[Record] 180609 (Sat) snakemake --cores 12 map

Notebook:	A01工作任務		
Created:	6/9/2018 6:42 PM	**Updated:**	6/10/2018 9:29 AM
Author:	clint		
Tags:	@2018 Duke Data+		

fix the path of picard in map.smk first

run the command

```
(env-py3) clintko@phl-biostats-ub1:/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe$ snakemake --cores 12 map
Building DAG of jobs...
Using shell: /bin/bash
Provided cores: 12
Rules claiming more threads will be scaled down.
Job counts:
        count   jobs
        2       MergeBamAlignment
        2       STAR_align
        2       TagReadWithGeneExon
        2       bam_hist
        2       bead_errors_metrics
        1       map
        1       multiqc_star
        2       plot_knee_plot
        1       plot_yield
        2       sort_sam
        17
```

This message is strange.

```
rule STAR_align:
    input: data/Surface_naph_filtered.fastq.gz, /data/clintko/DropSeq_Lung/GRCm38_v2/STAR_INDEX/SA_49/SA
    output: data/Surface_naph/Aligned.out.bam
    log: data/Surface_naph/Log.final.out
    jobid: 15
    wildcards: sample=Surface_naph
    threads: 12

/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/bpij4ovc.wrapper.py:18: SyntaxWarning: assertion is always true, p
erhaps remove parentheses?
  assert(fq1 is not None, "input-> fq1 is a required input parameter")
/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/bpij4ovc.wrapper.py:23: SyntaxWarning: assertion is always true, p
erhaps remove parentheses?
  assert(len(fq1) == len(fq2), "input-> equal number of files required for fq1 and fq2")
```

