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### Genomic Sequencing Data Analysis Workflow for Bioinformatics Core Facilities

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# From Sequencing to Discovery

## Genomic Sequencing Data Analysis Workflow for Bioinformatics Core Facilities

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The James



### Introduction

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

#### What?

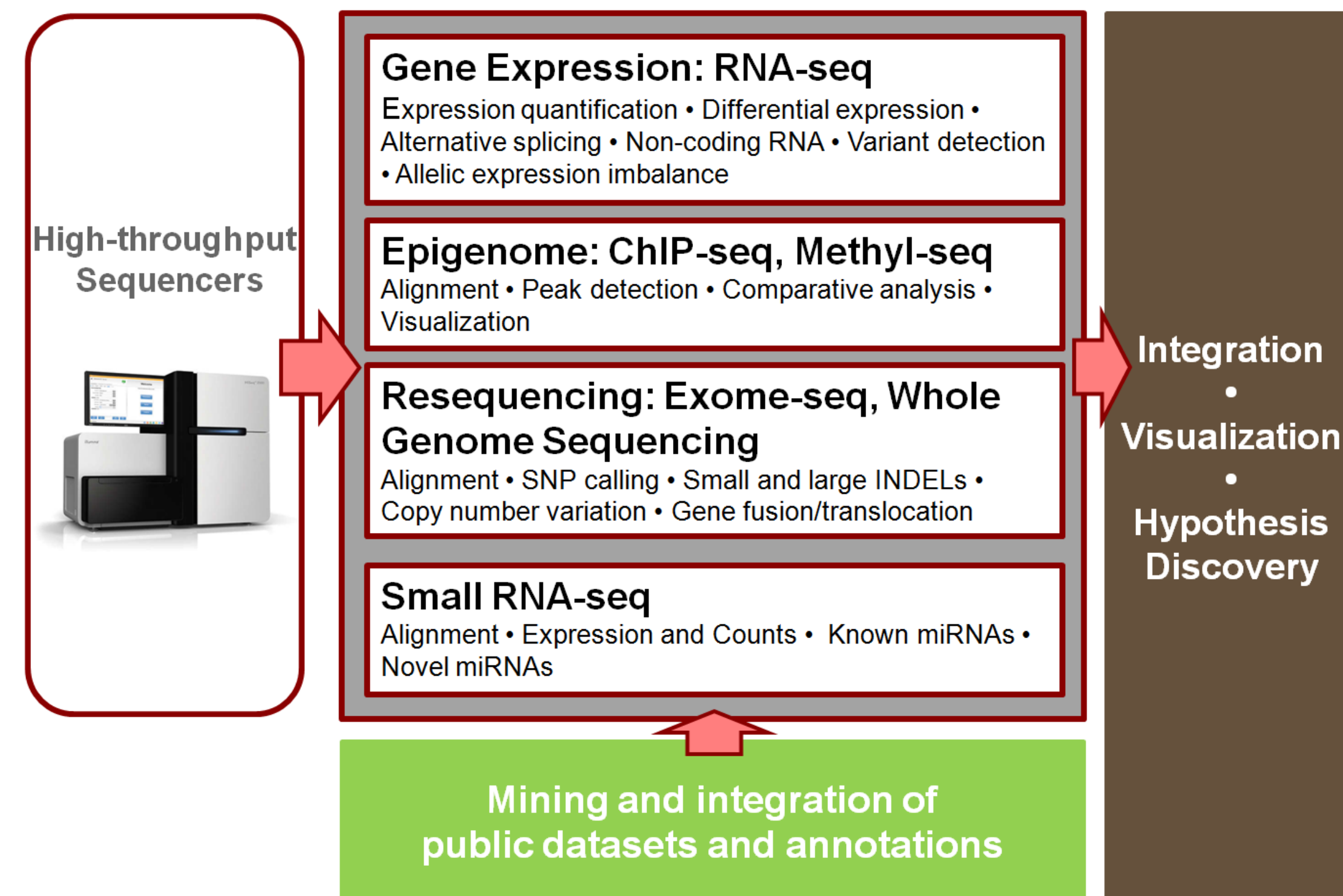
High-throughput genomic sequencing data analyses

