

Canu

canu -p **canu** -d **out_dir** -fast genomeSize=5000000 stopOnLowCoverage=0 minInputCoverage=0
useGrid=false minThreads=16 maxThreads=16 maxMemory=120 -nanopore-raw reads.fastq.gz

output filename prefix
output directory name
faster read overlapping (recommended in release notes for genomes <1 Gbp in size)
true size of the reference genome
prevents premature termination in cases of suboptimal input reads
these four options tailor Canu to the computational environment
input read type (changed to -pacbio-raw for PacBio reads)
input read filename

Flye

flye -o **out_dir** --plasmids --threads 16 --nano-raw reads.fastq.gz

output directory name
enable recovery of small plasmids
CPU threads to use
input read type (changed to --pacbio-raw for PacBio reads)
input read filename

Miniasm

miniasm_and_minipolish.sh reads.fastq.gz 16

input read filename
CPU threads to use

NECAT

necat.pl bridge config.txt

contains read filename, genome size and thread count

NextDenovo

seq_stat -g 5000000 input.fofn
nextDenovo nextdenovo_run.cfg
nextPolish nextpolish_run.cfg

true size of the reference genome
contains read filename
contains read filename, thread count and seed cutoff from seq_stat
contains read filename, thread count and assembly filename

Raven

raven --graphical-fragment-assembly graph.gfa --threads 16 reads.fastq.gz

output graph filename
CPU threads to use
input read filename

Redbean

wtdbg2.pl -o dbg -g 5000000 -t 16 -x ont reads.fastq.gz

output filename prefix
true size of the reference genome
CPU threads to use
assembly preset (changed to rs for PacBio reads)
input read filename

Shasta

gunzip -c reads.fastq.gz > reads.fastq
shasta --input reads.fastq --assemblyDirectory out_dir --threads 16

input read filename
the output directory name
CPU threads to use