

# pyrpipe report

file name:pyrpipe\_logs/2020-03-16-14\_33\_21\_pyrpipe.log

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## Summary

Time start: 2020-03-16 14:33:21 Time end: 2020-03-16 14:47:06  
Total time: 0:13:45

Num commands: 18

Num failed commands: 0

Num passed commands: 18

Total programs: 5

Programs: fasterq-dump,bbduk.sh,hisat2,samtools,stringtie

## Details

*command*

```
fasterq-dump -0 athal_out/SRR976159 -o SRR976159.fastq -e 8 -f SRR976159
```

*stdout*

```
spots read      : 4,728,806  
reads read      : 9,457,612  
reads written   : 9,457,612
```

*stderr*

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-03-16 14:33:28	0:00:39	

---

*command*

```
fasterq-dump -0 athal_out/SRR978411 -o SRR978411.fastq -e 8 -f SRR978411
```

*stdout*

```
spots read      : 4,200,625
reads read      : 8,401,250
reads written   : 8,401,250
```

*stderr*

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-03-16 14:34:08	0:00:41	

---

*command*

```
fasterq-dump -0 athal_out/SRR971778 -o SRR971778.fastq -e 8 -f SRR971778
```

*stdout*

```
spots read      : 5,432,321
reads read      : 10,864,642
reads written   : 10,864,642
```

*stderr*

Program	Return code	Start	Runtime	Version
fasterq-dump	0	20-03-16 14:34:49	0:00:53	

---

*command*

```
bbduk.sh in=athal_out/SRR976159/SRR976159_1.fastq
in2=athal_out/SRR976159/SRR976159_2.fastq out=athal_out/
SRR976159/SRR976159_1_bbduk.fastq out2=athal_out/SRR976159/
SRR976159_2_bbduk.fastq threads=8 ktrim=r k=23 mink=11
qtrim='rl' trimq=10 ref=adapters2.fa -Xmx2g
```

*stdout*

```
java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/software/
bbmap/current/ jgi.BBDuk in=athal_out/SRR976159/
SRR976159_1.fastq in2=athal_out/SRR976159/SRR976159_2.fastq
out=athal_out/SRR976159/SRR976159_1_bbduk.fastq
out2=athal_out/SRR976159/SRR976159_2_bbduk.fastq threads=8
```

```
ktrim=r k=23 mink=11 qtrim='rl' trimq=10 ref=adapters2.fa -
Xmx2g
Executing jgi.BBDuk [in=athal_out/SRR976159/
SRR976159_1.fastq, in2=athal_out/SRR976159/
SRR976159_2.fastq, out=athal_out/SRR976159/
SRR976159_1_bbduk.fastq, out2=athal_out/SRR976159/
SRR976159_2_bbduk.fastq, threads=8, ktrim=r, k=23, mink=11,
qtrim=rl, trimq=10, ref=adapters2.fa, -Xmx2g]
Version 38.73
```

```
Set threads to 8
maskMiddle was disabled because useShortKmers=true
0.099 seconds.
Initial:
Memory: max=2058m, total=2058m, free=2015m, used=43m

Added 3297 kmers; time:          0.414 seconds.
Memory: max=2058m, total=2058m, free=1961m, used=97m
```

```
Input is being processed as paired
Started output streams: 0.027 seconds.
Processing time:                56.747 seconds.
```

```
Input:                          9457612 reads
680948064 bases.
QTrimmed:                       319597 reads (3.38%)
1867256 bases (0.27%)
KTrimmed:                       10427 reads (0.11%)
483899 bases (0.07%)
Total Removed:                  1408 reads (0.01%)
2351155 bases (0.35%)
Result:                         9456204 reads (99.99%)
678596909 bases (99.65%)
```

```
Time:                           57.190 seconds.
Reads Processed:                 9457k    165.37k reads/sec
Bases Processed:                 680m     11.91m bases/sec
```

*stderr*

Program	Return code	Start	Runtime	Version
bbduk.sh	0	20-03-16 14:35:42	0:01:01	java -ea -Xmx2389m -Xms2389m -cp /home/usingh/lib_urmi/ softwares/bbmap/current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.