after 5~10 min (I think), I have seen it had already move to the next step

```
/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/bpij4ovc.wrapper.py:18: SyntaxWarning: assertion is always true, p
erhaps remove parentheses?
  assert(fq1 is not None, "input-> fq1 is a required input parameter")
/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/bpij4ovc.wrapper.py:23: SyntaxWarning: assertion is always true, p
erhaps remove parentheses?
  assert(len(fq1) == len(fq2), "input-> equal number of files required for fq1 and fq2")
Finished job 15.
1 of 17 steps (6%) done

rule sort_sam:
    input: data/Surface_naph/Aligned.out.bam
    output: data/Surface_naph.Aligned.sorted.bam
    jobid: 37
    wildcards: sample=Surface_naph

[Sat Jun 09 18:57:51 EDT 2018] picard.sam.SortSam INPUT=data/Surface_naph/Aligned.out.bam OUTPUT=data/Surface_naph.Aligned.sorted.bam SORT_ORDER
=queryname TMP_DIR=[/data/clintko/DropSeq_Lung/tmp]      VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEVEL=5 MAX_RECORDS_
N_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 18:57:51 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171-
b11-0ubuntu0.17.10.1-b11; Picard version: 2.10.3-SNAPSHOT
INFO    2018-06-09 18:59:33     SortSam Read    10,000,000 records.  Elapsed time: 00:01:42s.  Time for last 10,000,000:  102s.  Last read posit
ion: 7:109,520,567
```

```
[Sat Jun 09 18:57:51 EDT 2018] picard.sam.SortSam INPUT=data/Surface_naph/Aligned.out.bam OUTPUT=data/Surface_naph.Aligned.sorted.bam SORT_ORDER
=queryname TMP_DIR=[/data/clintko/DropSeq_Lung/tmp]    VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEVEL=5 MAX_RECORDS_I
N_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 18:57:51 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171-
b11-0ubuntu0.17.10.1-b11; Picard version: 2.10.3-SNAPSHOT
INFO    2018-06-09 18:59:33    SortSam Read    10,000,000 records.  Elapsed time: 00:01:42s.  Time for last 10,000,000: 102s.  Last read posit
ion: 7:109,520,567
INFO    2018-06-09 19:01:17    SortSam Read    20,000,000 records.  Elapsed time: 00:03:26s.  Time for last 10,000,000: 104s.  Last read posit
ion: 1:24,615,981
INFO    2018-06-09 19:03:02    SortSam Read    30,000,000 records.  Elapsed time: 00:05:10s.  Time for last 10,000,000: 104s.  Last read posit
ion: 2:84,641,967
INFO    2018-06-09 19:04:46    SortSam Read    40,000,000 records.  Elapsed time: 00:06:55s.  Time for last 10,000,000: 104s.  Last read posit
ion: 1:36,366,119
INFO    2018-06-09 19:06:30    SortSam Read    50,000,000 records.  Elapsed time: 00:08:38s.  Time for last 10,000,000: 103s.  Last read posit
ion: 11:48,805,613
INFO    2018-06-09 19:08:13    SortSam Read    60,000,000 records.  Elapsed time: 00:10:22s.  Time for last 10,000,000: 103s.  Last read posit
ion: 2:32,963,569
INFO    2018-06-09 19:09:57    SortSam Read    70,000,000 records.  Elapsed time: 00:12:06s.  Time for last 10,000,000: 103s.  Last read posit
ion: 17:33,824,342
INFO    2018-06-09 19:11:30    SortSam Finished reading inputs, merging and writing to output now.
INFO    2018-06-09 19:13:01    SortSam Wrote    10,000,000 records from a sorting collection.  Elapsed time: 00:15:10s.  Time for last 10,000,0
00:   89s.  Last read position: 7:45,122,453
INFO    2018-06-09 19:15:00    SortSam Wrote    20,000,000 records from a sorting collection.  Elapsed time: 00:17:08s.  Time for last 10,000,0
00:  118s.  Last read position: 7:90,441,976
INFO    2018-06-09 19:16:58    SortSam Wrote    30,000,000 records from a sorting collection.  Elapsed time: 00:19:06s.  Time for last 10,000,0
00:  118s.  Last read position: 9:25,101,348
INFO    2018-06-09 19:18:43    SortSam Wrote    40,000,000 records from a sorting collection.  Elapsed time: 00:20:52s.  Time for last 10,000,0
00:  105s.  Last read position: 4:117,967,849
INFO    2018-06-09 19:20:39    SortSam Wrote    50,000,000 records from a sorting collection.  Elapsed time: 00:22:48s.  Time for last 10,000,0
00:  116s.  Last read position: 3:37,715,039
INFO    2018-06-09 19:22:35    SortSam Wrote    60,000,000 records from a sorting collection.  Elapsed time: 00:24:44s.  Time for last 10,000,0
00:  116s.  Last read position: MT:6,755
INFO    2018-06-09 19:24:17    SortSam Wrote    70,000,000 records from a sorting collection.  Elapsed time: 00:26:26s.  Time for last 10,000,0
00:  101s.  Last read position: 14:49,713,271
[Sat Jun 09 19:26:04 EDT 2018] picard.sam.SortSam done. Elapsed time: 28.23 minutes.
Runtime.totalMemory()=4422893568
Removing temporary output file data/Surface_naph/Aligned.out.bam.
Finished job 37.
2 of 17 steps (12%) done
```

```
rule MergeBamAlignment:
    input: data/Surface_naph_trimmed_unmapped.bam, data/Surface_naph.Aligned.sorted.bam, /data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.dict
    output: data/Surface_naph.Aligned.merged.bam
    jobid: 30
    wildcards: sample=Surface_naph

[Sat Jun 09 19:26:06 EDT 2018] picard.sam.MergeBamAlignment UNMAPPED_BAM=data/Surface_naph_trimmed_unmapped.bam ALIGNED_BAM=[data/Surface_naph.A
ligned.sorted.bam] OUTPUT=data/Surface_naph.Aligned.merged.bam REFERENCE_SEQUENCE=/data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.fasta PAIRED_RUN=f
alse INCLUDE_SECONDARY_ALIGNMENTS=false    CLIP_ADAPTERS=true IS_BISULFITE_SEQUENCE=false ALIGNED_READS_ONLY=false MAX_INSERTIONS_OR_DELETIONS=1
 ATTRIBUTES_TO_REVERSE=[OQ, U2] ATTRIBUTES_TO_REVERSE_COMPLEMENT=[E2, SQ] READ1_TRIM=0 READ2_TRIM=0 ALIGNER_PROPER_PAIR_FLAGS=false SORT_ORDER=c
oordinate PRIMARY_ALIGNMENT_STRATEGY=BestMapq CLIP_OVERLAPPING_READS=true ADD_MATE_CIGAR=true UNMAP_CONTAMINANT_READS=false MIN_UNCLIPPED_BASES=
32 MATCHING_DICTIONARY_TAGS=[M5, LN] UNMAPPED_READ_STRATEGY=DO_NOT_CHANGE VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LE
VEL=5 MAX_RECORDS_IN_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 19:26:06 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171-
b11-0ubuntu0.17.10.1-b11; Picard version: 2.10.3-SNAPSHOT
INFO    2018-06-09 19:26:06    SamAlignmentMerger    Processing SAM file(s): [data/Surface_naph.Aligned.sorted.bam]
INFO    2018-06-09 19:26:25    AbstractAlignmentMerger Merged    1,000,000 records.  Elapsed time: 00:00:18s.  Time for last 1,000,000:   18s.
  Last read position: 11:96,953,694
INFO    2018-06-09 19:26:43    AbstractAlignmentMerger Merged    2,000,000 records.  Elapsed time: 00:00:37s.  Time for last 1,000,000:   18s.
  Last read position: 9:62,026,464
INFO    2018-06-09 19:27:06    AbstractAlignmentMerger Merged    3,000,000 records.  Elapsed time: 00:01:00s.  Time for last 1,000,000:   23s.
  Last read position: 7:27,133,572
INFO    2018-06-09 19:27:23    AbstractAlignmentMerger Merged    4,000,000 records.  Elapsed time: 00:01:17s.  Time for last 1,000,000:   17s.
  Last read position: 11:100,203,296
INFO    2018-06-09 19:27:46    AbstractAlignmentMerger Merged    5,000,000 records.  Elapsed time: 00:01:39s.  Time for last 1,000,000:   22s.
  Last read position: 6:66,930,244
INFO    2018-06-09 19:28:02    AbstractAlignmentMerger Merged    6,000,000 records.  Elapsed time: 00:01:56s.  Time for last 1,000,000:   16s.
  Last read position: 19:9,085,226
INFO    2018-06-09 19:28:19    AbstractAlignmentMerger Merged    7,000,000 records.  Elapsed time: 00:02:13s.  Time for last 1,000,000:   16s.
  Last read position: 2:37,836,448
INFO    2018-06-09 19:28:43    AbstractAlignmentMerger Merged    8,000,000 records.  Elapsed time: 00:02:36s.  Time for last 1,000,000:   23s.
  Last read position: 13:21,833,297
INFO    2018-06-09 19:28:59    AbstractAlignmentMerger Merged    9,000,000 records.  Elapsed time: 00:02:53s.  Time for last 1,000,000:   16s.
