Figure S1

dnaseq.py -t mpileup

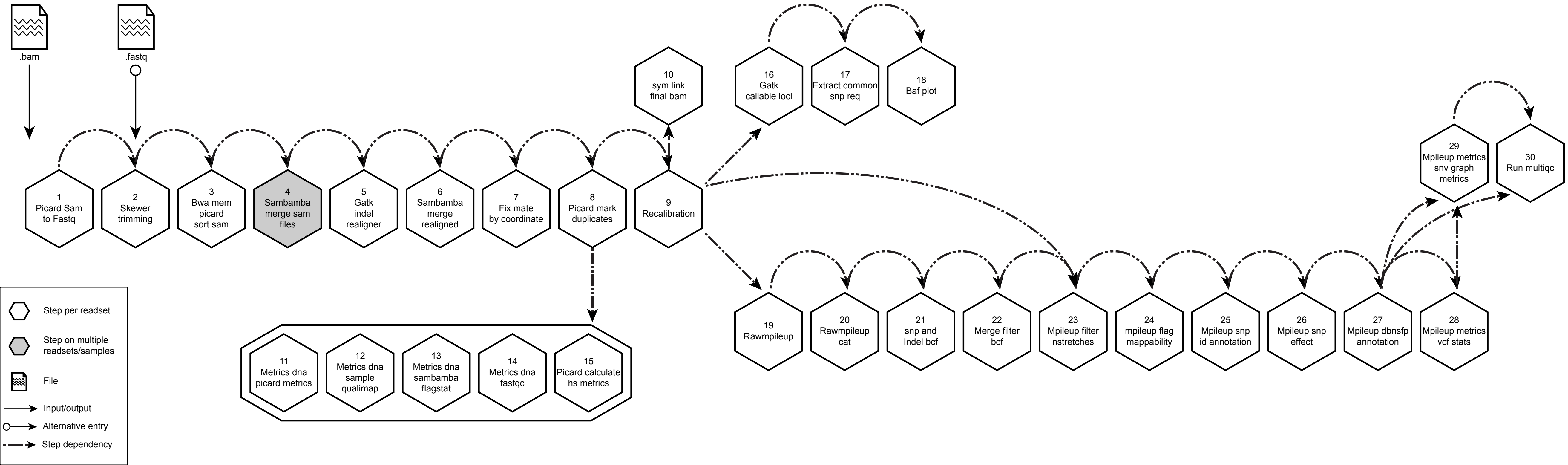


Figure S2

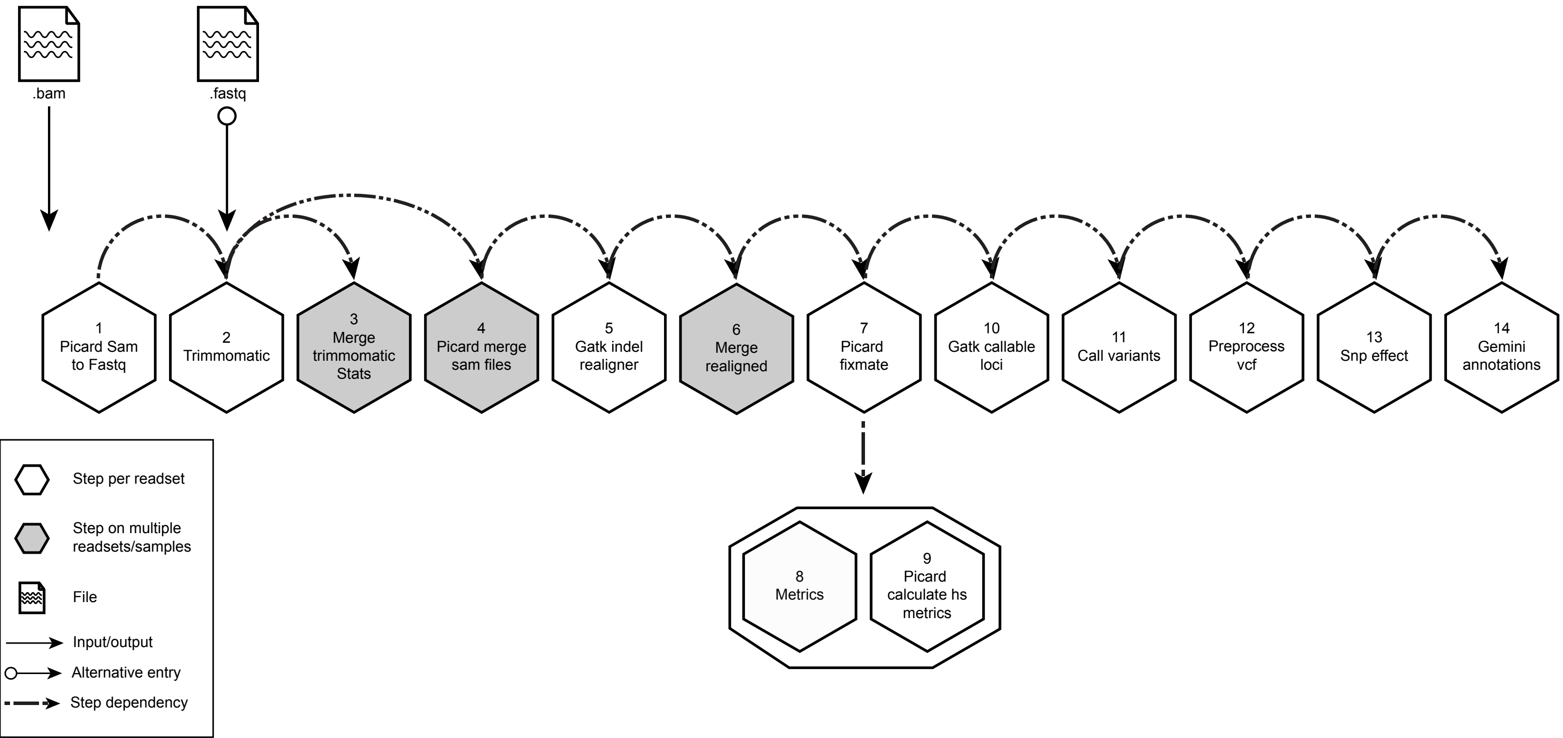

dnaseq_high_coverage.py
.bam
.fastq
1 Picard Sam to Fastq
2 Trimmomatic
3 Merge trimmomatic Stats
4 Picard merge sam files
5 Gatk indel realigner
6 Merge realigned
7 Picard fixmate
10 Gatk callable loci
11 Call variants
12 Preprocess vcf
13 Snp effect
14 Gemini annotations
8 Metrics
9 Picard calculate hs metrics
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S3