---

### *command*

```
bbduk.sh in=athal_out/SRR978411/SRR978411_1.fastq
in2=athal_out/SRR978411/SRR978411_2.fastq out=athal_out/
SRR978411/SRR978411_1_bbduk.fastq out2=athal_out/SRR978411/
SRR978411_2_bbduk.fastq threads=8 ktrim=r k=23 mink=11
qtrim='rl' trimq=10 ref=adapters2.fa -Xmx2g
```

### *stdout*

```
java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/software/
bbmap/current/ jgi.BBDuk in=athal_out/SRR978411/
SRR978411_1.fastq in2=athal_out/SRR978411/SRR978411_2.fastq
out=athal_out/SRR978411/SRR978411_1_bbduk.fastq
out2=athal_out/SRR978411/SRR978411_2_bbduk.fastq threads=8
ktrim=r k=23 mink=11 qtrim='rl' trimq=10 ref=adapters2.fa -
Xmx2g
```

```
Executing jgi.BBDuk [in=athal_out/SRR978411/
SRR978411_1.fastq, in2=athal_out/SRR978411/
SRR978411_2.fastq, out=athal_out/SRR978411/
SRR978411_1_bbduk.fastq, out2=athal_out/SRR978411/
SRR978411_2_bbduk.fastq, threads=8, ktrim=r, k=23, mink=11,
qtrim=rl, trimq=10, ref=adapters2.fa, -Xmx2g]
Version 38.73
```

Set threads to 8

maskMiddle was disabled because useShortKmers=true

0.030 seconds.

Initial:

Memory: max=2058m, total=2058m, free=2015m, used=43m

Added 3297 kmers; time: 0.072 seconds.

Memory: max=2058m, total=2058m, free=1950m, used=108m

Input is being processed as paired

Started output streams: 0.005 seconds.

Processing time: 48.863 seconds.

Input: 8401250 reads

604890000 bases.

QTrimmed: 247216 reads (2.94%)

1358333 bases (0.22%)

KTrimmed: 8251 reads (0.10%)

373837 bases (0.06%)

Total Removed: 1128 reads (0.01%)

1732170 bases (0.29%)

Result: 8400122 reads (99.99%)

603157830 bases (99.71%)

Time: 48.941 seconds.

Reads Processed:	8401k	171.66k reads/sec
Bases Processed:	604m	12.36m bases/sec

*stderr*

Program	Return code	Start	Runtime	Version
bbduk.sh	0	20-03-16 14:36:43	0:00:49	java -ea -Xmx2389m -Xms2389m -cp /home/usingh/lib_urmi/softwares/bbmap/current/jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.

*command*

```
bbduk.sh in=athal_out/SRR971778/SRR971778_1.fastq
in2=athal_out/SRR971778/SRR971778_2.fastq out=athal_out/
SRR971778/SRR971778_1_bbduk.fastq out2=athal_out/SRR971778/
SRR971778_2_bbduk.fastq threads=8 ktrim=r k=23 mink=11
qtrim='rl' trimq=10 ref=adapters2.fa -Xmx2g
```

*stdout*

```
java -ea -Xmx2g -Xms2g -cp /home/usingh/lib_urmi/softwares/
bbmap/current/ jgi.BBDuk in=athal_out/SRR971778/
SRR971778_1.fastq in2=athal_out/SRR971778/SRR971778_2.fastq
out=athal_out/SRR971778/SRR971778_1_bbduk.fastq
out2=athal_out/SRR971778/SRR971778_2_bbduk.fastq threads=8
ktrim=r k=23 mink=11 qtrim='rl' trimq=10 ref=adapters2.fa -
Xmx2g
```

```
Executing jgi.BBDuk [in=athal_out/SRR971778/
SRR971778_1.fastq, in2=athal_out/SRR971778/
SRR971778_2.fastq, out=athal_out/SRR971778/
SRR971778_1_bbduk.fastq, out2=athal_out/SRR971778/
SRR971778_2_bbduk.fastq, threads=8, ktrim=r, k=23, mink=11,
qtrim=rl, trimq=10, ref=adapters2.fa, -Xmx2g]
Version 38.73
```

```
Set threads to 8
maskMiddle was disabled because useShortKmers=true
0.013 seconds.
Initial:
Memory: max=2058m, total=2058m, free=2015m, used=43m

Added 3297 kmers; time:          0.025 seconds.
Memory: max=2058m, total=2058m, free=1961m, used=97m
```

```

Input is being processed as paired
Started output streams: 0.005 seconds.
Processing time:                61.344 seconds.

Input:                          10864642 reads
782254224 bases.
QTrimmed:                       196217 reads (1.81%)
1170368 bases (0.15%)
KTrimmed:                       13593 reads (0.13%)
576005 bases (0.07%)
Total Removed:                  1042 reads (0.01%)
1746373 bases (0.22%)
Result:                          10863600 reads (99.99%)
                                780507851 bases (99.78%)

Time:                            61.377 seconds.
Reads Processed:                10864k    177.02k reads/sec
Bases Processed:                782m     12.75m bases/sec

