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FastQC Standard Protocols

Works with: .fastq files (preferably merged by barcode/sample)

How to get FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/):
For Windows:
Download to your computing environment
Unzip file

For Hoffman:
Download FastQC to your Hoffman home directory
wget http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.4.zip
Unzip
unzip fastqc_v0.11.4.zip

Procedure / Work flow:
1. Convert .qseq files to .fastq (if necessary)
2. Merge .fastq by sample [cat file *.fq > merged.fq]
3. Transfer merged .fastq file from Hoffman to home computing environment (Use Globus, if necessary)
   - If Windows:
        Run executable .bat file
        File > Open > .fastq file
   - If Hoffman:
        After unzipping, go to FastQC directory
        Run: chmod 755 fastqc
        To run FastQC analysis, run: ./fastqc *pathToFastqFile.fq*
        Output will be an .html file in the directory with the analyzed .fastq file.
4. Output .html file must be viewed on a web browser

Script file, with all merged .fastq files in one directory:
```
#!/bin/bash
# Run fastqc for all fastq within one directory
## Job Submit command
### qsub -cwd -V -N QCfastq -l h_data=1G,h_rt=4:00:00 -m bea ./fastqc.sh
set -x
   for f in *.fastq; do
   /u/home/d/dmontoya/FastQC/fastqc -f fastq $f
done
```

Quality control of samples:
Take note of Total Sequences, Sequences flagged as poor quality, and %GC content

References & Resources:
Website: http://www.bioinformatics.babraham.ac.uk/projects/fastqc/