  Last read position: 10:120,224,719
INFO    2018-06-09 19:29:17    AbstractAlignmentMerger Merged    10,000,000 records.  Elapsed time: 00:03:10s.  Time for last 1,000,000:   17s.
```

```
Time for last 10,000,000:   124s.  Last read position: 10:63,022,740
INFO    2018-06-09 19:51:20     AbstractAlignmentMerger Written in coordinate order to output     40,000,000 records.  Elapsed time: 00:08:09s.
Time for last 10,000,000:   124s.  Last read position: 14:51,105,741
INFO    2018-06-09 19:53:25     AbstractAlignmentMerger Written in coordinate order to output     50,000,000 records.  Elapsed time: 00:10:13s.
Time for last 10,000,000:   124s.  Last read position: 19:10,502,675
INFO    2018-06-09 19:55:29     AbstractAlignmentMerger Written in coordinate order to output     60,000,000 records.  Elapsed time: 00:12:17s.
Time for last 10,000,000:   124s.  Last read position: */*
INFO    2018-06-09 19:56:17     AbstractAlignmentMerger Wrote 78586987 alignment records and 10204928 unmapped reads.
[Sat Jun 09 19:56:17 EDT 2018] picard.sam.MergeBamAlignment done. Elapsed time: 30.19 minutes.
Runtime.totalMemory()=2622488576
Removing temporary output file data/Surface_naph.Aligned.sorted.bam.
Finished job 30.
3 of 17 steps (18%) done

rule TagReadWithGeneExon:
    input: data/Surface_naph.Aligned.merged.bam, /data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.91.refFlat
    output: data/Surface_naph_gene_exon_tagged.bam
    jobid: 20
    wildcards: sample=Surface_naph

+ java -Xmx16g -Djava.io.tmpdir=/data/clintko/DropSeq_Lung/tmp -jar /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/jar/dropseq.jar TagReadWithG
neExon INPUT=data/Surface_naph.Aligned.merged.bam OUTPUT=data/Surface_naph_gene_exon_tagged.bam ANNOTATIONS_FILE=/data/clintko/DropSeq_Lung/GRC
38_v2/GRCm38.91.refFlat TAG=GE CREATE_INDEX=true
[Sat Jun 09 19:56:18 EDT 2018] org.broadinstitute.dropseqrna.metrics.TagReadWithGeneExon INPUT=data/Surface_naph.Aligned.merged.bam OUTPUT=data/
Surface_naph_gene_exon_tagged.bam TAG=GE ANNOTATIONS_FILE=/data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.91.refFlat CREATE_INDEX=true       STRAND_TA
=GS FUNCTION_TAG=XF USE_STRAND_INFO=true ALLOW_MULTI_GENE_READS=false VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEVEL=
5 MAX_RECORDS_IN_RAM=500000 CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 19:56:18 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171-
b11-0ubuntu0.17.10.1-b11; Picard version: 1.13(7bed8f4_1513008033)
INFO    2018-06-09 19:56:29     TagReadWithGeneExon     Processed        1,000,000 records.  Elapsed time: 00:00:10s.  Time for last 1,000,000:
9s.  Last read position: 1:24,614,113
INFO    2018-06-09 19:56:39     TagReadWithGeneExon     Processed        2,000,000 records.  Elapsed time: 00:00:20s.  Time for last 1,000,000:
0s.  Last read position: 1:55,080,243
INFO    2018-06-09 19:56:50     TagReadWithGeneExon     Processed        3,000,000 records.  Elapsed time: 00:00:32s.  Time for last 1,000,000:
1s.  Last read position: 1:133,157,943
INFO    2018-06-09 19:57:14     TagReadWithGeneExon     Processed        4,000,000 records.  Elapsed time: 00:00:56s.  Time for last 1,000,000:
4s.  Last read position: 2:5,882,854
INFO    2018-06-09 19:57:33     TagReadWithGeneExon     Processed        5,000,000 records.  Elapsed time: 00:01:14s.  Time for last 1,000,000:
8s.  Last read position: 2:61,800,213
INFO    2018-06-09 19:57:44     TagReadWithGeneExon     Processed        6,000,000 records.  Elapsed time: 00:01:26s.  Time for last 1,000,000:
1s.  Last read position: 2:152,736,743
INFO    2018-06-09 19:58:04     TagReadWithGeneExon     Processed        7,000,000 records.  Elapsed time: 00:01:45s.  Time for last 1,000,000:
9s.  Last read position: 2:157,104,875
INFO    2018-06-09 19:58:14     TagReadWithGeneExon     Processed        8,000,000 records.  Elapsed time: 00:01:56s.  Time for last 1,000,000:
```

```
6s.  Last read position: */*
INFO    2018-06-09 20:10:55     TagReadWithGeneExon     Processed        60,000,000 records.  Elapsed time: 00:14:37s.  Time for last 1,000,000:
8s.  Last read position: */*
INFO    2018-06-09 20:11:02     TagReadWithGeneExon     Processed        61,000,000 records.  Elapsed time: 00:14:43s.  Time for last 1,000,000:
6s.  Last read position: */*
INFO    2018-06-09 20:11:08     TagReadWithGeneExon     Processed        62,000,000 records.  Elapsed time: 00:14:50s.  Time for last 1,000,000:
6s.  Last read position: */*
INFO    2018-06-09 20:11:28     TagReadWithGeneExon     Processed        63,000,000 records.  Elapsed time: 00:15:10s.  Time for last 1,000,000:
0s.  Last read position: */*
INFO    2018-06-09 20:11:36     TagReadWithGeneExon     TOTAL READS [53400989] CORRECT_STRAND [51736108]  WRONG_STRAND [677113] AMBIGUOUS_STRAND
_FIXED [1561360] AMBIGUOUS REJECTED READS [987768]
[Sat Jun 09 20:11:36 EDT 2018] org.broadinstitute.dropseqrna.metrics.TagReadWithGeneExon done. Elapsed time: 15.30 minutes.
Runtime.totalMemory()=1485307904
Removing temporary output file data/Surface_naph.Aligned.merged.bam.
Finished job 20.
4 of 17 steps (24%) done

rule bead_errors_metrics:
    input: data/Surface_naph_gene_exon_tagged.bam
    output: data/Surface_naph_final.bam
    jobid: 7
    wildcards: sample=Surface_naph

+ java -Xmx16g -Djava.io.tmpdir=/data/clintko/DropSeq_Lung/tmp -jar /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/jar/dropseq.jar DetectBeadSyn
thesisErrors INPUT=data/Surface_naph_gene_exon_tagged.bam OUTPUT=data/Surface_naph_final.bam OUTPUT_STATS=logs/Surface_naph_synthesis_stats.txt
SUMMARY=logs/Surface_naph_synthesis_stats_summary.txt NUM_BARCODES=4000 PRIMER_SEQUENCE=AATGATACGGCGACCACCGAGATCTACACGCCTGTCCGCGGAAGCAGTGGTATCAA
CGCAGAGTAC
[Sat Jun 09 20:11:38 EDT 2018] org.broadinstitute.dropseqrna.beadsynthesis.DetectBeadSynthesisErrors OUTPUT_STATS=logs/Surface_naph_synthesis_st
ats.txt INPUT=[data/Surface_naph_gene_exon_tagged.bam] SUMMARY=logs/Surface_naph_synthesis_stats_summary.txt OUTPUT=data/Surface_naph_final.bam
PRIMER_SEQUENCE=AATGATACGGCGACCACCGAGATCTACACGCCTGTCCGCGGGAAGCAGTGGTATCAACGCAGAGTAC NUM_BARCODES=4000       EDIT_DISTANCE=0 CELL_BARCODE_TAG=XC MOLE
CULAR_BARCODE_TAG=XM GENE_EXON_TAG=GE STRAND_TAG=GS READ_MQ=10 MIN_UMIS_PER_CELL=25 MAX_NUM_ERRORS=1 VERBOSITY=INFO QUIET=false VALIDATION_STRIN
GENCY=STRICT COMPRESSION_LEVEL=5 MAX_RECORDS_IN_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 20:11:38 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171-
b11-0ubuntu0.17.10.1-b11; Picard version: 1.13(7bed8f4_1513008033)
INFO    2018-06-09 20:11:38     AbstractDetectBeadSynthesisErrors       Gathering barcodes for the top [4000] cells
WARNING: BAM index file /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/data/Surface_naph_gene_exon_tagged.bai is older than BAM /dat
a/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/data/Surface_naph_gene_exon_tagged.bam
INFO    2018-06-09 20:11:56     BAMTagHistogram Processed       10,000,000 records.  Elapsed time: 00:00:18s.  Time for last 10,000,000:   18s.  La
st read position: 3:135,465,874
INFO    2018-06-09 20:12:16     BAMTagHistogram Processed       20,000,000 records.  Elapsed time: 00:00:37s.  Time for last 10,000,000:   19s.  La
st read position: 7:45,122,513
INFO    2018-06-09 20:12:35     BAMTagHistogram Processed       30,000,000 records.  Elapsed time: 00:00:56s.  Time for last 10,000,000:   19s.  La
st read position: 10:63,022,740
INFO    2018-06-09 20:12:54     BAMTagHistogram Processed       40,000,000 records.  Elapsed time: 00:01:15s.  Time for last 10,000,000:   19s.  La
```

