

Output from NanoPreprocess

fast5_files

Basecalled
fast5

fastq_files

*.fq.gz file

alignment

*.bam and
*.bai files

QC_files

Sequencing
summary

Comparison
file (*.tsv)

Reference
(*.fa)

+ reference

TOMBO

Resquigging with tombo



Resquigged
single fast5

Get modifications

+ reference

NANOPOLISH

Indexing

Event align



Current data
per multifast5

Collapse data

+ bam file(s)

EPINANO

Indexing

Call variants



Variants

Calculate frequencies

Tombo's p-value per
position

Current data per position
and per read level

Features' frequencies per
position

Input files

Intermediate files

Results

* In parallel

NANOCOMPORE

Calculate nanocompore

Nanocompore's
p-value per
potision