Tophat for Illumina (version 1.5.0)

RNA-Seq FASTQ file:

[32: FASTQ Groomer on NCI_C2.fastq ‡]

Nucleotide-space: Must have Sanger-scaled quality values with ASCII offset 33

Use a built in reference genome or own from your history:

[Use a built-in genome ‡]

Built-ins genomes were created using default options

Select a reference genome:

[‡]

If your genome of interest is not listed, contact the Galaxy team

Is this library mate-paired?:

[Single-end ‡]

TopHat settings to use:

[Default settings ‡]

Use the Full parameter list to change default settings.

Execute