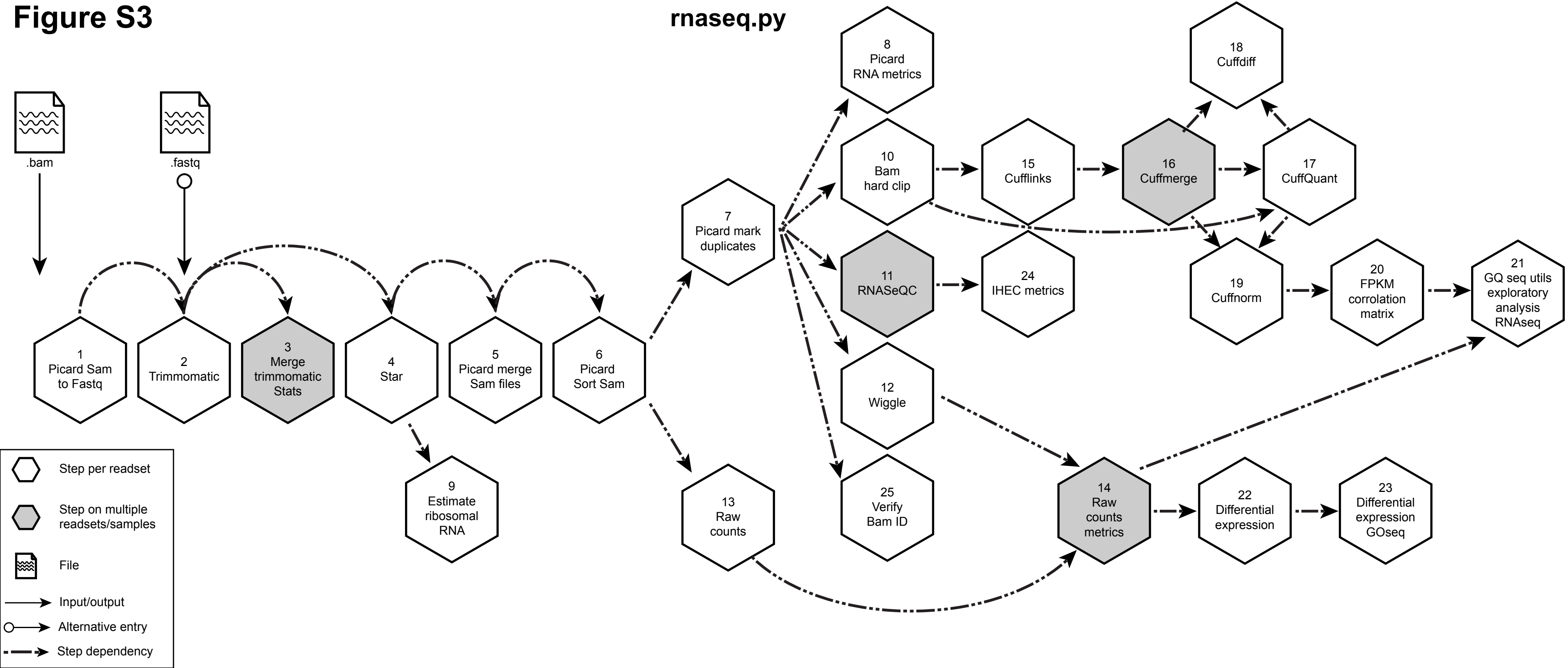

rnaseq.py
.bam
.fastq
1 Picard Sam to Fastq
2 Trimmomatic
3 Merge trimmomatic Stats
4 Star
5 Picard merge Sam files
6 Picard Sort Sam
7 Picard mark duplicates
8 Picard RNA metrics
9 Estimate ribosomal RNA
10 Bam hard clip
11 RNASeQC
12 Wiggle
13 Raw counts
14 Raw counts metrics
15 Cufflinks
16 Cuffmerge
17 CuffQuant
18 Cuffdiff
19 Cuffnorm
20 FPKM corrolation matrix
21 GQ seq utils exploratory analysis RNAseq
22 Differential expression
23 Differential expression GOseq
24 IHEC metrics
25 Verify Bam ID
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S4

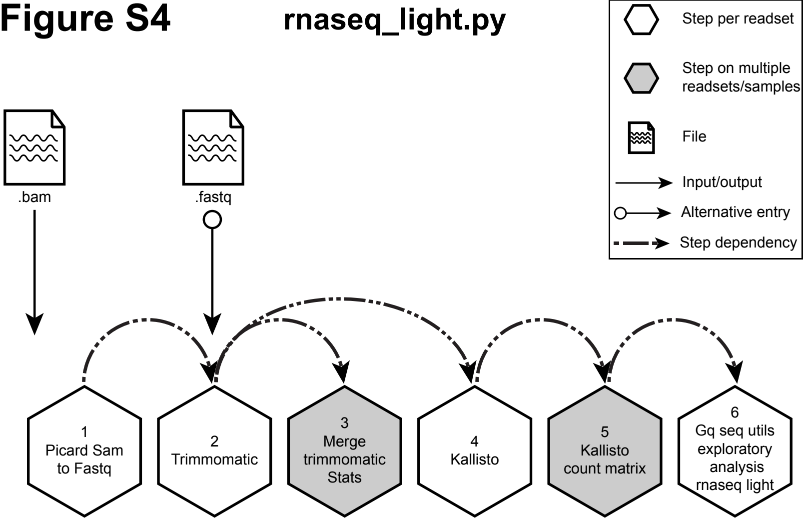

rnaseq_light.py
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency
.bam
.fastq
1 Picard Sam to Fastq
2 Trimmomatic
3 Merge trimmomatic Stats
4 Kallisto
5 Kallisto count matrix
6 Gq seq utils exploratory analysis rnaseq light

