

Runfolder Data Directory Hierarchy

Intensities
BaseCalls(Bustard)

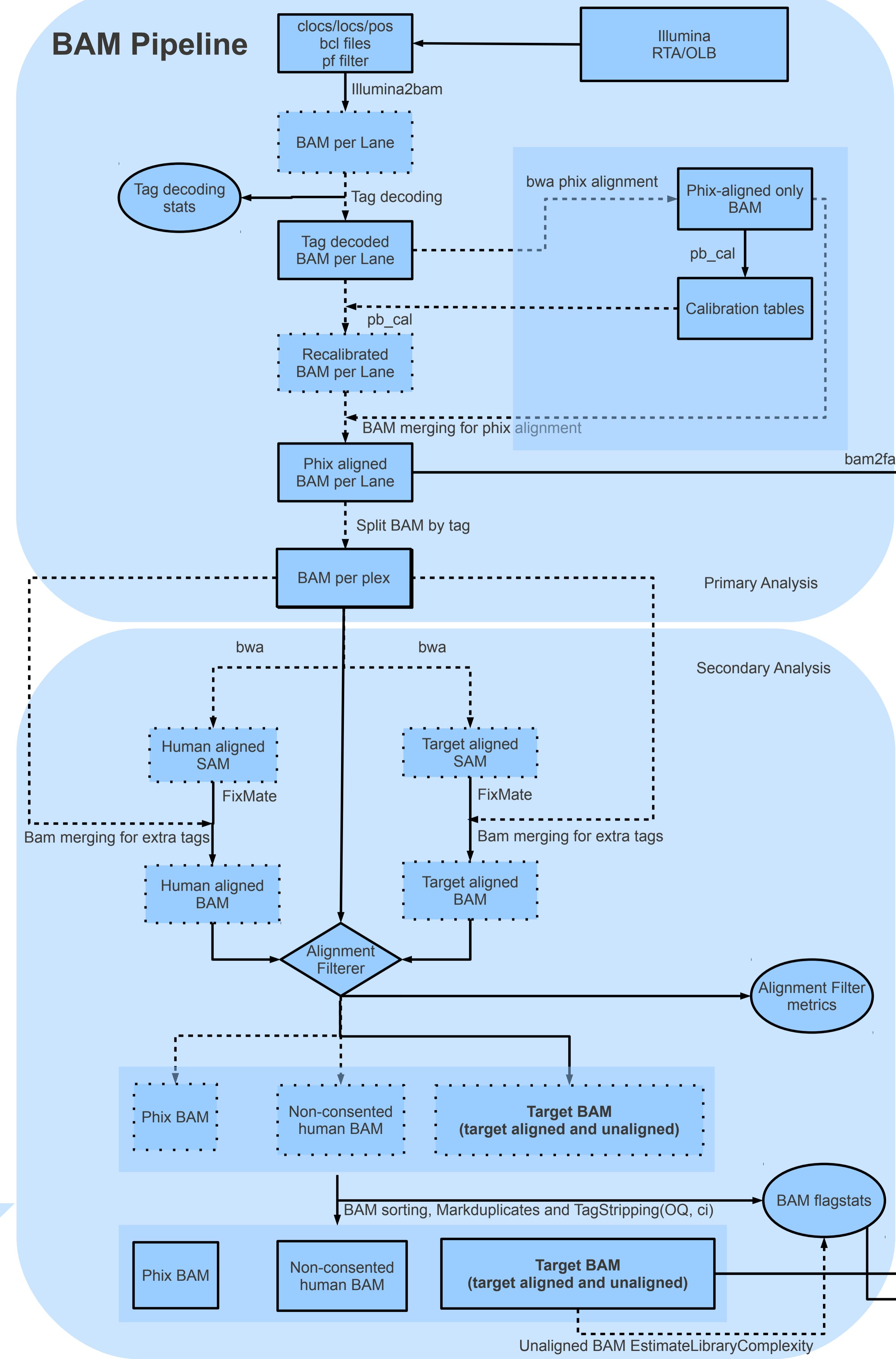
BAM_basecalls

PB_cal_bam(no_cal)
(Latest_Summary)

PB_cal_bam/lane?
(no_cal/lane*)

archive
(archive/lane*)

BAM Pipeline



QC Check
QC output JSON
under archive/qc or archive/lane*/qc

QX yield
GC fraction
Quality by cycle Heatmap

Fastqcheck
per lane and per plex

Fastq
(10K samplings)
per lane and per plex

archive
(archive/lane*)

.npg_cache_10000
under archive
or
archive/lane*

Insert size
Ref Match
Sequence Mismatch

Adapter check

GC bias

Genotype

Pulldown metrics

Total reads check