Alignment & m5C candidate calling operation for each source

input.fq

Align to reference → alignStats.tsv

Unaligned.fq

Align.bam

BAM processing

mpileup.tsv

Call m5C Candidates

call.tsv → call_stats.tsv

Input for next source
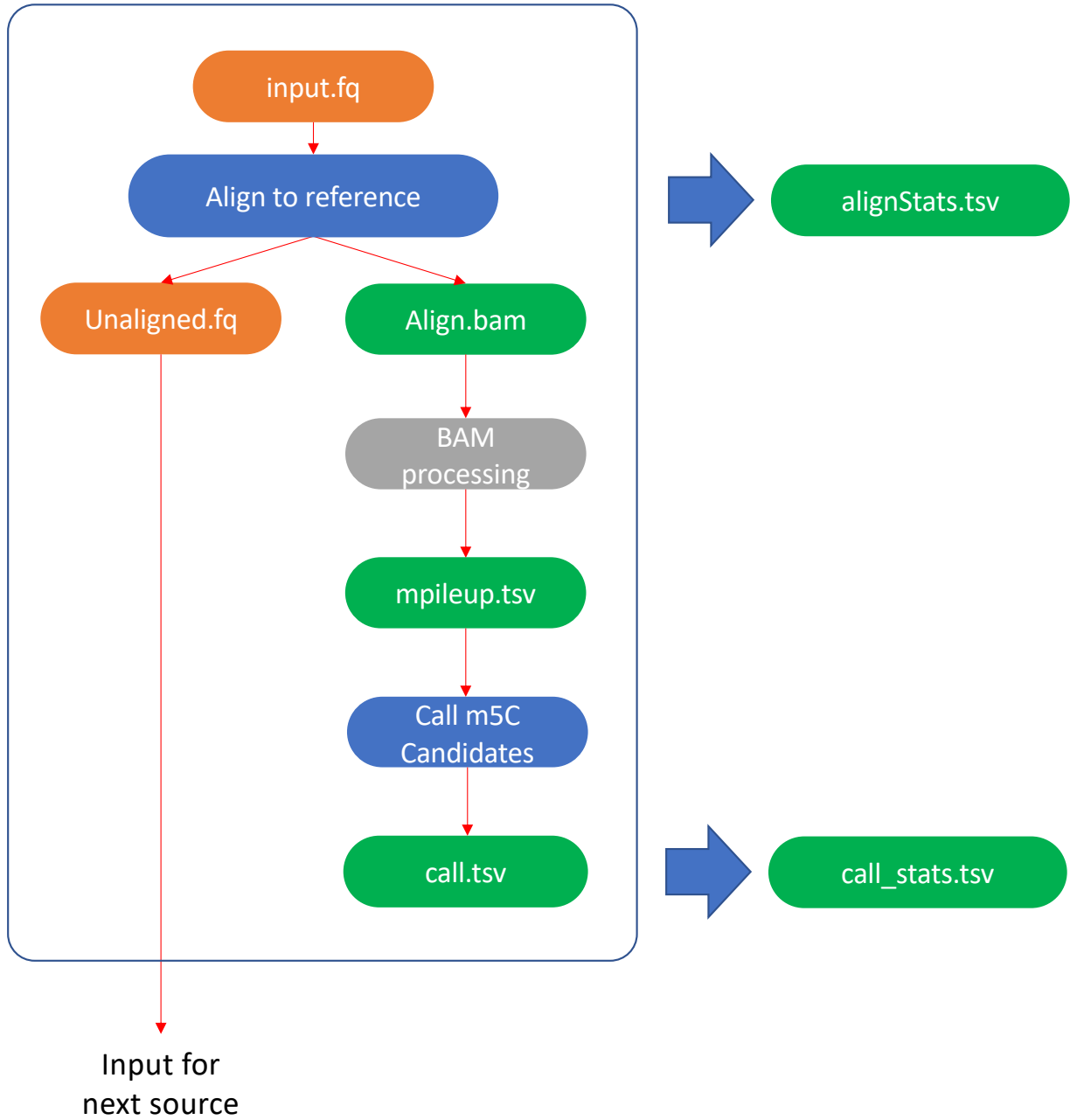
BAM processing step for each source

Align.bam

↓

Split bam

↓ ↓

Align.plus.bam   Align.minus.bam

↓ ↓ ↓

Samtools mpileup   Get reads with NH:i:1   Select reads aligned only to the minus strand and merge with unaligned reads

↓ ↓ ↓

mpileup_raw_all.tsv   Get reads with NH:i:2 or higher, but seen only once in the bam file   Unaligned.fq.gz

↓ ↓

align.plus.uniq.bam

↓

Samtools mpileup

↓

mpileup_raw_uniq.tsv

↓ ↓

rBis.mpileup_getStrand.py

↓ ↓

mpileup_all.tsv   mpileup_uniq.tsv

↓ ↓

rBis.mpileup_mergeTables.py

↓

mpileup.tsv