Figure S5

rnaseq_denovo_assembly.py

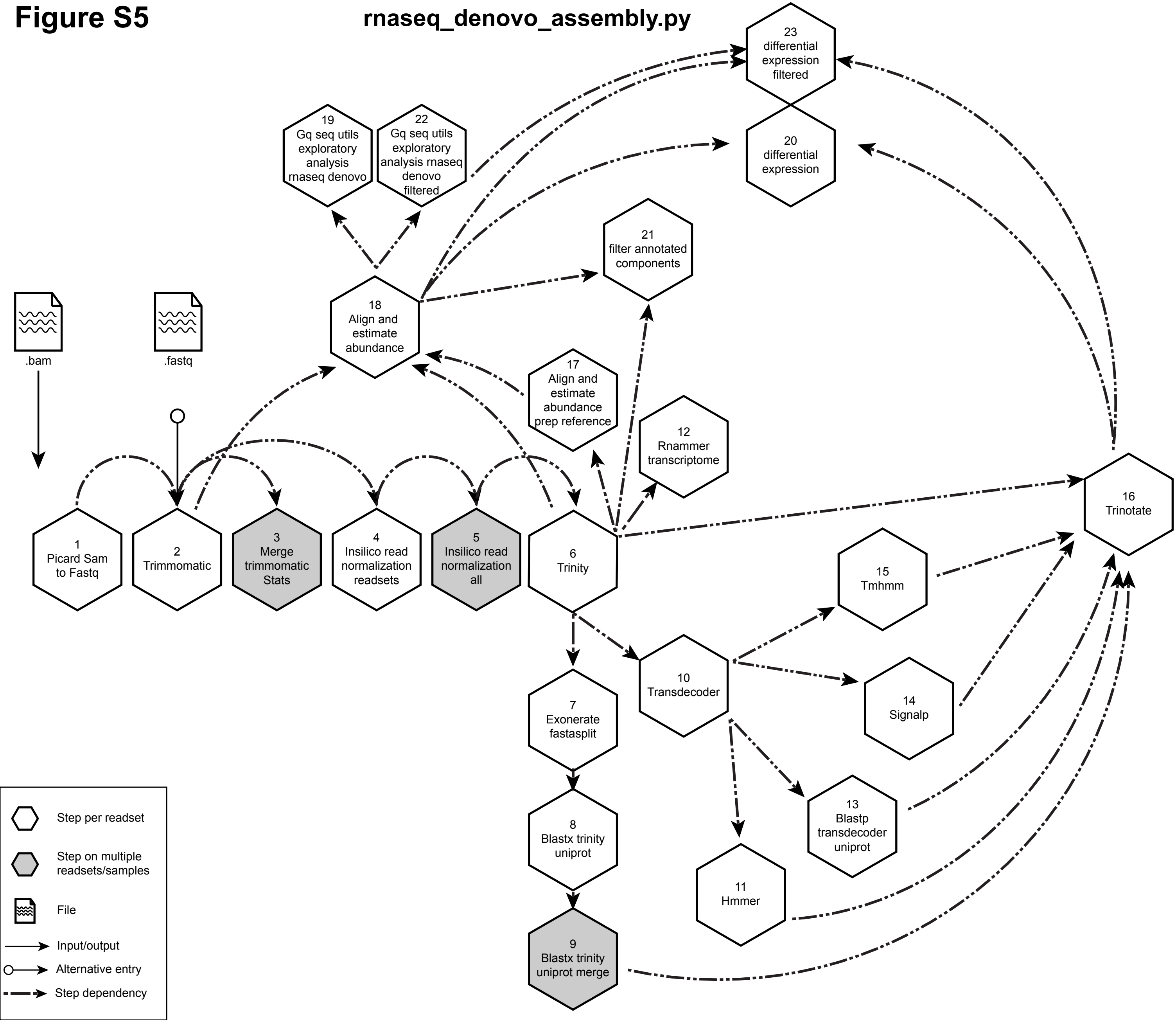


Figure S6

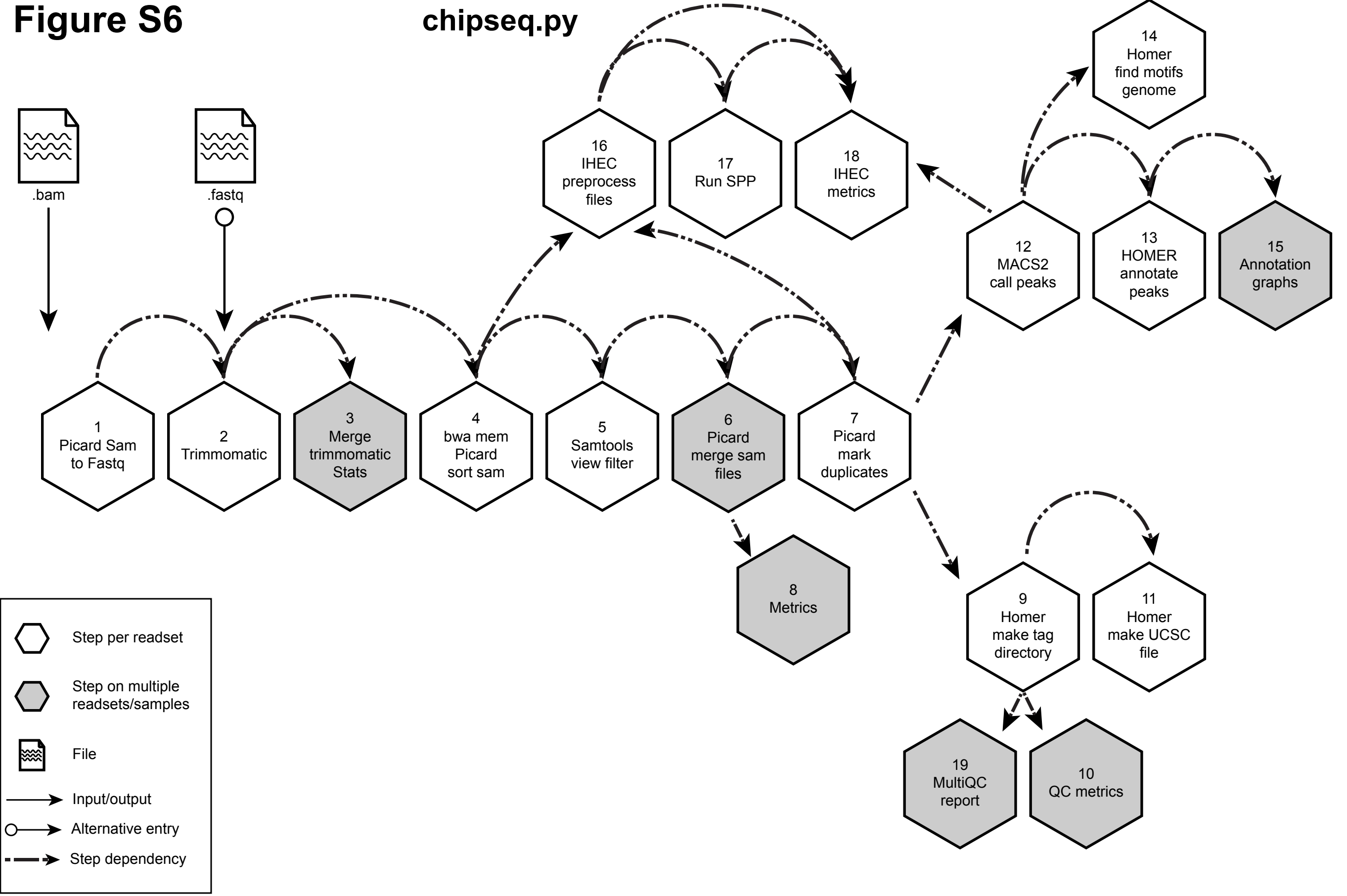

chipseq.py
.bam
.fastq
1 Picard Sam to Fastq
2 Trimmomatic
3 Merge trimmomatic Stats
4 bwa mem Picard sort sam
5 Samtools view filter
6 Picard merge sam files
7 Picard mark duplicates
8 Metrics
9 Homer make tag directory
10 QC metrics
11 Homer make UCSC file
12 MACS2 call peaks
13 HOMER annotate peaks
14 Homer find motifs genome
15 Annotation graphs
16 IHEC preprocess files
17 Run SPP
18 IHEC metrics
19 MultiQC report
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S7

