

NGS Data Mining and Integration for Biomarker Discovery in Cancer Project

AWS in Education research grant

Galaxy

Bowtie

Extremely fast, general purpose short read aligner

TopHat

Aligns RNA-Seq reads to the genome using Bowtie
Discovers splice sites

Cufflinks package

Cufflinks

Assembles transcripts

Cuffcompare

Compares transcript assemblies to annotation

Cuffmerge

Merges two or more transcript assemblies

Cuffdiff

Finds differentially expressed genes and transcripts
Detects differential splicing and promoter use

AWS Cloud

S3 Storage: 10 TB
raw/preprocessed data and analysis results

EC2 Instances: up to 25 auto-scaled
High-Memory Double Extra Large instances

