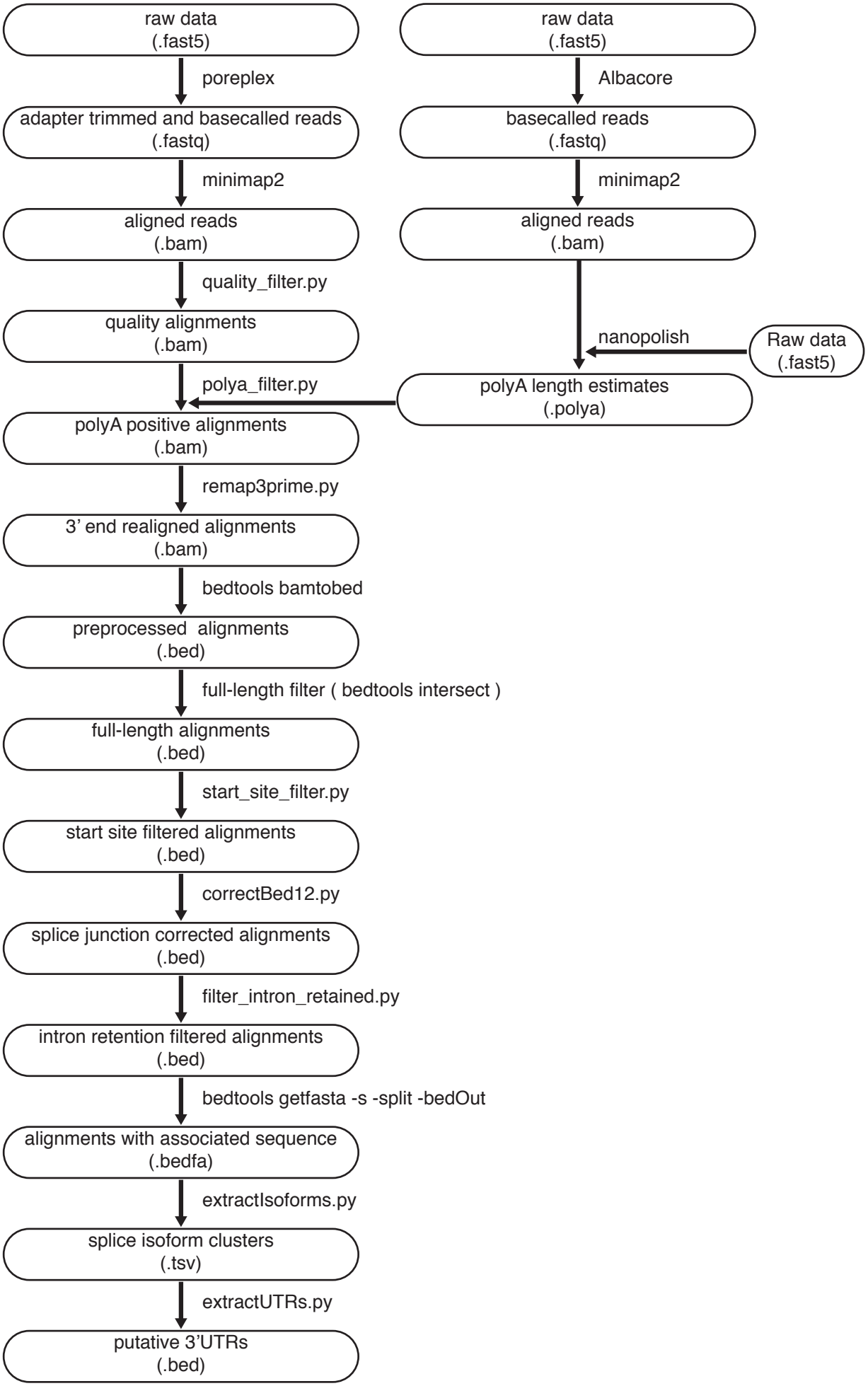
A


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