tumor_pair.py -t sv

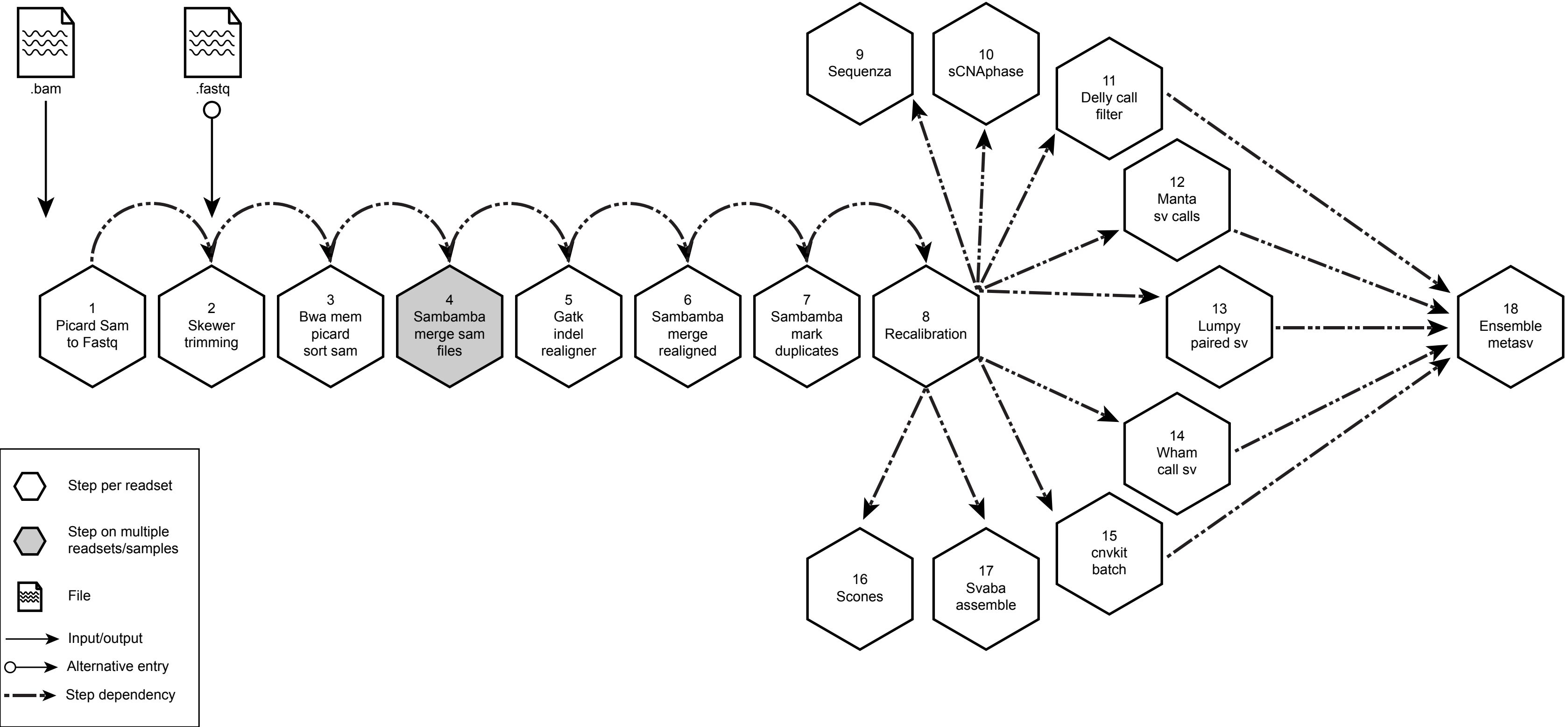
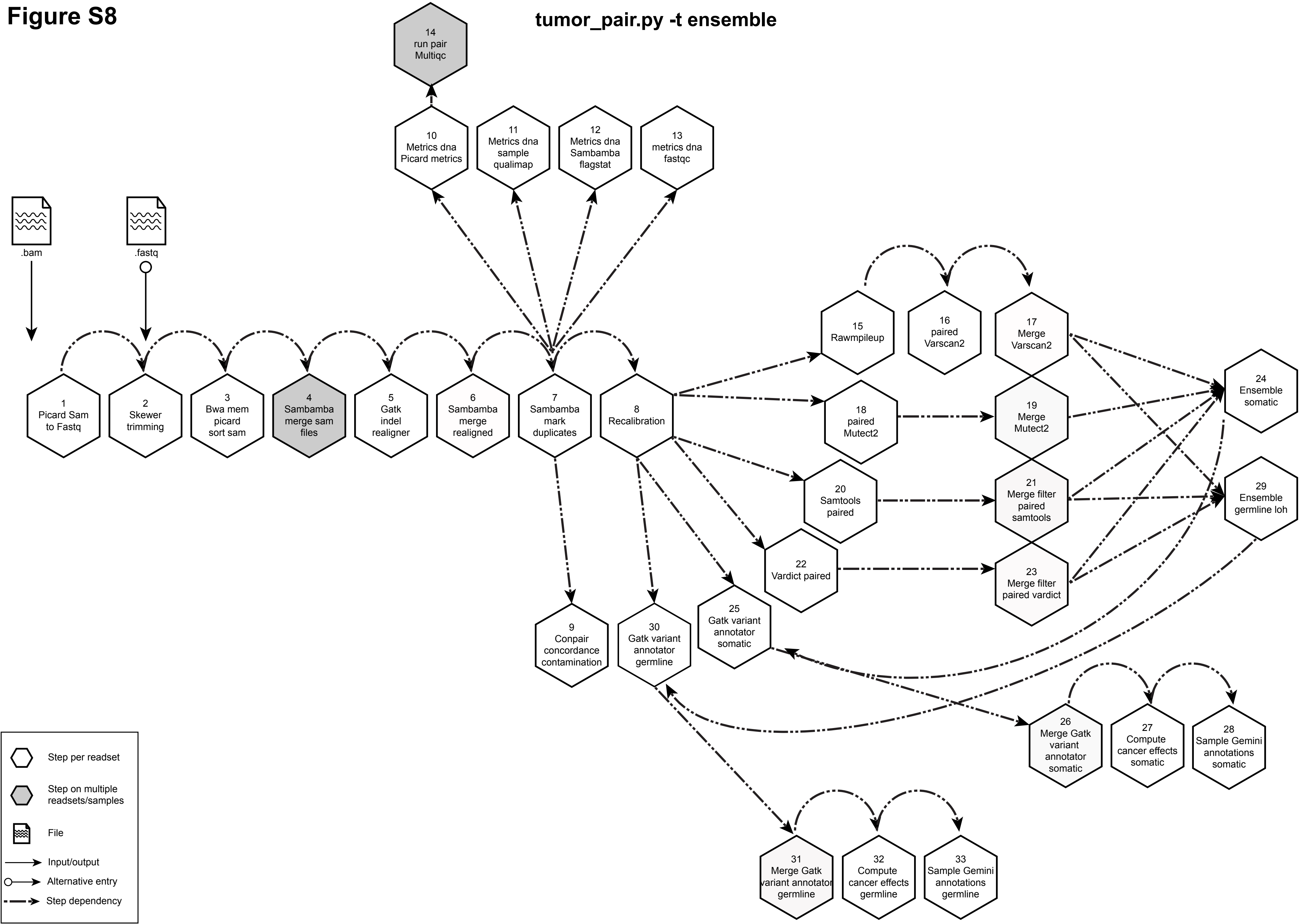