there are some strange warning

```
WARNING: BAM index file /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/data/Surface_naph_gene_exon_tagged.bai is older than BAM /dat
a/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/data/Surface_naph_gene_exon_tagged.bam
INFO    2018-06-09 20:13:47     UMIIterator     Processed        1,000,000 records.  Elapsed time: 00:00:13s.  Time for last 1,000,000:   13s.  Las
t read position: 1:161,241,131
```

Besides those weird warnings, it seems that everything is ok

```
000:     6s.   Last read position: X:106,019,664
INFO    2018-06-09 20:32:16    DetectBeadSynthesisErrors    Processed    53,000,000 records.   Elapsed time: 00:09:28s.   Time for last 1,000,
000:    18s.   Last read position: MT:11,265
INFO    2018-06-09 20:32:22    DetectBeadSynthesisErrors    Processed    54,000,000 records.   Elapsed time: 00:09:34s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:32:29    DetectBeadSynthesisErrors    Processed    55,000,000 records.   Elapsed time: 00:09:41s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:32:48    DetectBeadSynthesisErrors    Processed    56,000,000 records.   Elapsed time: 00:10:00s.   Time for last 1,000,
000:    19s.   Last read position: */*
INFO    2018-06-09 20:32:54    DetectBeadSynthesisErrors    Processed    57,000,000 records.   Elapsed time: 00:10:07s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:33:01    DetectBeadSynthesisErrors    Processed    58,000,000 records.   Elapsed time: 00:10:13s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:33:21    DetectBeadSynthesisErrors    Processed    59,000,000 records.   Elapsed time: 00:10:33s.   Time for last 1,000,
000:    19s.   Last read position: */*
INFO    2018-06-09 20:33:27    DetectBeadSynthesisErrors    Processed    60,000,000 records.   Elapsed time: 00:10:39s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:33:47    DetectBeadSynthesisErrors    Processed    61,000,000 records.   Elapsed time: 00:10:59s.   Time for last 1,000,
000:    19s.   Last read position: */*
INFO    2018-06-09 20:33:53    DetectBeadSynthesisErrors    Processed    62,000,000 records.   Elapsed time: 00:11:06s.   Time for last 1,000,
000:     6s.   Last read position: */*
INFO    2018-06-09 20:34:00    DetectBeadSynthesisErrors    Processed    63,000,000 records.   Elapsed time: 00:11:12s.   Time for last 1,000,
000:     6s.   Last read position: */*
[Sat Jun 09 20:34:17 EDT 2018] org.broadinstitute.dropseqrna.beadsynthesis.DetectBeadSynthesisErrors done. Elapsed time: 22.66 minutes.
Runtime.totalMemory()=7057965056
Removing temporary output file data/Surface_naph_gene_exon_tagged.bam.
Finished job 7.
5 of 17 steps (29%) done
```

