protocols.io

Reads trimming & Quality control & Reads alignment

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Abstract

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Protocol

fastQC of raw reads
Step 1.

/home/CAM/qlin/RCP1_OX_Transcriptome/fastQC/raw

trim reads by trimmomatic
Step 2.

/home/CAM/qlin/RCP1_OX_Transcriptome/trimmomatic

fastQC of trimmed reads
Step 3.

/home/CAM/qlin/RCP1_OX_Transcriptome/fastQC/t1

/home/CAM/qlin/RCP1_OX_Transcriptome/fastQC/t3

align trimmed reads to genome assembly
Step 4.

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t1

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t2

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t3

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t4

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t5

count genome coverage
Step 5.

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t1/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t1/depth*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t2/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t2/depth*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t3/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t3/depth*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t4/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t4/depth*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t5/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/STAR/t5/depth*

choose the best trimmed reads and align them to genome assembly by HISAT2
Step 6.

/home/CAM/qlin/RCP1_OX_Transcriptome/HISAT2/t6

Verify the genome coverage
Step 7.

/home/CAM/qlin/RCP1_OX_Transcriptome/HISAT2/t6/view*

/home/CAM/qlin/RCP1_OX_Transcriptome/HISAT2/t6/depth*