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IPA assembly for Hifi PacBio reads

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1

Works for me

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ABSTRACT

This protocol is regarding the assembly of plant genomes using HiFi data (PacBio Sequel II) using Improved Phase Assembly (IPA) tool.

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KEYWORDS

Improved Phased assembly, CCS reads, PacBio Sequel II

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MATERIALS TEXT

Requirements to use IPA assembly:

1) CCS.bam files, from PacBio sequel II.

2) Install IPA tool using the link provided below:

<https://github.com/PacificBiosciences/pbipa>

3) We performed the genome assembly in "High performance computing (HPC)" system, at University of Queensland, using following commands:

```
$ conda create --prefix /mnt/beegfs/usr/ipaM
```

```
$ conda activate /mnt/beegfs/usr/ipaM
```

```
$ conda install pbipa
```

```
$ ipa validate
```

```
$ ipa local --nthreads 24 --njobs 1 -i m64123_200919_084320.ccs.bam -i m64123_201004_151034.ccs.bam
```

1 Steps to generate the genome assembly of different plant species using IPA (Improved phased assembly):

1) ccs.bam files generated by PacBio Sequel II (HiFi) platform for all the plant species were used to assemble the genome using IPA tool.

2) IPA was installed

2) IPA was initiated using Conda environment

2

```
$ conda create --prefix /mnt/beegfs/user/ipaM
$ conda activate /mnt/beegfs/user/ipaM
$ conda install pbipa
$ ipa validate
ipa local --nthreads 24 --njobs 1 -i m64123_200919_084320.ccs.bam -i \
m64123_201004_151034.ccs.bam
```

Above screen shot shows the commands used for using IPA, using Conda environment.