#### Why?

To answer an increasingly diverse range of biological questions

#### How?

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



Applications of Next Generation Sequencing (NGS)

### Motivation, Challenges and Goals

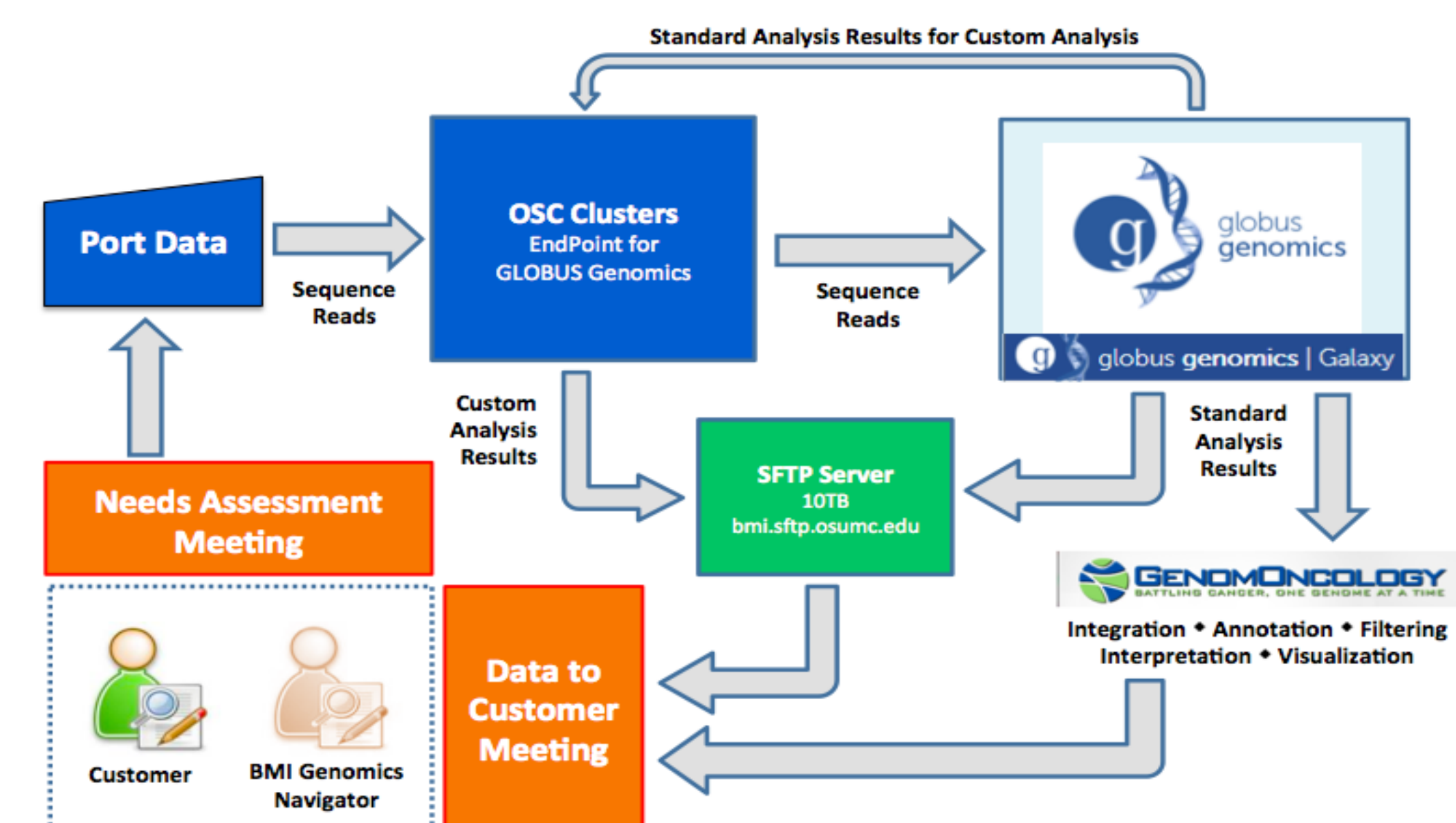
#### Motivations:

- 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.

