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Protocol status: Working

The pipeline of Hi-C assembly

In 6 collections

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ABSTRACT

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

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Quality control

- 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).

Note

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

Valid pairs reads extraction

- 2 Extract valid pairs reads according the HiC-Pro result.

Assembly

- 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

Note

1-Note: Using default parameter

Note

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