

Additional File 7

```
bwa aln -l 1024 -f ./sample.1x.sai ./reference.fasta ./sample.1x.fq
```

```
bwa samse -r @RG\t"ID:simulated"\t"SM:sample.1x -f./sample.1x.sam ./reference.fasta ./sample.1x.sai ./sample.1x.fq
```

```
samtools view -bS ./sample.1x.sam > ./sample.1x.bam
```

```
samtools sort ./sample.1x.bam ./sample.1x.bam_sorted
```

```
samtools index ./sample.1x.bam_sorted.bam
```

```
java -Xmx4g -jar ./GenomeAnalysisTK.jar -T PrintReads -R ./reference.fasta -I ./sample.1x.bam_sorted.bam -o ./sample.1x.sorted.qualrecal.bam
```

```
java -Xmx4g -jar ./GenomeAnalysisTK.jar -T RealignerTargetCreator -R ./reference.fasta -I ./sample.1x.bam_sorted.bam -o ./sample.1x.sorted.indel.intervals
```

```
java -Xmx4g -jar ./GenomeAnalysisTK.jar -T IndelRealigner -R ./reference.fasta -I ./sample.1x.sorted.qualrecal.bam -targetIntervals ./sample.1x.sorted.indel.intervals \
-o ./sample.1x.sorted.qualrecal.indelrealign.bam
```

```
samtools flagstat ./sample.1x.sorted.qualrecal.indelrealign.bam > ./sample.1x.sorted.qualrecal.indelrealign.bam.flagstat.txt
```

```
samtools index ./sample.1x.sorted.qualrecal.indelrealign.bam
```

```
samtools mpileup -Bg -f ./reference.fasta ./sample.1x.sorted.qualrecal.indelrealign.bam > ./sample.1x.sorted.qualrecal.indelrealign.bam.pileup
```

```
bcftools view -LNcgV ./sample.1x.sorted.qualrecal.indelrealign.bam.pileup > ./sample.1x.sorted.qualrecal.indelrealign.raw.bcf
```

```
vcfutils.pl varFilter -Q 20 -D 30 -d 1 ./sample.1x.sorted.qualrecal.indelrealign.raw.bcf > ./sample.1x.sorted.qualrecal.indelrealign.q20.vcf
```