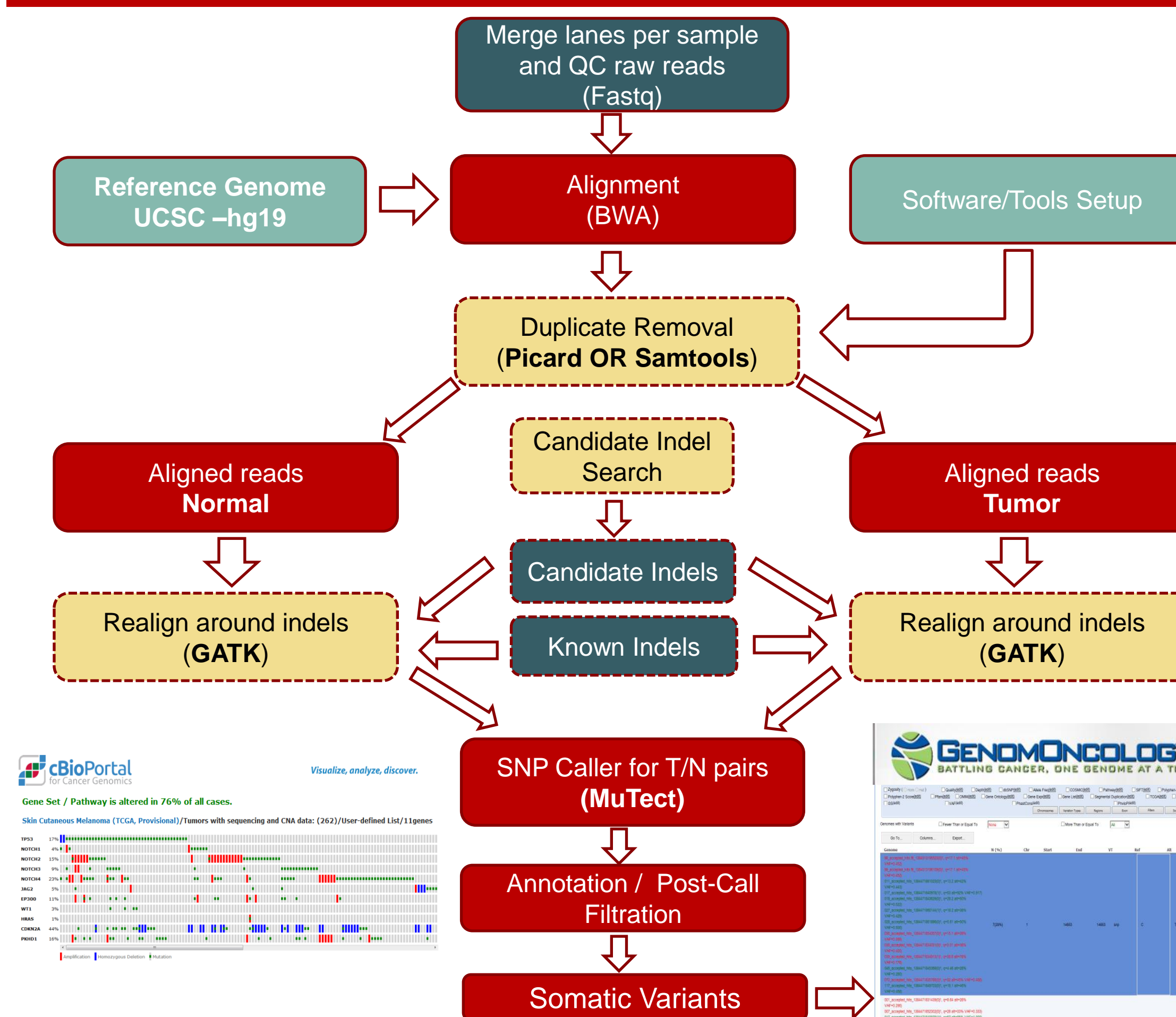
### Data Workflow and Management



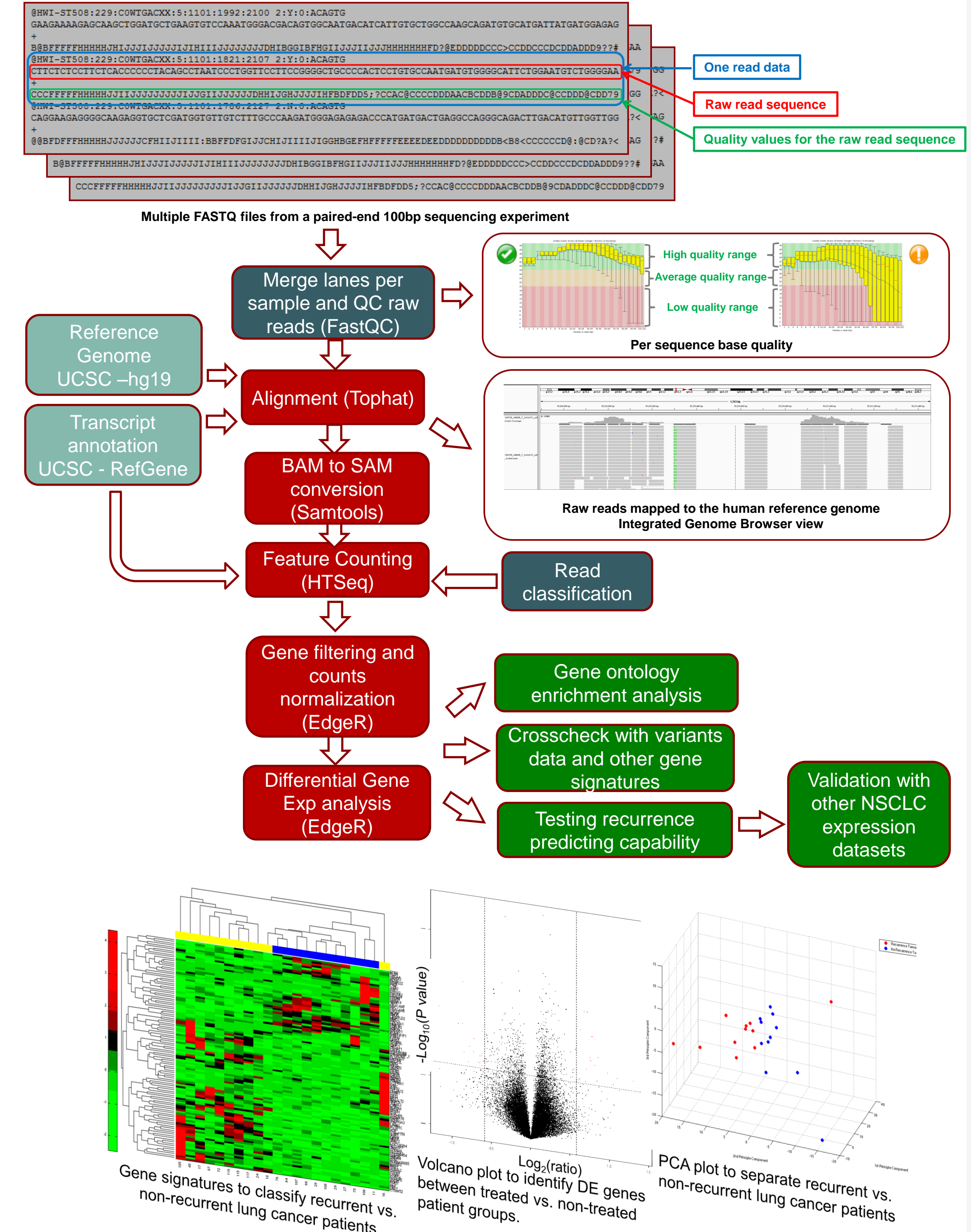
**Globus Genomics:** An end-to-end sequencing analysis framework, which leverage advanced tools and data management through Amazon **cloud computing** to provide cost-effective services that meet bioscience researchers' needs.

**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



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