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IPA assembly for PacBio Hifi reads

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Works for me

dx.doi.org/10.17504/protocols.io.buxvnxn6[The University of Queensland](#)

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ABSTRACT

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

EXTERNAL LINK

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

DOI

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PROTOCOL CITATION

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KEYWORDS

Improved Phase Assembly (IPA), CCS reads, PacBio Sequel II, Genome, Assembly

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IMAGE ATTRIBUTION

The image used in the thumbnail is the picture of the *Macadamia tetraphylla* (provided by Robert Henry).

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Requirements to run IPA assembly:

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

2) The IPA tool was installed using the following link:

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

3) Genomes were assembled in the 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 (input files)

1 Steps:

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

2) The IPA tool was installed using the conda environment, following the link:

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

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```
$ 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
```

The above screenshot shows the commands used for generating the IPA assembly