

## Galaxy Workflow ' transcripts-assembly-se-dataset-collection'

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Step	Annotation
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Step 1: Input dataset collection	
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<b>Input Dataset Collection</b>	
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<i>select at runtime</i>	
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Step 2: Input dataset	
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<b>input</b>	
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<i>select at runtime</i>	
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Step 3: FASTQ Groomer	
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<b>File to groom</b>	
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Output dataset 'output' from step 1	
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<b>Input FASTQ quality scores type</b>	
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Sanger & Illumina 1.8+	
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<b>Advanced Options</b>	
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Hide Advanced Options	
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Step 4: HISAT2	
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<b>Input data format</b>	
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FASTQ	
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<b>Single end or paired reads?</b>	
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Individual unpaired reads	
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<b>Reads</b>	
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Output dataset 'output_file' from step 3	
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<b>Write unaligned reads (in fastq format) to separate file(s)</b>	
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False	
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<b>Write aligned reads (in fastq format) to separate file(s)</b>	
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False	
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<b>Source for the reference genome to align against</b>	
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Use a genome from history	
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<b>Select the reference genome</b>	
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Output dataset 'output' from step 2	
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<b>Primary alignments</b>	
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Not available.	
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<b>Maximum number of seeds that will be extended</b>	
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Not available.

### **Report secondary alignments**

False

### **Alignment options**

Use default values

### **Input options**

Use default values

### **Scoring options**

Use default values

### **Spliced alignment parameters**

Use default values

### **Paired alignment parameters**

Use default values

## **Step 5: Flagstat**

### **BAM File to report statistics of**

Output dataset 'output\_alignments' from step 4

## **Step 6: StringTie**

### **Mapped reads to assemble transcripts from**

Output dataset 'output\_alignments' from step 4

### **Use GFF file to guide assembly**

Do not use GFF/GTF

### **Options**

Use defaults

## **Step 7: StringTie merge**

### **Transcripts**

Output dataset 'output\_gtf' from step 6

### **Reference annotation to include in the merging**

*select at runtime*

### **Minimum input transcript length to include in the merge**

50

### **Minimum input transcript coverage to include in the merge**

0

### **Minimum input transcript FPKM to include in the merge**

1.0

### **Minimum input transcript TPM to include in the merge**

1.0

### **Minimum isoform fraction**

0.01

**Gap between transcripts to merge together**

250

**Keep merged transcripts with retained introns**

False