Canu

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 · these two options prevent premature termination in cases of suboptimal input reads

```
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
```

these four options tailor Canu to the computational environment · input read type (changed to -pacbio-raw for PacBio reads) · input read filename

Flye

output directory name · enable recovery of small plasmids · enable uneven coverage mode · true size of the reference genome · CPU threads to use · input read type (changed to --pacbio-raw for PacBio reads) · input read filename

```
flye -o out_dir --plasmids --meta --genome-size 5m --threads 16 --nano-raw reads.fastq.gz
```

Miniasm

input read filename · CPU threads to use

```
miniasm_and_minipolish.sh reads.fastq.gz 16
```

Raven

output graph filename · CPU threads to use · input read filename

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

Redbean

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

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

Shasta

input read filename · the output directory name · CPU threads to use

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