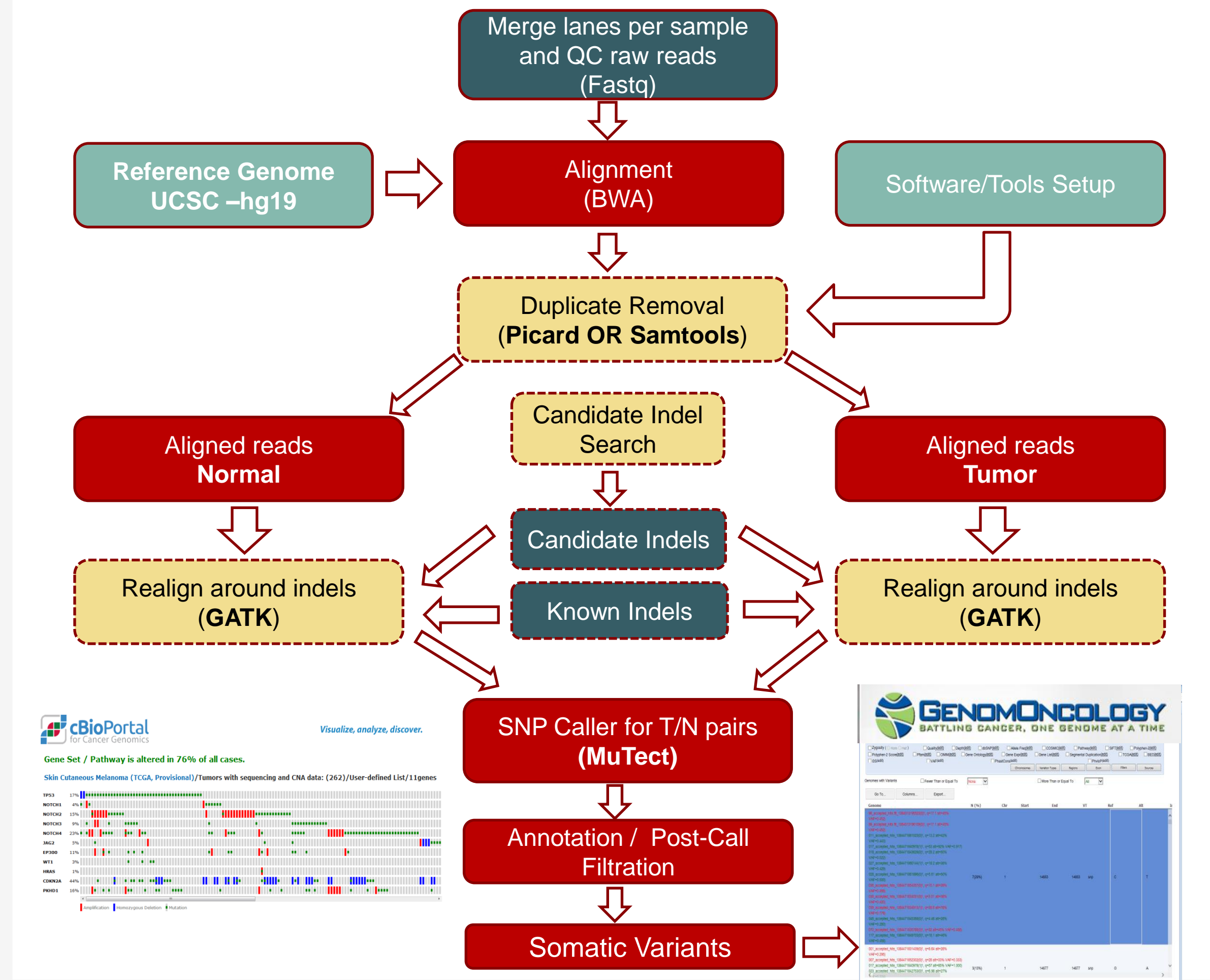
Data Workflow and Management



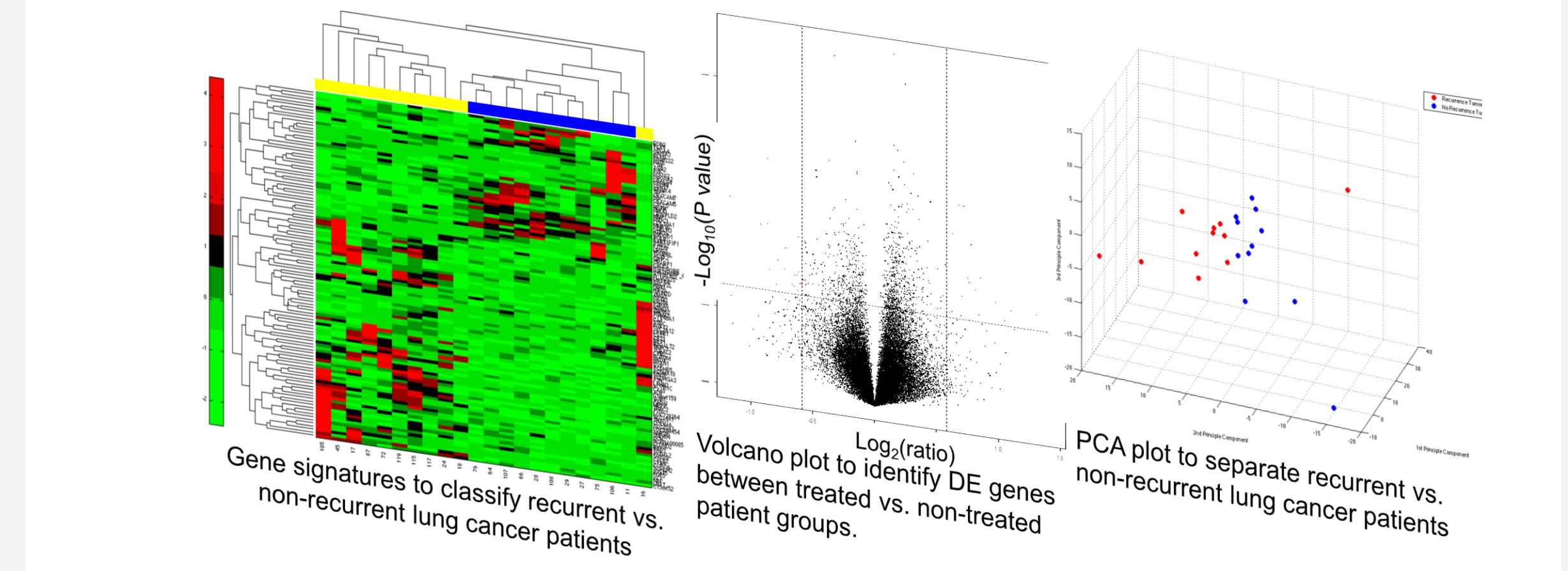
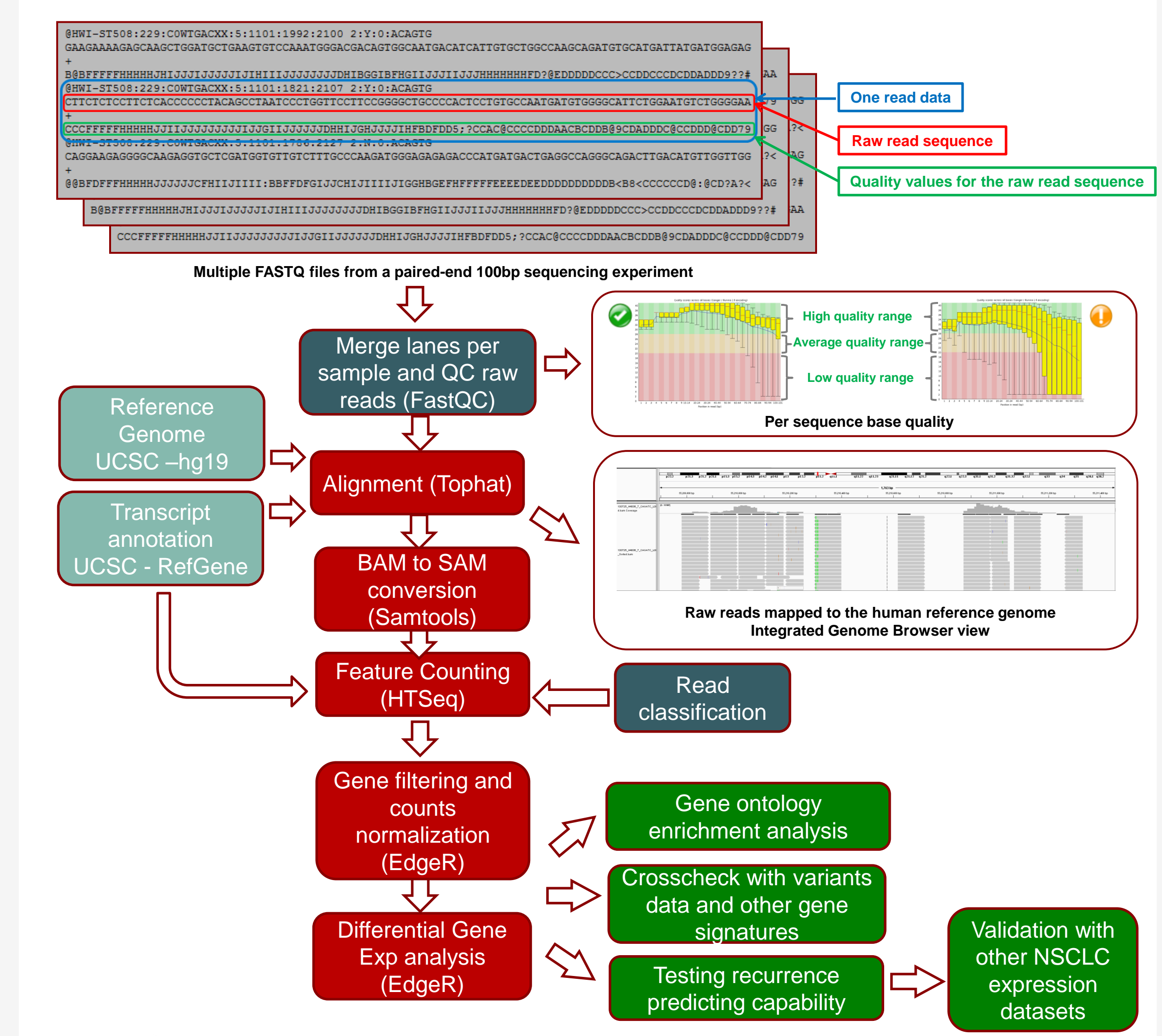
Globus Genomics: An end-to-end sequencing analysis framework, which leverage advanced tools and data management through Amazon **cloud computing** to provide cost-effective services that meet bioscience researchers' needs.