Figure S8



tumor_pair.py -t ensemble

Figure S9

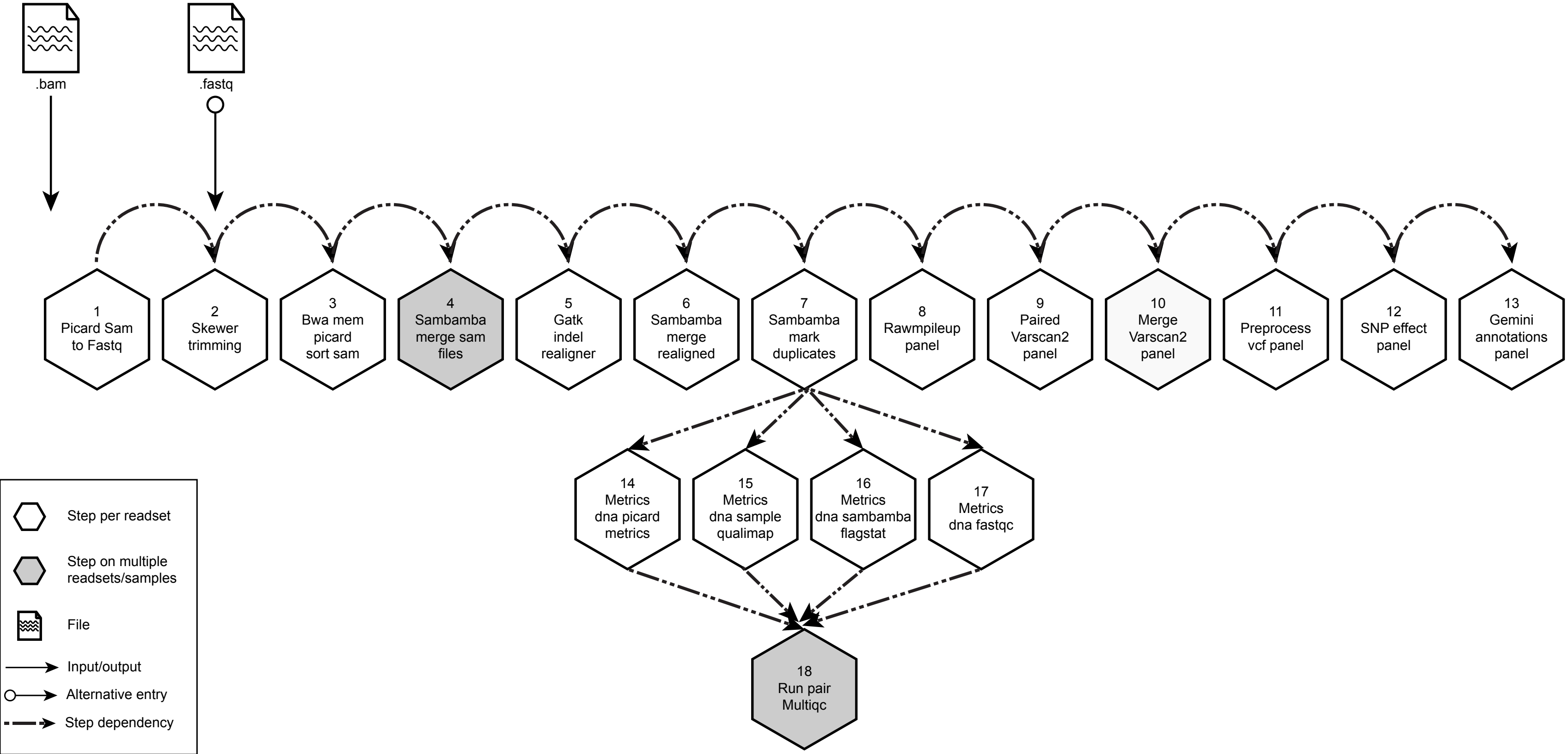

tumor_pair.py -t fastpass
.bam
.fastq
1 Picard Sam to Fastq
2 Skewer trimming
3 Bwa mem picard sort sam
4 Sambamba merge sam files
5 Gatk indel realigner
6 Sambamba merge realigned
7 Sambamba mark duplicates
8 Rawmpileup panel
9 Paired Varscan2 panel
10 Merge Varscan2 panel
11 Preprocess vcf panel
12 SNP effect panel
13 Gemini annotations panel
14 Metrics dna picard metrics
15 Metrics dna sample qualimap
16 Metrics dna sambamba flagstat
17 Metrics dna fastqc
18 Run pair Multiqc
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S10