I wonder what this means? it appears at the start of mapping as well

```
rule STAR_align:
    input: data/Gland_homeo_filtered.fastq.gz, /data/clintko/DropSeq_Lung/GRCm38_v2/STAR_INDEX/SA_49/SA
    output: data/Gland_homeo/Aligned.out.bam
    log: data/Gland_homeo/Log.final.out
    jobid: 10
    wildcards: sample=Gland_homeo
    threads: 12

/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/271sfnzw.wrapper.py:18: SyntaxWarning: assertion is always true,
erhaps remove parentheses?
  assert(fq1 is not None, "input-> fq1 is a required input parameter")
/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/271sfnzw.wrapper.py:23: SyntaxWarning: assertion is always true,
erhaps remove parentheses?
  assert(len(fq1) == len(fq2), "input-> equal number of files required for fq1 and fq2")
Finished job 10.
6 of 17 steps (35%) done
```

```
rule bam_hist:
    input: data/Surface_naph_final.bam
    output: logs/Surface_naph_hist_out_cell.txt
    jobid: 4
    wildcards: sample=Surface_naph


rule sort_sam:
    input: data/Gland_homeo/Aligned.out.bam
    output: data/Gland_homeo.Aligned.sorted.bam
    jobid: 35
    wildcards: sample=Gland_homeo
```

```
localrule plot_yield:
    input: logs/Surface_naph_CELL_barcode.txt, logs/Gland_homeo_CELL_barcode.txt, logs/Surface_naph_UMI_barcode.txt, logs/Gland_homeo_UMI_barcod
e.txt, logs/Surface_naph_reads_left.txt, logs/Gland_homeo_reads_left.txt, data/Surface_naph/Log.final.out, data/Gland_homeo/Log.final.out, logs/
Surface_naph_reads_left_trim.txt, logs/Gland_homeo_reads_left_trim.txt
    output: plots/yield.pdf
    jobid: 3

+ java -Xmx16g -Djava.io.tmpdir=/data/clintko/DropSeq_Lung/tmp -jar /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/jar/dropseq.jar BAMTagHistogr
am TAG=XC I=data/Surface_naph_final.bam READ_QUALITY=10 O=logs/Surface_naph_hist_out_cell.txt
```

error occur when requiring multiqc

```
localrule multiqc_star:
    input: data/Surface_naph/Log.final.out, data/Gland_homeo/Log.final.out
    output: reports/star.html
    jobid: 5

[Sat Jun 09 20:42:48 EDT 2018] org.broadinstitute.dropseqrna.metrics.BAMTagHistogram INPUT=data/Surface_naph_final.bam OUTPUT=logs/Surface_naph
hist_out_cell.txt TAG=XC READ_QUALITY=10     FILTER_PCR_DUPLICATES=false VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEV
L=5 MAX_RECORDS_IN_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 20:42:48 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171
b11-0ubuntu0.17.10.1-b11; Picard version: 1.13(7bed8f4_1513008033)
[Sat Jun 09 20:42:48 EDT 2018] picard.sam.SortSam INPUT=data/Gland_homeo/Aligned.out.bam OUTPUT=data/Gland_homeo.Aligned.sorted.bam SORT_ORDER=
ueryname TMP_DIR=[/data/clintko/DropSeq_Lung/tmp]     VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEVEL=5 MAX_RECORDS_IN
RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 20:42:48 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171
b11-0ubuntu0.17.10.1-b11; Picard version: 2.10.3-SNAPSHOT
/bin/bash: multiqc: command not found
Traceback (most recent call last):
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/_u1b9sn0.wrapper.py", line 24, in <module>
    "multiqc"
  File "/local_data/env-py3/lib/python3.6/site-packages/snakemake/shell.py", line 130, in __new__
    raise sp.CalledProcessError(retcode, cmd)
subprocess.CalledProcessError: Command ' set -euo pipefail;  multiqc -m star --force -o reports -n star.html data/Gland_homeo data/Surface_naph
' returned non-zero exit status 127.
    Error in rule multiqc_star:
        jobid: 5
        output: reports/star.html

RuleException:
CalledProcessError in line 62 of /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk:
Command ' set -euo pipefail;  /local_data/env-py3/bin/python3 /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/_u1
9sn0.wrapper.py ' returned non-zero exit status 1.
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk", line 62, in __rule_multiqc_star
  File "/usr/lib/python3.6/concurrent/futures/thread.py", line 56, in run
Loading required package: viridisLite
Warning: Ignoring unknown parameters: binwidth, bins, pad
Warning: Ignoring unknown parameters: binwidth, bins, pad
pdf
  2
Finished job 3.
7 of 17 steps (41%) done
```

