

ONT long read
fast5 format

Illumina short read
fastq format

Preprocessing

Basecalling

Guppy

Trim and demultiplex

Porechop

Isoform detection

Isoform detection

FLTSA

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