

CDC/21_2nd QC

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20193852 문유빈

- ▷ 21_2nd를 qc 돌려야 하는데 앞서 과정에서 21_1st로 돌렸음
 - ▽ 해당 프로세스 중지한 후 21_2nd로 qc 진행

1. Script 수정

1-1) 01.QC_C_yb.sh

```
inPath="/data/Original_data/CDC/21_2nd/shotgun/"
outPath="/home/guest01/2021/yb/yb01/CDC_JJ/Analysis/"

for file in $(ls ${inPath}2021_C*_1.fastq.gz)
do
    stub=${file%_1.fastq.gz}
    stub2=${stub#${inPath}}
    sample=${stub2}
    echo $sample
    mkdir $outPath$sample
    mkdir $outPath$sample/QcReads

    /home/bioware/FaQCs/FaQCs.pl -p $inPath$stub2\_1.fastq.gz $inPath$stub2\_2.fastq.gz
    -q 20 -min L 50 -avg q 0 -n 1 -lc 0.85 -5end 0 -3end 0 -split_size 100000 -d $outPath/$
sample/QcReads -t 0 -adapter > $outPath$sample\QC.log
done
```

- ** 저번엔 _C, _J, _K 3개를 한번에 시행해서 좀 더 오랜 시간이 걸렸음
 - *** _C, _J, _K를 따로 진행하면 시간 줄어들, 따로 진행하기 위해 설정
- 2021_C*_1.fastq.gz => 2021_C로 시작하고 _1.fastq.gz로 끝나는 모든 것

```
[guest01@smel0:script]$ cd /data/Original_data/CDC/21_2nd/shotgun/
[guest01@smel0:shotgun]$ ll
total 451140368
-rw-rw-r-- 1 bbang9 SMEL 2398341546 Jan 6 10:04 2021_CF1H_112_1.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2467365605 Jan 6 10:04 2021_CF1H_112_2.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2842289046 Jan 6 10:30 2021_CF1H_114_1.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2977861872 Jan 6 10:30 2021_CF1H_114_2.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2321897466 Jan 6 10:30 2021_CF1H_124_1.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2349397171 Jan 6 10:30 2021_CF1H_124_2.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2423358133 Jan 6 10:05 2021_CF1H_132_1.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2520622086 Jan 6 10:05 2021_CF1H_132_2.fastq.gz
-rw-rw-r-- 1 bbang9 SMEL 2189473125 Jan 6 10:30 2021_CF1H_134_1.fastq.gz
```

실제 언니
21_2nd 디렉

1-2) 01.QC_J_yb.sh

```
inPath="/data/Original_data/CDC/21_2nd/shotgun/"
outPath="/home/guest01/2021/yb/yb01/CDC_JJ/Analysis/"

for file in $(inPath)2021_J*_1.fastq.gz
do
    stub=${file%_1.fastq.gz}
    stub2=${stub#inPath}
    sample=$stub2
    echo $sample
    mkdir $outPath$sample
    mkdir $outPath$sample/QcReads

    /home/bioware/FaQCs/FaQCs.pl -p $inPath$stub2\_1.fastq.gz $inPath$stub2\_2.fastq.gz
    -q 20 -min_L 50 -avg_q 0 -n 1 -lc 0.85 -5end 0 -3end 0 -split_size 100000 -d $outPath/$
sample/QcReads -t 8 -adapter > $outPath$sample\QC.log
done
```

** J만 실행하는 스크립트

1-3) 01.QC_K_yb.sh

```
inPath="/data/Original_data/CDC/21_2nd/shotgun/"
outPath="/home/guest01/2021/yb/yb01/CDC_JJ/Analysis/"

for file in $(inPath)2021_K*_1.fastq.gz
do
    stub=${file%_1.fastq.gz}
    stub2=${stub#inPath}
    sample=$stub2
    echo $sample
    mkdir $outPath$sample
    mkdir $outPath$sample/QcReads

    /home/bioware/FaQCs/FaQCs.pl -p $inPath$stub2\_1.fastq.gz $inPath$stub2\_2.fastq.gz
    -q 20 -min_L 50 -avg_q 0 -n 1 -lc 0.85 -5end 0 -3end 0 -split_size 100000 -d $outPath/$
sample/QcReads -t 8 -adapter > $outPath$sample\QC.log
done
```

