SeekViralReads results for sample *"sample"*

Adapters removal by cutadapt

command line:

```
cutadapt  -n 5 -a CAGCGGACGCCTATGTGATGG -g CATCACATAGGCGTCCGCTG -A CAGCGGACGCCTATGTGATGG -G
```

Results summary

variable	value
Total read pairs processsed	1,000
R1 with adapters	43 (4.3%)
R2 with adapters	33 (3.3%)
R1 total length before	249,799 bp
R1 total length after	247,655 bp
R2 total length before	244,066 bp
R2 total length after	242,511 bp
Total length of filtered sequences (R1+R2)	490,166 bp (99.3%)
Reads pairs written	1,000 (100.0%)

Quality trimming by cutadapt

command line:

```
cutadapt  -a CAGCGGACGCCTATGTGATGG -g CATCACATAGGCGTCCGCTG -A CAGCGGACGCCTATGTGATGG -G CATC
```

Results summary:

variable	value
Total reads pairs processsed	1,000
R1 with adapters	38 (3.8%)
R2 with adapters	43 (4.3%)

variable	value
R1 total length before	247,655 bp
R1 total length after	224,446 bp
R2 total length before	242,511 bp
R2 total length after	182,841 bp
Total length of quality trimmed sequences	407,287 bp (83.1%)
Reads pairs written	940 (94.0%)

Mapping on contaminent sequences

```
bwa mem -t 15 Data/Bacterial16S_and_Aedes_vexans_genome.fasta cleaned_sample_R1.fastq cleane
```

Stats

variable	value
Reads input	1880
Mapped	907
Mapped %	46.09%