methylseq.py

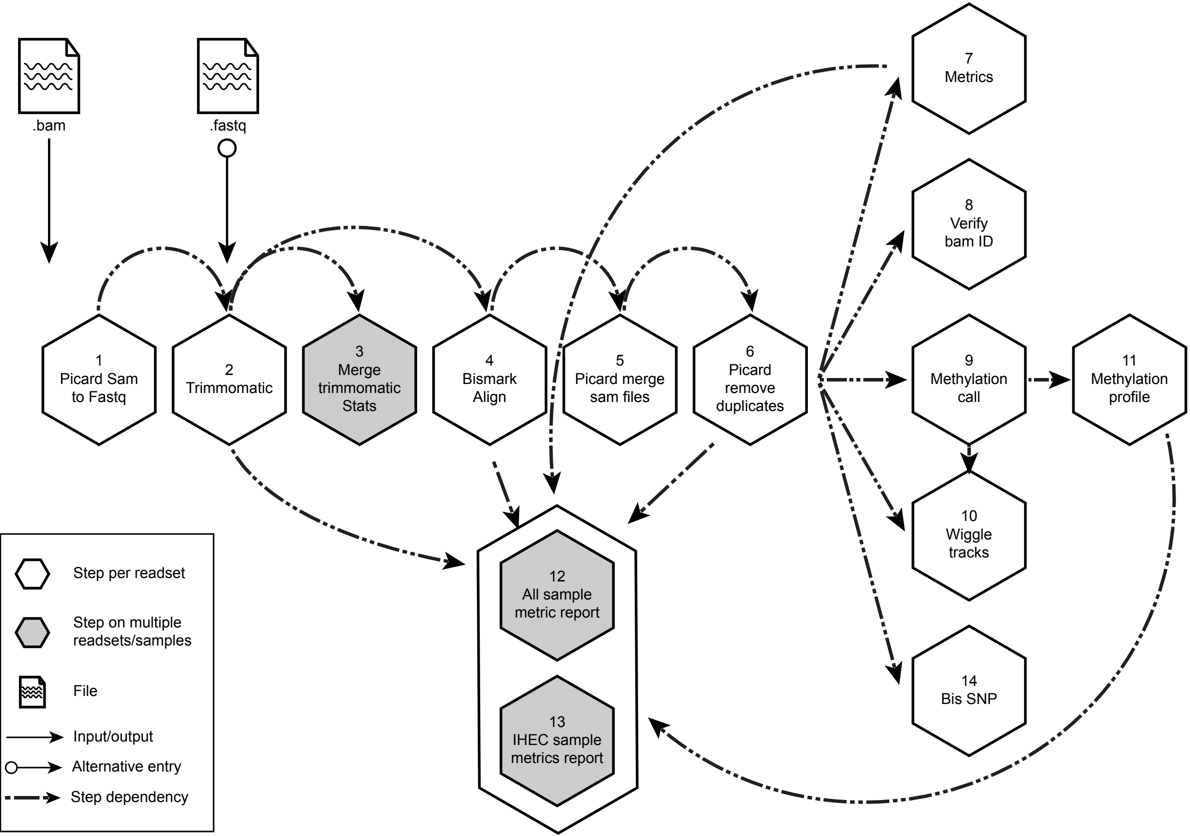


Figure S11

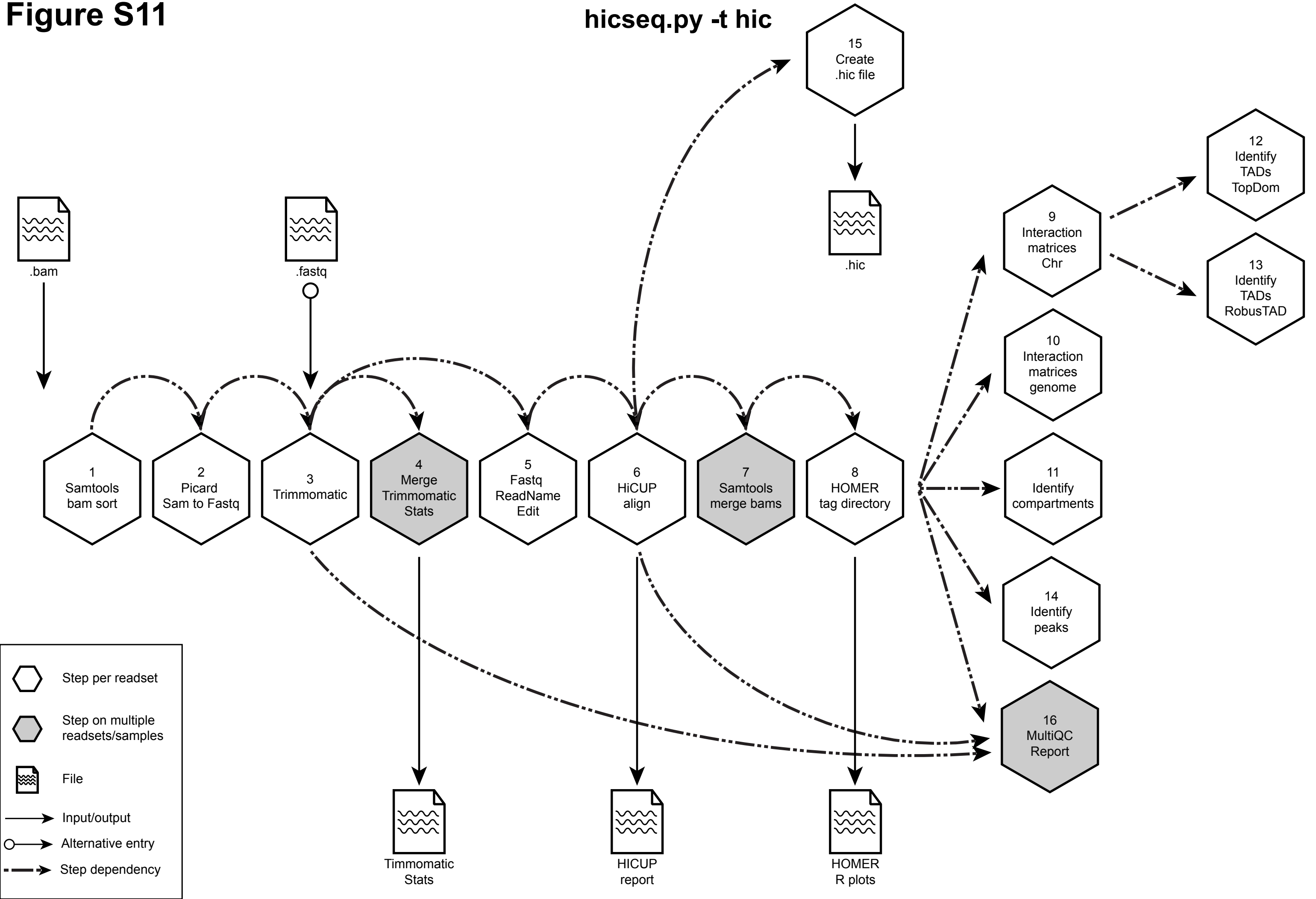

hicseq.py -t hic
.bam
.fastq
1 Samtools bam sort
2 Picard Sam to Fastq
3 Trimmomatic
4 Merge Trimmomatic Stats
5 Fastq ReadName Edit
6 HiCUP align
7 Samtools merge bams
8 HOMER tag directory
9 Interaction matrices Chr
10 Interaction matrices genome
11 Identify compartments
12 Identify TADs TopDom
13 Identify TADs RobusTAD
14 Identify peaks
15 Create .hic file
16 MultiQC Report
.hic
Timmomatic Stats
HICUP report
HOMER R plots
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S12

