

Galaxy Workflow ' mirdeep2-microRNA-detection'

Step	Annotation
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Step 1: Input dataset	
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input <i>select at runtime</i>	
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Step 2: Input dataset	
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input <i>select at runtime</i>	
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Step 3: Input dataset	
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input <i>select at runtime</i>	
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Step 4: Input dataset	
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input <i>select at runtime</i>	
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Step 5: Input dataset	
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input <i>select at runtime</i>	
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Step 6: mirdeep2_mapper	
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Read input file	
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Output dataset 'output' from step 1	
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Reference genome from history	
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Output dataset 'output' from step 2	
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Parse to fasta format	
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True	
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Remove reads with non-canonical letters	
--	--

True	
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Clip 3' adapter sequence (optional)	
--	--

Empty.	
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Discard reads shorter than int nts	
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18	
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Collapse reads	
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True	
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Map with one mismatch	
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False	
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Map up to int nts	
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5	
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Display analysis code in report?

False

Step 7: mirdeep2

Read input file

Output dataset 'reads_collapsed' from step 6

Reference genome from history

Output dataset 'output' from step 2

reads mappings

Output dataset 'reads_collapsed_vs_genome' from step 6

miRBase mature miRNA for this species

Output dataset 'output' from step 3

miRBase mature miRNA from related species

Output dataset 'output' from step 4

precursor sequences

Output dataset 'output' from step 5

minimum read stack height

Not available.

minimum score cut-off

0

randfold analysis

False

maximum number of precursors

50000

Search in species

All species

mature_ref_miRNAs contain miRBase v18 identifiers?

False

Display analysis code in report?

False