This is the first error that appear so far

```
subprocess.CalledProcessError: Command ' set -euo pipefail;  multiqc -m star --force -o reports -n star.html data/Gland_homeo data/Surface_naph
' returned non-zero exit status 127.
    Error in rule multiqc_star:
        jobid: 5
        output: reports/star.html

RuleException:
CalledProcessError in line 62 of /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk:
Command ' set -euo pipefail;  /local_data/env-py3/bin/python3 /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/_u1b
9sn0.wrapper.py ' returned non-zero exit status 1.
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk", line 62, in __rule_multiqc_star
  File "/usr/lib/python3.6/concurrent/futures/thread.py", line 56, in run
```

```
subprocess.CalledProcessError: Command ' set -euo pipefail;  multiqc -m star --force -o reports -n star.html data/Gland_homeo data/Surface_naph
' returned non-zero exit status 127.
    Error in rule multiqc_star:
        jobid: 5
        output: reports/star.html

RuleException:
CalledProcessError in line 62 of /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk:
Command ' set -euo pipefail;  /local_data/env-py3/bin/python3 /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/_u1l
9sn0.wrapper.py ' returned non-zero exit status 1.
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk", line 62, in __rule_multiqc_star
  File "/usr/lib/python3.6/concurrent/futures/thread.py", line 56, in run
Loading required package: viridisLite
Warning: Ignoring unknown parameters: binwidth, bins, pad
Warning: Ignoring unknown parameters: binwidth, bins, pad
pdf
  2
Finished job 3.
7 of 17 steps (41%) done
INFO    2018-06-09 20:43:07    BAMTagHistogram Processed    10,000,000 records.  Elapsed time: 00:00:18s.  Time for last 10,000,000:    18s.  La
st read position: 3:135,466,484
INFO    2018-06-09 20:43:26    BAMTagHistogram Processed    20,000,000 records.  Elapsed time: 00:00:37s.  Time for last 10,000,000:    18s.  La
st read position: 7:45,122,520
INFO    2018-06-09 20:43:44    BAMTagHistogram Processed    30,000,000 records.  Elapsed time: 00:00:55s.  Time for last 10,000,000:    18s.  La
st read position: 10:67,014,984
INFO    2018-06-09 20:44:03    BAMTagHistogram Processed    40,000,000 records.  Elapsed time: 00:01:14s.  Time for last 10,000,000:    18s.  La
st read position: 14:52,088,502
INFO    2018-06-09 20:44:21    BAMTagHistogram Processed    50,000,000 records.  Elapsed time: 00:01:32s.  Time for last 10,000,000:    18s.  La
st read position: 19:11,482,001
INFO    2018-06-09 20:44:26    SortSam Read    10,000,000 records.  Elapsed time: 00:01:38s.  Time for last 10,000,000:    98s.  Last read posi
ion: 17:23,900,655
INFO    2018-06-09 20:44:36    BAMTagHistogram Processed    60,000,000 records.  Elapsed time: 00:01:47s.  Time for last 10,000,000:    15s.  La
st read position: */*
[Sat Jun 09 20:44:41 EDT 2018] org.broadinstitute.dropseqrna.metrics.BAMTagHistogram done. Elapsed time: 1.89 minutes.
Runtime.totalMemory()=2700083200
Finished job 4.
8 of 17 steps (47%) done
INFO    2018-06-09 20:46:06    SortSam Read    20,000,000 records.  Elapsed time: 00:03:17s.  Time for last 10,000,000:    99s.  Last read posi
ion: 17:23,919,328
INFO    2018-06-09 20:47:46    SortSam Read    30,000,000 records.  Elapsed time: 00:04:57s.  Time for last 10,000,000:    99s.  Last read posi
ion: 17:23,882,564
INFO    2018-06-09 20:49:26    SortSam Read    40,000,000 records.  Elapsed time: 00:06:38s.  Time for last 10,000,000:    100s.  Last read posi
ion: 4:137,395,582
INFO    2018-06-09 20:51:06    SortSam Read    50,000,000 records.  Elapsed time: 00:08:17s.  Time for last 10,000,000:    99s.  Last read posi
```

it turns out to run the pipeline, at least 20 GB memory is required. Below is the screenshot of command "top"

```
60243 clintko    20   0 20.310g 6.069g  20508 S 100.0  4.8  10:47.10 java
 1647 root      -51   0      0      0      0 S   6.0  0.0 308:47.26 irq/75-nvidia
 1670 root      -51   0      0      0      0 S   5.0  0.0 237:33.18 irq/90-nvidia
60444 clintko    20   0  46736   4272   3296 R   0.7  0.0   0:00.07 top
 2392 gdm        20   0 614704  24388  18740 S   0.3  0.0   1:44.14 gsd-color
42192 wxiaoaa    20   0 1954088 236140 132516 S   0.3  0.2   1:11.52 Web Content
60400 root       20   0      0      0      0 S   0.3  0.0   0:00.15 kworker/12:1
    1 root       20   0 220628   8236   5572 S   0.0  0.0   0:06.36 systemd
```

