Supplementary material - Title page

SERS detection of the biomarker hydrogen cyanide from *Pseudomonas aeruginosa* cultures isolated from cystic fibrosis patients

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Supplementary material

```
#!/bin/bash
ISO=$1 #Input: list of isolate names.

while read line
do

    echo "$line is being aligned with BWA (v.0.7.12) aln paired end function (sampe)"
    bwa aln lasR.fna $line.L*_1.fq.gz > "$line"_read1.sai
    bwa aln lasR.fna $line.L*_2.fq.gz > "$line"_read2.sai
    bwa sampe lasR.fna "$line"_read1.sai "$line"_read2.sai $line.L*_1.fq.gz $line.L*_2.fq.gz > "$line"_aligned.sam

    echo "$line is going through round one in SAMtools v.0.1.18"
    samtools view -Shb -F4 "$line"_aligned.sam > "$line"_aligned.bam
    samtools sort "$line"_aligned.bam "$line"_aligned_sort
    samtools index "$line"_aligned_sort.bam

    echo "$line read groups are added by Picard (v.1.140)"
    java -Xmx2g -jar picard-tools-1.140/picard.jar AddOrReplaceReadGroups INPUT="$line"_aligned_sort.bam OUTPUT="$line"_aligned.RG.bam RGID=CF RGLB=CF_LIB1 RGPL=Illumina RGPU=CF_RG1_UNIT1 RGSM=$line VALIDATION_STRINGENCY=LENIENT

    echo "$line pileups and raw files are being produced by SAMtools v0.1.18"
    samtools mpileup -q 20 -C50 -BDSsugf lasR.fna "$line"_aligned.RG.bam | bcftools view -vg - > "$line"_raw.vcf
done<$ISO
```