

The pipeline of Hi-C assembly

Xin Liu

Abstract

From here, You can know detail methods of Hi-C assembly of the Betta splendens genome.

Citation: Xin Liu The pipeline of Hi-C assembly. **protocols.io**

dx.doi.org/10.17504/protocols.io.qradv2e

Published: 08 Jun 2018

Protocol

Quality control

Step 1.

Get raw Hi-C sequencing data in Fastq format and reference genome(the result of SOAPdenovo2) . Filter the input raw sequences by using HiC-Pro (v. 2.8.0).

📌 NOTES

Hongling Zhou 06 Jun 2018

Using parameters'MIN_INSERT_SIZE = 50 MAX_INSERT_SIZE = 2000',others are default parameters

Valid pairs reads extraction

Step 2.

Extract valid pairs reads according the HiC-Pro result.

Assembly

Step 3.

1. Run Juicer (v. 1.5) to prepare data for 3D de novo (v.170123) assembly with valid pairs reads.

2. Run 3D de novo (v.170123) assembly to assemble into chromosome

📌 NOTES

Hongling Zhou 06 Jun 2018

1-Note: Using default parameter

Hongling Zhou 06 Jun 2018

2-Note: Using parameter '-m haploid -s 4 -c 21'