This is strange. Why does it stop? The message mention the process stopped b/c of one error. The only error occurred is caused by multiqc, which help generating html file. I don't think this will cause problems during the preprocessing.


```
Finished job 4.
8 of 17 steps (47%) done
INFO    2018-06-09 20:46:06    SortSam Read    20,000,000 records.  Elapsed time: 00:03:17s.  Time for last 10,000,000:   99s.  Last read posi
ion: 17:23,919,328
INFO    2018-06-09 20:47:46    SortSam Read    30,000,000 records.  Elapsed time: 00:04:57s.  Time for last 10,000,000:   99s.  Last read posi
ion: 17:23,882,564
INFO    2018-06-09 20:49:26    SortSam Read    40,000,000 records.  Elapsed time: 00:06:38s.  Time for last 10,000,000:  100s.  Last read posi
ion: 4:137,395,582
INFO    2018-06-09 20:51:06    SortSam Read    50,000,000 records.  Elapsed time: 00:08:17s.  Time for last 10,000,000:   99s.  Last read posi
ion: 9:25,101,145
INFO    2018-06-09 20:52:45    SortSam Read    60,000,000 records.  Elapsed time: 00:09:57s.  Time for last 10,000,000:   99s.  Last read posi
ion: 19:33,976,621
INFO    2018-06-09 20:54:25    SortSam Read    70,000,000 records.  Elapsed time: 00:11:36s.  Time for last 10,000,000:   99s.  Last read posi
ion: 17:23,919,170
INFO    2018-06-09 20:56:05    SortSam Read    80,000,000 records.  Elapsed time: 00:13:16s.  Time for last 10,000,000:  100s.  Last read posi
ion: 17:23,882,650
INFO    2018-06-09 20:56:19    SortSam Finished reading inputs, merging and writing to output now.
INFO    2018-06-09 20:57:47    SortSam Wrote   10,000,000 records from a sorting collection.  Elapsed time: 00:14:58s.  Time for last 10,000,
00:   86s.  Last read position: 17:23,882,548
INFO    2018-06-09 20:59:42    SortSam Wrote   20,000,000 records from a sorting collection.  Elapsed time: 00:16:53s.  Time for last 10,000,
00:  115s.  Last read position: 7:90,441,976
INFO    2018-06-09 21:01:26    SortSam Wrote   30,000,000 records from a sorting collection.  Elapsed time: 00:18:37s.  Time for last 10,000,
00:  103s.  Last read position: 11:120,729,738
INFO    2018-06-09 21:03:01    SortSam Wrote   40,000,000 records from a sorting collection.  Elapsed time: 00:20:12s.  Time for last 10,000,
00:   95s.  Last read position: 7:90,441,976
INFO    2018-06-09 21:04:54    SortSam Wrote   50,000,000 records from a sorting collection.  Elapsed time: 00:22:06s.  Time for last 10,000,
00:  113s.  Last read position: 17:23,882,582
INFO    2018-06-09 21:06:34    SortSam Wrote   60,000,000 records from a sorting collection.  Elapsed time: 00:23:45s.  Time for last 10,000,
00:   99s.  Last read position: 19:33,976,491
INFO    2018-06-09 21:08:26    SortSam Wrote   70,000,000 records from a sorting collection.  Elapsed time: 00:25:38s.  Time for last 10,000,
00:  112s.  Last read position: 5:146,835,574
INFO    2018-06-09 21:10:04    SortSam Wrote   80,000,000 records from a sorting collection.  Elapsed time: 00:27:16s.  Time for last 10,000,
00:   98s.  Last read position: 17:23,882,548
[Sat Jun 09 21:10:23 EDT 2018] picard.sam.SortSam done. Elapsed time: 27.58 minutes.
Runtime.totalMemory()=4827119616
Removing temporary output file data/Gland_homeo/Aligned.out.bam.
Finished job 35.
9 of 17 steps (53%) done
Shutting down, this might take some time.
Exiting because a job execution failed. Look above for error message
Complete log: /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/log/2018-06-09T184909.666092.snakemake.log
(env-py3) clintko@phl-biostats-ub1:/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe$
```

I rerun the snakemake mapping. Notice that the job counts are different than the first time I executed. I wondered why?


```
(env-py3) clintko@phl-biostats-ub1:/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe$ snakemake --cores 12 map
Building DAG of jobs...
Using shell: /bin/bash
Provided cores: 12
Rules claiming more threads will be scaled down.
Job counts:
        count   jobs
        1       MergeBamAlignment
        1       TagReadWithGeneExon
        1       bam_hist
        1       bead_errors_metrics
        1       map
        1       multiqc_star
        2       plot_knee_plot
        8

localrule multiqc_star:
    input: data/Surface_naph/Log.final.out, data/Gland_homeo/Log.final.out
    output: reports/star.html
    jobid: 6

localrule plot_knee_plot:
    input: logs/Surface_naph_hist_out_cell.txt
    output: plots/Surface_naph_knee_plot.pdf
    jobid: 8
    wildcards: sample=Surface_naph

rule MergeBamAlignment:
    input: data/Gland_homeo_trimmed_unmapped.bam, data/Gland_homeo.Aligned.sorted.bam, /data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.dict
    output: data/Gland_homeo.Aligned.merged.bam
    jobid: 23
    wildcards: sample=Gland_homeo
```

