

ONT long read
fast5 format

Illunima short read
fastq format

Preprocessing

Basecalling
Guppy

Trim and demultiplex
Porechop

Isoform detection

Isoform detection
FLAMES

Map and quantify

Map to genome
Minimap2

Map to transcriptome
Minimap2

Map to genome
Subread

Gene-level quantify
featureCounts

Transcript-level quantify
Minimap2

Gene-level quantify
featureCounts

Exon-level quantify
featureCounts

Differential gene expression
limma

Differential transcript usage
DRIMSeq, voom-diffSplice

Differential gene expression
limma

Differential splicing
voom-diffSplice

Differential analysis