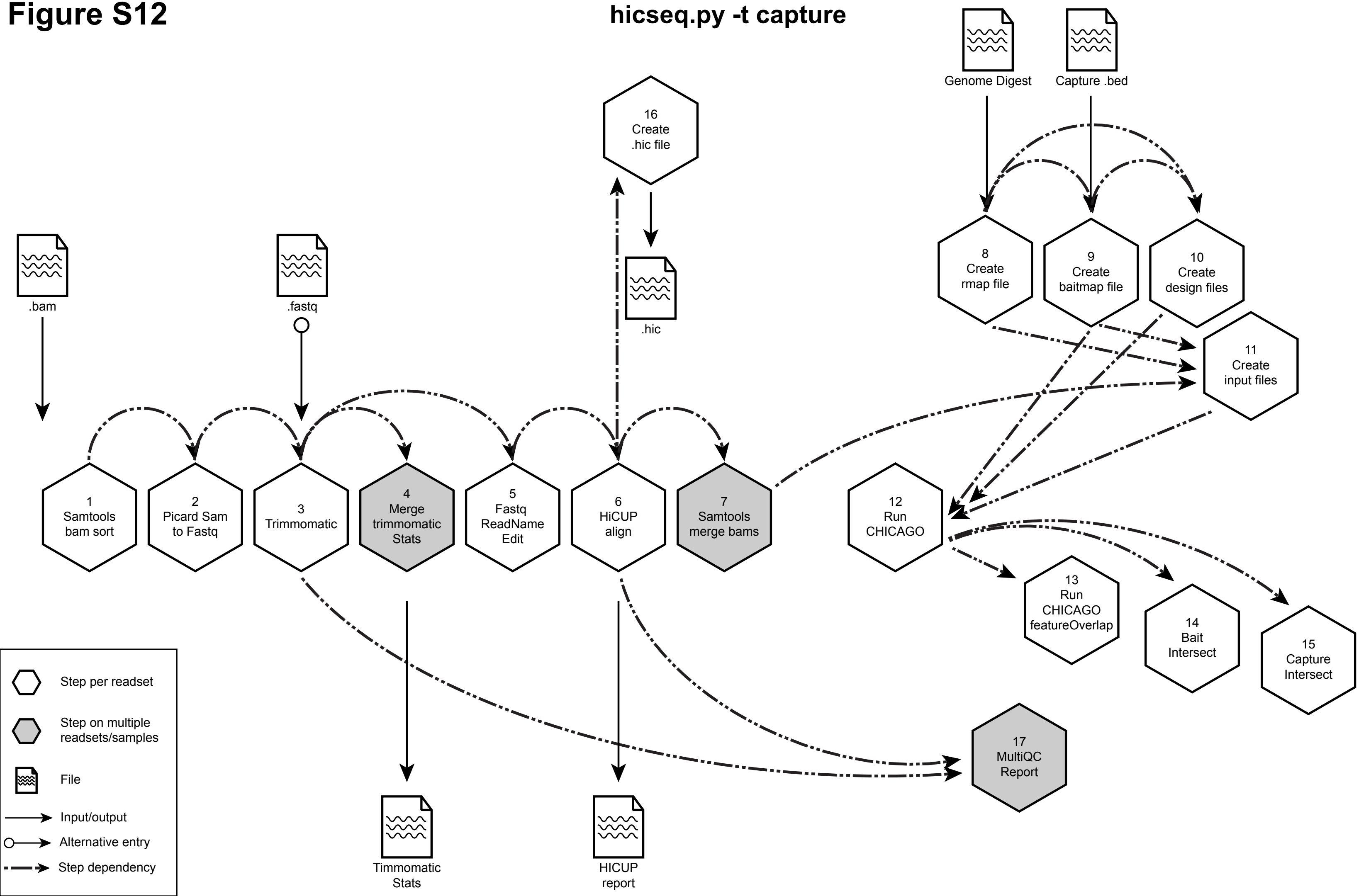

hicseq.py -t capture
Genome Digest
Capture .bed
16 Create .hic file
.hic
8 Create rmap file
9 Create baitmap file
10 Create design files
11 Create input files
.bam
.fastq
1 Samtools bam sort
2 Picard Sam to Fastq
3 Trimmomatic
4 Merge trimmomatic Stats
5 Fastq ReadName Edit
6 HiCUP align
7 Samtools merge bams