it encounter the error very quick

```
rule MergeBamAlignment:
    input: data/Gland_homeo_trimmed_unmapped.bam, data/Gland_homeo.Aligned.sorted.bam, /data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.dict
    output: data/Gland_homeo.Aligned.merged.bam
    jobid: 23
    wildcards: sample=Gland_homeo

[Sat Jun 09 21:19:36 EDT 2018] picard.sam.MergeBamAlignment UNMAPPED_BAM=data/Gland_homeo_trimmed_unmapped.bam ALIGNED_BAM=[data/Gland_homeo.Al
gned.sorted.bam] OUTPUT=data/Gland_homeo.Aligned.merged.bam REFERENCE_SEQUENCE=/data/clintko/DropSeq_Lung/GRCm38_v2/GRCm38.fasta PAIRED_RUN=fal
e INCLUDE_SECONDARY_ALIGNMENTS=false    CLIP_ADAPTERS=true IS_BISULFITE_SEQUENCE=false ALIGNED_READS_ONLY=false MAX_INSERTIONS_OR_DELETIONS=1 A
TRIBUTES_TO_REVERSE=[OQ, U2] ATTRIBUTES_TO_REVERSE_COMPLEMENT=[E2, SQ] READ1_TRIM=0 READ2_TRIM=0 ALIGNER_PROPER_PAIR_FLAGS=false SORT_ORDER=coo
dinate PRIMARY_ALIGNMENT_STRATEGY=BestMapq CLIP_OVERLAPPING_READS=true ADD_MATE_CIGAR=true UNMAP_CONTAMINANT_READS=false MIN_UNCLIPPED_BASES=32
MATCHING_DICTIONARY_TAGS=[M5, LN] UNMAPPED_READ_STRATEGY=DO_NOT_CHANGE VERBOSITY=INFO QUIET=false VALIDATION_STRINGENCY=STRICT COMPRESSION_LEVE
=5 MAX_RECORDS_IN_RAM=500000 CREATE_INDEX=false CREATE_MD5_FILE=false GA4GH_CLIENT_SECRETS=client_secrets.json
[Sat Jun 09 21:19:36 EDT 2018] Executing as clintko@phl-biostats-ub1 on Linux 4.13.0-43-generic amd64; OpenJDK 64-Bit Server VM 1.8.0_171-8u171
b11-0ubuntu0.17.10.1-b11; Picard version: 2.10.3-SNAPSHOT
/bin/bash: multiqc: command not found
Traceback (most recent call last):
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/ln8qpr6b.wrapper.py", line 24, in <module>
    "multiqc"
  File "/local_data/env-py3/lib/python3.6/site-packages/snakemake/shell.py", line 130, in __new__
    raise sp.CalledProcessError(retcode, cmd)
subprocess.CalledProcessError: Command ' set -euo pipefail;  multiqc -m star --force -o reports -n star.html data/Surface_naph data/Gland_homeo
' returned non-zero exit status 127.
Error in rule multiqc_star:
    jobid: 6
    output: reports/star.html

RuleException:
CalledProcessError in line 62 of /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk:
Command ' set -euo pipefail;  /local_data/env-py3/bin/python3 /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/scripts/ln8
pr6b.wrapper.py ' returned non-zero exit status 1.
  File "/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/rules/map.smk", line 62, in __rule_multiqc_star
  File "/usr/lib/python3.6/concurrent/futures/thread.py", line 56, in run
INFO    2018-06-09 21:19:36    SamAlignmentMerger    Processing SAM file(s): [data/Gland_homeo.Aligned.sorted.bam]
Warning message:
Removed 195968 rows containing missing values (geom_point).
Finished job 8.
1 of 8 steps (12%) done
```

It reaches to the end quickly (I mean it only reach to the 2 of 8 steps

```
INFO    2018-06-09 21:37:32    AbstractAlignmentMerger Merged    58,000,000 records.  Elapsed time: 00:17:55s.  Time for last 1,000,000:    16s
  Last read position: 17:23,919,325
INFO    2018-06-09 21:39:37    AbstractAlignmentMerger Written in coordinate order to output    10,000,000 records.  Elapsed time: 00:01:59s.
Time for last 10,000,000:  118s.  Last read position: 5:115,345,746
INFO    2018-06-09 21:41:44    AbstractAlignmentMerger Written in coordinate order to output    20,000,000 records.  Elapsed time: 00:04:05s.
Time for last 10,000,000:  126s.  Last read position: 9:89,699,346
INFO    2018-06-09 21:43:47    AbstractAlignmentMerger Written in coordinate order to output    30,000,000 records.  Elapsed time: 00:06:09s.
Time for last 10,000,000:  123s.  Last read position: 12:55,490,460
INFO    2018-06-09 21:46:02    AbstractAlignmentMerger Written in coordinate order to output    40,000,000 records.  Elapsed time: 00:08:24s.
Time for last 10,000,000:  135s.  Last read position: 17:23,882,624
INFO    2018-06-09 21:47:50    AbstractAlignmentMerger Written in coordinate order to output    50,000,000 records.  Elapsed time: 00:10:11s.
Time for last 10,000,000:  107s.  Last read position: 17:31,141,180
INFO    2018-06-09 21:50:08    AbstractAlignmentMerger Written in coordinate order to output    60,000,000 records.  Elapsed time: 00:12:29s.
Time for last 10,000,000:  138s.  Last read position: */*
INFO    2018-06-09 21:51:53    AbstractAlignmentMerger Wrote 81100041 alignment records and 10914531 unmapped reads.
[Sat Jun 09 21:51:53 EDT 2018] picard.sam.MergeBamAlignment done. Elapsed time: 32.29 minutes.
Runtime.totalMemory()=835190784
Removing temporary output file data/Gland_homeo.Aligned.sorted.bam.
Finished job 23.
2 of 8 steps (25%) done
Shutting down, this might take some time.
Exiting because a job execution failed. Look above for error message
Complete log: /data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe/.snakemake/log/2018-06-09T211933.817711.snakemake.log
(env-py3) clintko@phl-biostats-ub1:/data/clintko/DropSeq_Lung/Drop-seq_tools-1.13/dropSeqPipe$
```