NGMASTER – *in silico* Multi-Antigen Sequence Typing for *Neisseria gonorrhoeae*

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Appendix

Appendix 1: List of commands and parameters used

RAW SEQUENCE TRIMMING AND ADAPTER CLIPPING

For paired-end 150 and 300 bp reads:

```
$ trimmomatic PE -phred33 R1.fastq.gz R2.fastq.gz clipped_R1.fq.gz
/dev/null clipped_R2.fq.gz /dev/null ILLUMINACLIP:NexteraPE-PE.fa:1:30:11
LEADING:20 TRAILING:20
```

For paired-end 100 bp reads:

```
$ trimmomatic PE -phred33 R1.fastq.gz R2.fastq.gz clipped_R1.fq.gz
/dev/null clipped_R2.fq.gz /dev/null ILLUMINACLIP:TruSeq2-PE.fa:1:30:11
LEADING:20 TRAILING:20
```

GENOME ASSEMBLY

MEGAHIT:

```
$ megahit --out-dir megahit -1 clipped_R1.fq.gz -2 clipped_R2.fq.gz
--min-contig-len 500 --presets bulk
```

SPAdes:

```
$ spades.py -o spades --careful -k 21,33,55,77,87,97,107,117,127
--tmp-dir /tmp -1 clipped_R1.fq.gz -2 clipped_R2.fq.gz
```

SPAdes with repeat resolution disabled:

```
$ spades.py -o spades --careful --disable-rr
-k 21,33,55,77,87,97,107,117,127 --tmp-dir /tmp
-1 clipped_R1.fq.gz -2 clipped_R2.fq.gz
```

REMAPPING READS BACK TO DRAFT ASSEMBLY
(see https://github.com/tseemann/snippy)

```
$ snippy --outdir sample --ref sample_spades.fa
--R1 sample_clipped_R1.fq.gz --R2 sample_clipped_R2.fq.gz
```

NGMASTER

```
$ ngmaster *.fa > results.txt
```