A

raw data
(.fast5)
poreplex
adapter trimmed and basecalled reads
(.fastq)
minimap2
aligned reads
(100%) (.bam)
quality_filter.py
quality alignments
(91.6%) (.bam)
polya_filter.py
polyA positive alignments
(82.7%) (.bam)
remap3prime.py
3' end realigned alignments
(82.7%) (.bam)
bedtools bamtobed
preprocessed alignments
(82.7%) (.bed)
TSS_filter.py
start site filtered alignments
(62.1%) (.bed)
correctBed12.py
splice junction corrected alignments
(60.0%) (.bed)
filter_intron_retained.py
intron retention filtered alignments
(59.3%) (.bed)
bedtools getfasta -s -split -bedOut
alignments with associated sequence
(59.3%) (.bedfa)
three_prime_filter.py
3' filtered alignments
(58.8%) (.bed)
extractIsoforms.py
stringent splice isoform clusters
(.tsv)
extractUTRs.py
stringent putative 3'UTRs
(.bed)
raw data
(.fast5)
Albacore
basecalled reads
(.fastq)
minimap2
aligned reads
(.bam)
nanopolish
Raw data
(.fast5)
polyA length estimates
(.polya)