SNP/INDEL calling

Pavel Dobrynin, Dobzhansky Center for Genome Bioinformatics, Saint Petersburg State University

1. Reference genome
2. Raw reads (.fastq files)
3. Bowtie2 (or BWA)
4. Samtools

Check list

1. Unzip raw reads
2. Use FastQC
3. Trimming (optional)
4. Use FastQC (optional)

Check quality

1. Unzip bowtie2
2. Make bowtie2
3. Unzip samtools
4. Make samtools

Prepare tools

```
/Your Path/bowtie2-build ./H37Rv.fasta test
```

Make bowtie2 index

```
/Your Path/bowtie2 –p2 -x test -1
testR1.fastq -2 testR2.fastq > test.sam
```

Align reads to reference

```
/Your Path/samtools view –bS test.sam > test.bam
```

SAM to BAM

```
/Your Path/samtools sort test.bam
test.sorted
```

Sort BAM

```
/Your Path/samtools rmdup test.sorted.bam
test.rm.bam
```

Remove PCR duplicates

```
samtools mpileup -ugf ./H37Rv.fasta
try.rm.bam | bcftools view -bvcg - > test.bcf
```

Variant calling