```

*stderr*

Program	Return code	Start	Runtime	Version
bbduk.sh	0	20-03-16 14:37:32	0:01:02	java -ea -Xmx2389m -Xms2389m -cp /home/usingh/lib_urmi/ softwares/bbmap/current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in /docs/.

*command*

```

hisat2 -1 athal_out/SRR976159/SRR976159_1_bbduk.fastq -2
athal_out/SRR976159/SRR976159_2_bbduk.fastq -S athal_out/
SRR976159/SRR976159_hisat2.sam -p 10 -x athal_out/athalIndex/
athalInd --dta-cufflinks

```

*stdout*

```

4728102 reads; of these:
  4728102 (100.00%) were paired; of these:
    206355 (4.36%) aligned concordantly 0 times
    4408674 (93.24%) aligned concordantly exactly 1 time
    113073 (2.39%) aligned concordantly >1 times
    ----
    206355 pairs aligned concordantly 0 times; of these:

```

```

    41812 (20.26%) aligned discordantly 1 time
    ----
    164543 pairs aligned 0 times concordantly or
discordantly; of these:
    329086 mates make up the pairs; of these:
        180236 (54.77%) aligned 0 times
        143903 (43.73%) aligned exactly 1 time
        4947 (1.50%) aligned >1 times
98.09% overall alignment rate

```

*stderr*

Program	Return code	Start	Runtime	Version
hisat2	0	20-03-16 14:38:34	0:01:20	/home/usingh/lib_urmi/software/hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

*command*

```

hisat2 -1 athal_out/SRR978411/SRR978411_1_bbduk.fastq -2
athal_out/SRR978411/SRR978411_2_bbduk.fastq -S athal_out/
SRR978411/SRR978411_hisat2.sam -p 10 -x athal_out/athalIndex/
athalInd --dta-cufflinks

```

*stdout*

```

4200061 reads; of these:
    4200061 (100.00%) were paired; of these:
        197395 (4.70%) aligned concordantly 0 times
        3894710 (92.73%) aligned concordantly exactly 1 time
        107956 (2.57%) aligned concordantly >1 times
    ----
    197395 pairs aligned concordantly 0 times; of these:
        41081 (20.81%) aligned discordantly 1 time
    ----
    156314 pairs aligned 0 times concordantly or
discordantly; of these:
    312628 mates make up the pairs; of these:
        173942 (55.64%) aligned 0 times
        133563 (42.72%) aligned exactly 1 time

```

5123 (1.64%) aligned >1 times  
97.93% overall alignment rate

*stderr*

Program	Return code	Start	Runtime	Version
hisat2	0	20-03-16 14:39:55	0:01:10	/home/usingh/lib_urmi/software/ hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

*command*

```
hisat2 -1 athal_out/SRR971778/SRR971778_1_bbduk.fastq -2  
athal_out/SRR971778/SRR971778_2_bbduk.fastq -S athal_out/  
SRR971778/SRR971778_hisat2.sam -p 10 -x athal_out/athalIndex/  
athalInd --dta-cufflinks
```

*stdout*

```
5431800 reads; of these:  
  5431800 (100.00%) were paired; of these:  
    643042 (11.84%) aligned concordantly 0 times  
    4607041 (84.82%) aligned concordantly exactly 1 time  
    181717 (3.35%) aligned concordantly >1 times  
    ----  
    643042 pairs aligned concordantly 0 times; of these:  
      17692 (2.75%) aligned discordantly 1 time  
    ----  
    625350 pairs aligned 0 times concordantly or  
discordantly; of these:  
      1250700 mates make up the pairs; of these:  
        1132021 (90.51%) aligned 0 times  
        112866 (9.02%) aligned exactly 1 time  
        5813 (0.46%) aligned >1 times  
89.58% overall alignment rate
```

