

## Tophat for Illumina (version 1.5.0)

### RNA-Seq FASTQ file:

29: FASTQ Groomer on data CBG\_1b.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:

Zebrafish (Danio rerio): danRer7

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