

Canu

canu -p **canu** -d **out_dir** -fast genomeSize=5m stopOnLowCoverage=0 stopOnReadQuality=false
useGrid=false minThreads=16 maxThreads=16 maxMemory=63 -nanopore-raw reads.fastq.gz

the output filename prefix
the output directory name
faster read overlapping (recommended in release notes for genomes <1 Gbp in size)
the true size of the reference genome
these two options prevent 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 --meta --genome-size 5m --threads 16 --nano-raw reads.fastq.gz

the output directory name
enable recovery of small plasmids
enable uneven coverage mode
the true size of the reference genome
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

Raven

raven --threads 16 reads.fastq.gz

CPU threads to use
input read filename

Redbean

wtdbg2.pl -o **dbg** -g 5m -t 16 -x ont reads.fastq.gz

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

Shasta

seqtk seq -A reads.fastq.gz > reads.fasta
shasta --input reads.fasta --assemblyDirectory out_dir --threads 16

input read filename
the output directory name
CPU threads to use