*stderr*



Program	Return code	Start	Runtime	Version
hisat2	0	20-03-16 14:41:04	0:01:23	/home/usingh/lib_urmi/software/ hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}

---

*command*

```
samtools view -o athal_out/SRR976159/SRR976159_hisat2.bam -@ 6 -b athal_out/SRR976159/SRR976159_hisat2.sam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
samtools	0	20-03-16 14:42:27	0:00:37	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

---

*command*

```
samtools sort -o athal_out/SRR976159/SRR976159_hisat2_sorted.bam -@ 6 athal_out/SRR976159/SRR976159_hisat2.bam
```

*stdout*

```
[bam_sort_core] merging from 0 files and 6 in-memory blocks...
```

*stderr*

Program	Return code	Start	Runtime	Version
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samtools	0	20-03-16 14:43:05	0:00:18	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.
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---

*command*

```
samtools view -o athal_out/SRR978411/SRR978411_hisat2.bam -@ 6 -b athal_out/SRR978411/SRR978411_hisat2.sam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
samtools	0	20-03-16 14:43:23	0:00:29	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

---

*command*

```
samtools sort -o athal_out/SRR978411/SRR978411_hisat2_sorted.bam -@ 6 athal_out/SRR978411/SRR978411_hisat2.bam
```

*stdout*

```
[bam_sort_core] merging from 0 files and 6 in-memory blocks...
```

*stderr*

Program	Return code	Start	Runtime	Version
samtools	0	20-03-16 14:43:52	0:00:17	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

---

*command*

```
samtools view -o athal_out/SRR971778/SRR971778_hisat2.bam -@ 6 -b athal_out/SRR971778/SRR971778_hisat2.sam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
samtools	0	20-03-16 14:44:10	0:00:37	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

---

*command*

```
samtools sort -o athal_out/SRR971778/SRR971778_hisat2_sorted.bam -@ 6 athal_out/SRR971778/SRR971778_hisat2.bam
```

*stdout*

```
[bam_sort_core] merging from 0 files and 6 in-memory blocks...
```

*stderr*

Program	Return code	Start	Runtime	Version
samtools	0	20-03-16 14:44:47	0:00:26	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.

---

*command*

```
stringtie -o athal_out/SRR976159/SRR976159_hisat2_sorted_stringtie.gtf -p 8 -G athal_out/Arabidopsis_thaliana.TAIR10.45.gtf athal_out/SRR976159/SRR976159_hisat2_sorted.bam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
stringtie	0	20-03-16 14:45:14	0:00:40	2.0.4

---

*command*

```
stringtie -o athal_out/SRR978411/
SRR978411_hisat2_sorted_stringtie.gtf -p 8 -G athal_out/
Arabidopsis_thaliana.TAIR10.45.gtf athal_out/SRR978411/
SRR978411_hisat2_sorted.bam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
stringtie	0	20-03-16 14:45:54	0:00:33	2.0.4

---

*command*