12 Run CHICAGO
13 Run CHICAGO featureOverlap
14 Bait Intersect
15 Capture Intersect
17 MultiQC Report
Timmomatic Stats
HICUP report
Step per readset
Step on multiple readsets/samples
File
Input/output
Alternative entry
Step dependency

Figure S13

ampliconseq.py

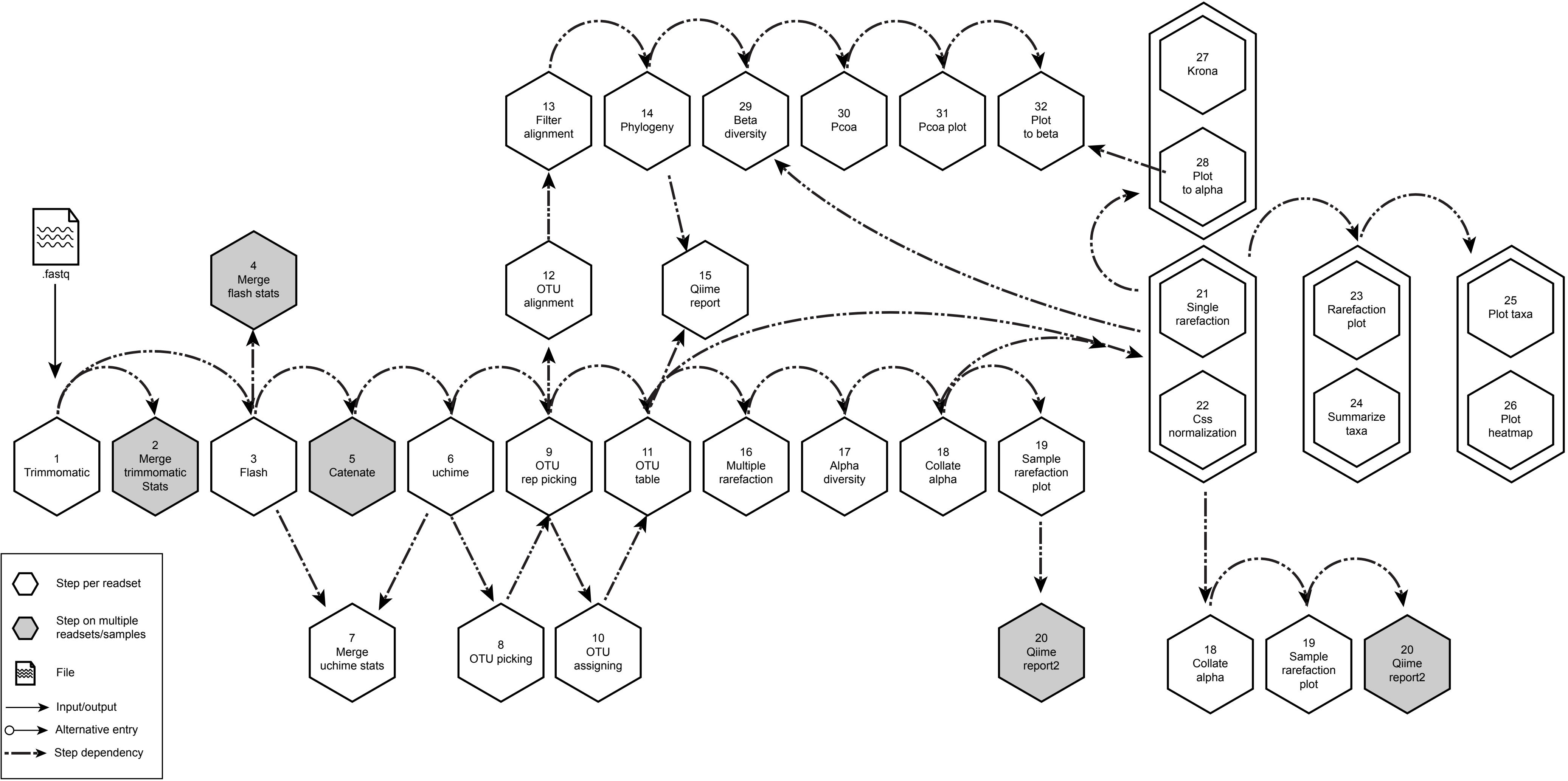


Figure S14

pacbio_assembly.py