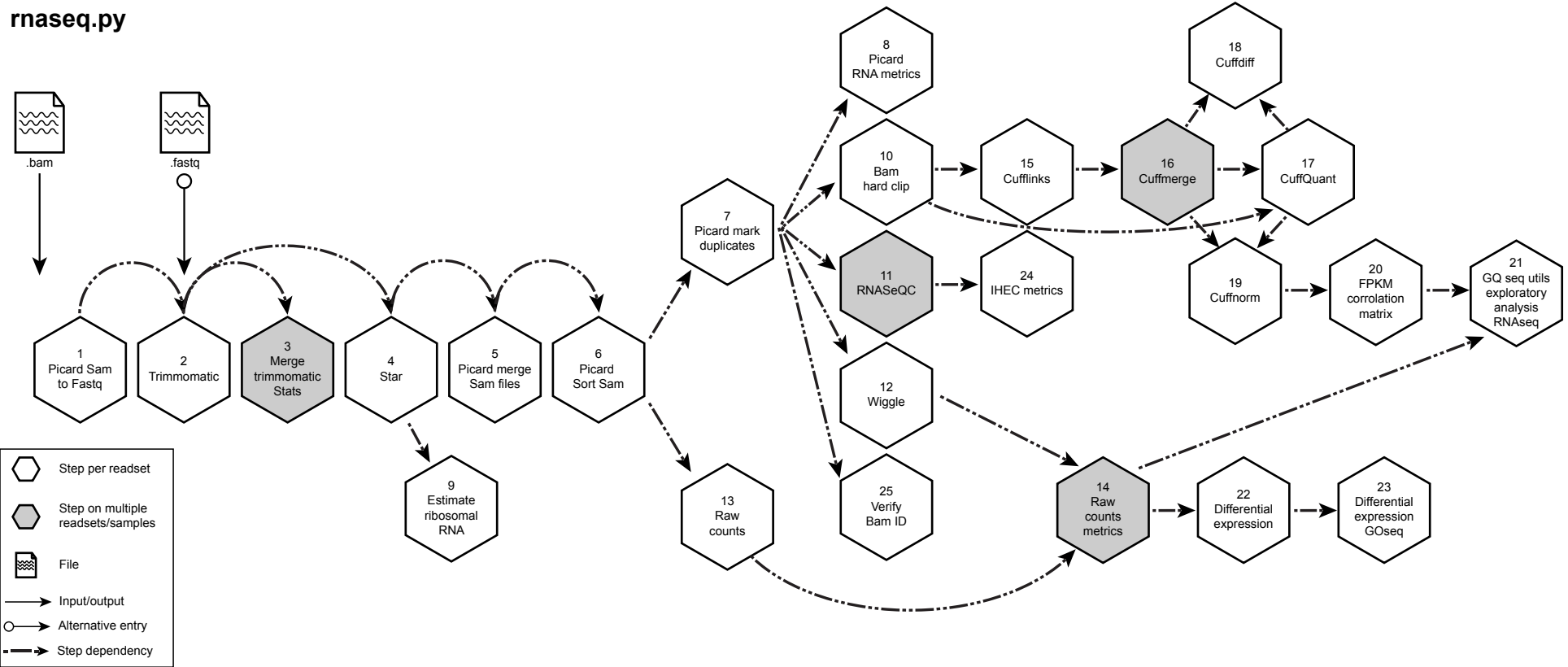
rnaseq.py


.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