```
stringtie -o athal_out/SRR971778/
SRR971778_hisat2_sorted_stringtie.gtf -p 8 -G athal_out/
Arabidopsis_thaliana.TAIR10.45.gtf athal_out/SRR971778/
SRR971778_hisat2_sorted.bam
```

*stdout*

*stderr*

Program	Return code	Start	Runtime	Version
stringtie	0	20-03-16 14:46:27	0:00:39	2.0.4

---

## Environment Information

Programs		
name	version	path

fasterq-dump		/home/usingh/lib_urmi/softwares/sratoolkit.2.10.0-centos_linux64/bin/fasterq-dump
bbduk.sh	java -ea -Xmx2389m -Xms2389m -cp /home/usingh/lib_urmi/softwares/bbmap/current/ jgi.BBDuk --version BBMap version 38.73 For help, please run the shellscript with no parameters, or look in / docs/.	/home/usingh/lib_urmi/softwares/bbmap/bbduk.sh
hisat2	/home/usingh/lib_urmi/softwares/hisat2-2.1.0/hisat2-align-s version 2.1.0 64-bit Built on login-node03 Wed Jun 7 15:53:42 EDT 2017 Compiler: gcc version 4.8.2 (GCC) Options: -O3 -m64 -msse2 -funroll-loops -g3 -DPOPCNT_CAPABILITY Sizeof {int, long, long long, void*, size_t, off_t}: {4, 8, 8, 8, 8, 8}	/home/usingh/lib_urmi/softwares/hisat2-2.1.0/hisat2
samtools	samtools 1.9 Using htslib 1.9 Copyright (C) 2018 Genome Research Ltd.	/home/usingh/anaconda3/envs/pyrpipeTest/bin/samtools
stringtie	2.0.4	/home/usingh/lib_urmi/softwares/stringtie-2.0.4.Linux_x86_64/stringtie

System Information	
Time at collection	20-03-16 14:33:21
Python	Python 3.7.5 (default, Oct 25 2019, 15:51:11) [GCC 7.3.0]
Operating system	Linux-3.16.0-4-amd64-x86_64-with-debian-8.11
CPU	8 logical CPU cores

sys.modules
'sys'
'builtins'
'_frozen_importlib'
'_imp'
'_thread'
'_warnings'

'_weakref'
'zipimport'
'_frozen_importlib_external'
'_io'
'marshal'
'posix'
'encodings'
'codecs'
'_codecs'
'encodings.aliases'
'encodings.utf_8'
'_signal'
'__main__'
'encodings.latin_1'
'io'
'abc'
'_abc'
'_bootlocale'
'_locale'
'site'
'os'
'stat'
'_stat'
'posixpath'
'genericpath'
'os.path'
'_collections_abc'
'_sitebuiltins'
'types'
'importlib'
'importlib._bootstrap'
'importlib._bootstrap_external'
'warnings'
'importlib.util'
'importlib.abc'
'importlib.machinery'
'contextlib'
'collections'
'operator'
'_operator'
'keyword'
'heapq'
'_heapq'
'itertools'

'reprlib'
'_collections'
'functools'
'_functools'
'google'
'google.cloud'
'google.logging'
'mpl_toolkits'
'sphinxcontrib'
'runpy'
'pkgutil'
'weakref'
'_weakrefset'
'ipykernel'
'ipykernel._version'
'ipykernel.connect'
'_future_ '
'json'
'json.decoder'
're'
'enum'
'sre_compile'
'_sre'
'sre_parse'
'sre_constants'
'copyreg'
'json.scanner'
'_json'
'json.encoder'
'subprocess'
'time'
'signal'
'errno'
'_posixsubprocess'
'select'
'selectors'
'collections.abc'
'math'
'threading'
'traceback'
'linecache'
'tokenize'
'token'
'IPython'

'IPython.core'
'IPython.core.getipython'
'IPython.core.release'
'IPython.core.application'
'atexit'
'copy'
'glob'
'fnmatch'
'logging'
'string'
'_string'
'shutil'
'zlib'
'bz2'
'_compression'
'_bz2'
'lzma'
'_lzma'
'pwd'
'grp'
'traitlets'
'traitlets.traitlets'
'inspect'
'dis'
'opcode'
'_opcode'
'six'
'struct'
'_struct'
'traitlets.utils'
'traitlets.utils.getargspec'
'traitlets.utils.importstring'
'ipython_genutils'
'ipython_genutils._version'
'ipython_genutils.py3compat'
'ipython_genutils.encoding'
'locale'
'platform'
'traitlets.utils.sentinel'
'traitlets.utils.bunch'
'traitlets._version'
'traitlets.config'
'traitlets.config.application'
'decorator'



'traitlets.config.configurable'
'traitlets.config.loader'
'argparse'
'gettext'
'ast'
'_ast'
'ipython_genutils.path'
'random'
'hashlib'
'_hashlib'
'_blake2'
'_sha3'
'bisect'
'_bisect'
'_random'
'ipython_genutils.text'
'textwrap'
'ipython_genutils.importstring'
'IPython.core.crashhandler'
'pprint'
'IPython.core.ultratb'
'pydoc'
'urllib'
'urllib.parse'
'IPython.core.debugger'
'bdb'
'IPython.utils'
'IPython.utils.PyColorize'
'IPython.utils.coloransi'
'IPython.utils.ipstruct'
'IPython.utils.colorable'
'pygments'
'pygments.util'
'IPython.utils.py3compat'
'IPython.utils.encoding'
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<b>sys.path</b>
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