

Parameters tuning and scheme of the steps to determine genomic instability from NGS data, steps were performed according cnvkit software documentation <https://cnvkit.readthedocs.io/en/stable/>. In bold tuned parameters specified in the process.

```
cnvkit.py coverage sample.bam ngs.bed -o sample.targetcoverage.cnn
```

```
cnvkit.py coverage sample.bam ngs_antitargets.bed -o sample.antitargetcoverage.cnn
```

```
cnvkit.py fix sample.targetcoverage.cnn sample.antitargetcoverage.cnn Reference.cnn -o sample.cnn
```

```
cnvkit.py segment sample.cnr -t 0.001 -o sample.cns
```

```
cnvkit.py call sample.cns -y -m clonal --purity -o sample.cns
```

```
java -Xmx108g -jar GenomeAnalysisTK.jar -T MuTect2 -R ref.fasta -I:tumor sample.bam -L ngs.bed -o sample_mu_ot.vcf
```

LOH regions annotation

```
bedtools intersect -a sample_mu_ot.vcf -b panel_of_samples.bed -header > sample_het.vcf
```

```
cnvkit.py call sample.cns -y -v sample_het.vcf -o sample_loh.cns
```