GenomAnalytics : A web-based interface to annotate, interpret, visualize and share the NGS analysis results from human samples through an integrated, intuitive and interactive platform.

Mutation Analysis on DNA Sequencing Data



Gene Expression Analysis on RNA-Seq Data



Motivation, Challenges and Goals

- Motivations:**
- Next Generation Sequencing (NGS) is becoming a common tool in the practice of biomedical research and is the future of how medicine will be practiced.
 - Decreased cost in NGS technologies lead to increased amount of data generated both in size and complexity.
- Challenges** are big data analysis, management, interpretation, mining, visualization and sharing.
- Our **goal** is to develop scalable, extendable pipelines and data workflows that support large-scale re-sequencing experiments which in turn will provide high quality, standardized, low-cost NGS data analysis in a reasonably short turnaround time to all investigators.

Contact Us

Philip Payne, PhD
Co-Director
Philip.Payne@osumc.edu

Jeff Parvin, MD PhD
Co-Director
Jeffrey.Parvin@osumc.edu

Kun Huang, PhD
Co-Director
Kun.Huang@osumc.edu

Gulcin Ozer, PhD
Technical Director
Gulcin.Ozer@osumc.edu

Jie Zhang, PhD
Research Scientist
Jie.Zhang@osumc.edu

Selen Yilmaz, MS
Bioinformatics Specialist
AyseSelen.Yilmaz@osumc.edu

Baris Hancioglu, PhD
Bioinformatics Specialist
Baris.Hancioglu@osumc.edu