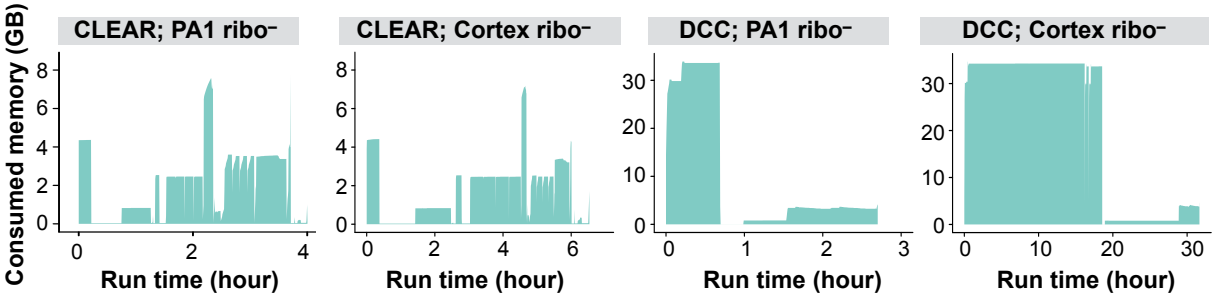
A

Tool	Sample	Read type	No. of reads or fragments	Elapsed time (hour)	Memory consumption (GB)
CIRCexplorer3 -CLEAR	PA1	single-end	125,735,340	4.0	7.7
	Cortex	paired-end	114,797,948	6.5	7.2
DCC	PA1	single-end	125,735,340	2.7	33.9
	Cortex	paired-end	114,797,948	31.7	34.7

B



C

CLEAR

one command:

```
clear_quant -1 PA1.fq -g hg38.fa -i hisat2_index -j bowtie1_index -G gene.gtf -o out_dir -p 10
```

DCC

multiple steps:

```
STAR  --runThreadN 10\
      --genomeDir star_index
      --genomeLoad NoSharedMemory\
      --readFilesIn PA1.fq\
      --outFileNamePrefix PA1_star\
      --outReadsUnmapped Fastx\
      --outSAMattributes NH  HI  AS  nM  NM  MD  jM  jI  XS\
      --outSJfilterOverhangMin 15  15  15  15\
      --outFilterMultimapNmax 20\
      --outFilterScoreMin 1\
      --outFilterMatchNminOverLread 0.7\
      --outFilterMismatchNmax 999\
      --outFilterMismatchNoverLmax 0.05\
      --alignIntronMin 20\
      --alignIntronMax 1000000\
      --alignMatesGapMax 1000000\
      --alignSJoverhangMin 15\
      --alignSJDBoverhangMin 10\
      --alignSoftClipAtReferenceEnds No\
      --chimSegmentMin 15\
      --chimScoreMin 15\
      --chimScoreSeparation 10\
      --chimJunctionOverhangMin 15\
      --sjdbGTFfile gene.gtf\
      --quantMode GeneCounts\
      --twopassMode Basic\
      --chimOutType Junctions SeparateSAMold
samtools view -bS PA1_starAligned.out.sam > PA1_starAligned.out.bam
samtools sort PA1_starAligned.out.bam > PA1_starAligned.sorted.bam
samtools index PA1_starAligned.sorted.bam
ls | grep bam$ | grep -v mate > bam_files.txt
ls | grep junction$ | grep -v mate > samplesheet
circtools detect @samplesheet -T 10 -N -D -an gene.gtf -F -Nr 1 1 -fg -G -A hg38.fa -B @bam_files.txt
```