** K만 실행하는 스크립트

1-4) 결과 : script 3개

```
[guest01@smel0:CDC_JJ]$ cd script/
[guest01@smel0:script]$ ll
total 12
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:06 01.QC_C_yb.sh
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:38 01.QC_J_yb.sh
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:37 01.QC_K_yb.sh
```

2. Nohup 실행

2-1) smel0에서 C 진행

```
[guest01@smel0:script]$ nohup ./01.QC_C_yb.sh > /home/guest01/2021/yb/yb01/CDC_JJ/script/01.QC_C.nhlog &  
[1] 67599  
[guest01@smel0:script]$ nohup: ignoring input and redirecting stderr to stdout
```

2-2) smel1에서 J 진행

```
[guest01@smel1:script]$ nohup ./01.QC_J_yb.sh > /home/guest01/2021/yb/yb01/CDC_JJ/script/01.QC_J.nhlog &  
[1] 84559  
[guest01@smel1:script]$ nohup: ignoring input and redirecting stderr to stdout
```

2-3) smel1에서 K 진행

```
[guest01@smel1:script]$ nohup ./01.QC_K_yb.sh > /home/guest01/2021/yb/yb01/CDC_JJ/script/01.QC_K.nhlog &  
[1] 84608  
[guest01@smel1:script]$ nohup: ignoring input and redirecting stderr to stdout
```

3. 실행 상황

*script 폴더에 nhlog 파일 3개 생성됨

```
[guest01@smel-cluster:script]$ ll  
total 24  
-rw-rw-r-- 1 guest01 guest01 14 Feb 16 11:40 01.QC_C.nhlog  
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:06 01.QC_C_yb.sh  
-rw-rw-r-- 1 guest01 guest01 14 Feb 16 11:41 01.QC_J.nhlog  
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:38 01.QC_J_yb.sh  
-rw-rw-r-- 1 guest01 guest01 14 Feb 16 11:42 01.QC_K.nhlog  
-rwxrwxr-x 1 guest01 guest01 535 Feb 16 11:37 01.QC_K_yb.sh
```

*실행한 터미널에서 jobs 입력시 상황 표시

```
[guest01@smel1:Analysis]$ jobs  
[1]+  Running                  nohup ./01.QC_K_yb.sh > /home/guest01/2021/yb/yb01/CDC_JJ/script/01.QC_K.nhlog & (wd: ~/2021/yb/yb01/CDC_JJ/script)
```

3-1) J 끝

```
[1]+ Done                               nohup ./01.QC_J_yb.sh > /home/guest01/2021/yb/yb01/CDC_JJ/
script/01.QC_J.nhlog (wd: ~/2021/yb/yb01/CDC_JJ/script)
(wd now: ~/2021/yb/yb01/CDC_JJ/Analysis/2021_JF2H_424)
```

** 끝나면 해당 터미널에서 위와 같은 메시지 뜸

3-2) K, C 순으로 끝남

```
-rw-rw-r-- 1 guest01 guest01 46334 Feb 17 20:43 QC.log
drwxrwxr-x 2 guest01 guest01 4096 Feb 17 20:44 QcReads
[guest01@smel0:2021_KF2H_224]$ cd QcReads/
[guest01@smel0:QcReads]$ ll
total 21593992
-rw-rw-r-- 1 guest01 guest01 11021756495 Feb 17 20:43 QC.1.trimmed.fastq
-rw-rw-r-- 1 guest01 guest01 11018068075 Feb 17 20:44 QC.2.trimmed.fastq
-rw-rw-r-- 1 guest01 guest01      104 Feb 17 19:48 QC.fastqCount.txt
-rw-rw-r-- 1 guest01 guest01    260331 Feb 17 20:44 QC_qc_report.pdf
-rw-rw-r-- 1 guest01 guest01      1169 Feb 17 20:44 QC.stats.txt
-rw-rw-r-- 1 guest01 guest01    72146235 Feb 17 20:44 QC.unpaired.trimmed.fastq
```

=> 끝난 상황, 상세한 설명은 저번 QC 파일에 있음