Galaxy Workflow ' trinity-transcriptome-assembly-se-dataset-collection'

Step **Annotation**

Step 1: Input dataset collection

input
select at runtime

Step 2: FASTQ Groomer

File to groom
Output dataset 'output' from step 1

Input FASTQ quality scores type
Sanger & Illumina 1.8+

Advanced Options
Hide Advanced Options

Step 3: Trinity

Paired or Single-end data?
Single

Single-end reads
Output dataset 'output_file' from step 2

Strand specific data
False

Run in silico normalization of reads
True

Additional Options:

Minimum Contig Length
200

Use the genome guided mode?
No

Error-corrected or circular consensus (CCS) pac bio reads
select at runtime

Minimum count for K-mers to be assembled
1